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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN HEART

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human heart is described. Also described are single exon nucleic acid probes expressed in the
heart and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

CROSS-REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_HEART.txt, created
25 24 January 2001, having 20,186,946 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

Field of the Invention

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The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

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heart and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of mRNA – are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

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amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

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While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

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Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

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et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the heart and vascular system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that
20 contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as causative, these disorders are for the most part believed to have polygenic etiologies. There is a need for methods
25 and apparatus that permit prediction, diagnosis and prognosis of diseases of the human heart, particularly those diseases with polygenic etiology.

Summary of the Invention

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The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present
35 invention also provides apparatus for verifying the

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expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful
5 for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in
10 sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a
15 sample derived from human heart, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least
20 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

25 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.
30 Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

35 Suitably, said set of single exon nucleic acid

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probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 19,771 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

 In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

 Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

 Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

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polyacetal, polysulfone, celluloseacetate,
cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention; there is
provided a microarray comprising a spatially addressable
5 set of single exon nucleic acid probes in accordance with
the first aspect of the invention.

In one embodiment, a genome-derived single-exon
microarray is packaged together with such an ordered set of
amplifiable probes corresponding to the probes, or one or
10 more subsets of probes, thereon. In alternative
embodiments, the ordered set of amplifiable probes is
packaged separately from the genome-derived single exon
microarray.

In another aspect, the invention provides genome-
15 derived single exon nucleic acid probes useful for gene
expression analysis, and particularly for gene expression
analysis by microarray. In particular embodiments of this
aspect, the present invention provides human single-exon
probes that include specifically-hybridizable fragments of
20 SEQ ID Nos. 9,981 - 19,771, wherein the fragment hybridizes
at high stringency to an expressed human gene. In
particular embodiments, the invention provides single exon
probes comprising SEQ ID Nos. 1 - 9,980.

Accordingly, in a third aspect of the invention,
25 there is provided a single exon nucleic acid probe for
measuring human gene expression in a sample derived from
human heart which is a nucleic acid molecule comprising a
nucleotide sequence as set out in any of SEQ ID NOs.: 1 -
9,980 or a complementary sequence or a fragment thereof
30 wherein said probe hybridizes at high stringency to a
nucleic acid expressed in the human heart.

In one embodiment, a single exon nucleic acid
probe in accordance with the third aspect comprises a
nucleotide sequence as set out in any of SEQ ID NOs.: 9,981
35 - 19,771 or a complementary sequence or a fragment thereof.

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In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding
5 a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 19,772 - 29,119 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

Preferably, a single exon nucleic acid probe in
10 accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or
15 preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length.
20 It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in
25 accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid
30 probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those
35 skilled in the art.

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In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a
5 single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition,
10 comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to
15 prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human heart, comprising:

contacting the single exon microarray in
20 accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then

measuring the label detectably bound to each
25 probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from
30 genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said
35 probe is a single exon probe having a fragment identical in

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sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a single exon
microarray in accordance with the first aspect of the
invention, and said fragment is selectively hybridizable at
5 high stringency.

In a eighth aspect of the invention, there is
provided a method of assigning exons to a single gene,
comprising:

identifying a plurality of exons from genomic
10 sequence in accordance with the seventh aspect of the
invention; and then

measuring the expression of each of said exons in
a plurality of tissues and/or cell types using
hybridization to single exon microarrays having a probe
15 with said exon,

wherein a common pattern of expression of said
exons in said plurality of tissues and/or cell types
indicates that the exons should be assigned to a single
gene.

20 In an ninth aspect of the invention, there is
provided a nucleic acid sequence as set out in any of SEQ
ID NOS: 1 - 19,771 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is
provided a peptide encoded by a sequence comprising a
25 sequence as set out in any of SEQ ID NOS: 9,981 - 19,771,
or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
encoded by a sequence comprising a sequence set out in any
of SEQ ID NOS.: 1 - 9,980.

30 In a further aspect, the invention provides
peptides comprising an amino acid sequence translated from
the DNA fragments, said amino acid sequences comprising SEQ
ID NOS.: 9,981 - 19,771.

Accordingly in a eleventh aspect of the invention
35 there is provided a peptide comprising a sequence as set

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out in any of SEQ ID NOs: 19,772 - 29,119, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

10

Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic

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acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as

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PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

5 As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the
10 larger nucleic acid molecule.

 As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

15 As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

20 As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9
25 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

 As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means
30 any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

 As used herein, a "Mondrian" means a visual
35 display in which a single genomic sequence is annotated

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with predicted and experimentally confirmed functional information.

5 Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

10 FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence
15 data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

20 FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted
25 lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray.
30 The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the
35 expression of verified sequences that showed expression

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with signal intensity greater than 3 in at least one
tissue, with: FIG. 7A showing the expression as measured by
microarray hybridization in each of the 10 measured
tissues, and the expression as measured "bioinformatically"
5 by query of EST, NR and SwissProt databases; with FIG. 7B
showing the legend for display of physical expression
(ratio) in FIG. 7A; and with FIG. 7C showing the legend for
scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3
10 signal intensity for arrayed sequences that were identical
to sequences in existing EST, NR and SwissProt databases or
that were dissimilar (unknown), where black denotes the
signal intensity for all sequence-verified products with a
BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30})
15 ("unknown") and a dotted line denotes sequence-verified
spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases
25,000 to 130,000), containing the carbamyl phosphate
20 synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming,
25 Annotating, and Displaying Functional Regions From Genomic
Sequence Data

FIG. 1 is a flow chart illustrating in broad
outline a process for predicting functional regions from
30 genomic sequence, confirming and characterizing the
functional activity of such regions experimentally, and
then associating and displaying the information so obtained
in meaningful and useful relationship to the original
sequence data.

35 The initial input into process 10 of the present

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invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records
5 corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector
10 sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence
15 identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence.
20 Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in
25 information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the
30 htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than
35 human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*

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brigsii, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification

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and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps

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can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

5 Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

10 For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process
15 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into
20 process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database
25 contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

30 Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

35 For example, if the function sought to be

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identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added

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relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

5 One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further
10 described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of
15 the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

 If query 20 incorporates multiple criteria, such
20 as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

25 If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query
30 20 can be generated that takes into account the initial negative result.

 When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired
35 analytical approach and the particular analytical methods

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thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent
5 analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu
10 repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the
15 genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by
20 proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases
25 and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or
30 codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the
35 specific nucleotide references to one that is unrecognized

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by the subsequent bioinformatic algorithms, such as "X".
Alternatively, but at present less preferred, the undesired
sequence can be excised from the returned genomic sequence,
leaving gaps.

5 Preprocessing 24 can further include selection
from among duplicative sequences of that one sequence of
highest quality. Higher quality can be measured as a lower
percentage of, fewest number of, or least densely clustered
occurrence of ambiguous nucleotides, defined as those
10 nucleotides that are identified in the genomic sequence
using symbols indicating ambiguity. Higher quality can
also or alternatively be valued by presence in the longest
contig.

 Preprocessing 24 can, and often will, also
15 include formatting of the data as specifically appropriate
for passage to the analytical algorithms of process 25.
Such formatting can and typically will include, *inter alia*,
addition of a unique sequence identifier, either derived
from the original accession number in genomic sequence
20 database 100, or newly applied, and can further include
additional annotation. Formatting can include conversion
from one to another sequence listing standard, such as
conversion to or from FASTA or the like, depending upon the
input expected by the subsequent process.

25 Preprocessing, which can be optional depending
upon the function desired to be identified and the
informational requirements of the methods for effecting
such identification, is followed by sequence processing 25,
where sequences with the desired function are identified
30 within the genomic sequence.

 As mentioned above, such functions can include,
but are not limited to, encoding protein, regulating
transcription, regulating message transport after
transcription into mRNA, regulating message splicing after
35 transcription, of regulating message degradation, and the

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like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

5 The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not
10 hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

15 Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

20 Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be
25 performed using any of a variety of known programs that identify regions with lower sequence variability.

 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in
30 Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

35 Increased reliability can be obtained when

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consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

5 Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a
10 given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset
15 thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene
20 prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5%
25 of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among
30 different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset
35 thereof, with another approach, such as comparative

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sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the
5 predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

10 Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

15 In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

20 For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that
25 have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses
30 amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully
35 to amplify. Where subsequent gene expression assay relies

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upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in

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process 200, and as further identified as suitable by
process 300, are amplified from genomic DNA using the
polymerase chain reaction (PCR). Although PCR is
conveniently used, other amplification approaches can also
5 be used.

Amplification schemes can be designed to capture
the entirety of each predicted ORF in an amplicon with
minimal additional (that is, intronic or intergenic)
sequence. Because ORFs predicted from human genomic
10 sequence using the methods of the present invention differ
in length, such an approach results in amplicons of varying
length.

However, most predicted ORFs are shorter than 500
bp in length, and although amplicons of at least about 100
15 or 200 base pairs can be immobilized as probes on nucleic
acid microarrays, early experimental results using the
methods of the present invention have suggested that longer
amplicons, at least about 400 or 500 base pairs, are more
effective. Furthermore, certain advantages derive from
20 application to the microarray of amplicons of defined size.

Therefore, amplification schemes can
alternatively, and preferably, be designed to amplify
regions of defined size, preferably at least about 300, 400
or 500 bp, centered about each predicted ORF. Such an
25 approach results in a population of amplicons of limited
size diversity, but that typically contain intronic and/or
intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs
predicted from human genomic sequence according to the
30 methods of the present invention exceed 500 bp in length.
Portions of such extended ORFs, preferably at least about
300, 400 or 500 bp in length, can be amplified. However, it
has been discovered that the percentage success at
amplifying pieces of such ORFs is low, and that such
35 putative exons are more effectively amplified when larger

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fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as
5 PRIMER3 (available online for use at
<http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of
10 genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can
15 be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of
20 primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The
25 common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming
30 sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been
35 obtained, or a closely related species, and can

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conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline

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silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, 5 polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly 10 advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more 15 typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying 20 nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, 25 Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. 30 For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of 35 background noise in such microarrays.

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As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or
5 alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose
10 certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the
15 expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed
20 using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in
25 Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography
30 techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at
35 least 1000, typically at least 2000, preferably 5000 and

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upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays

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based thereupon – are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

5 Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined – subsequently arrayed for expression measurements could not, therefore, have been represented as
10 probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention – that is, the one third of sequences that had previously been accessioned in EST or other
15 expression databases – are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful
20 cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the
25 genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the
30 desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

35 Thus, the genome-derived single exon microarrays

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of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes

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disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-
5 including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence
10 of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or
15 amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays
20 need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is,
25 independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include
30 artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would
35 contribute to nonspecific hybridization.

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Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding
5 region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression
10 measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a
15 single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the
20 average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-
25 spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95
30 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the
35 probes in the genome-derived single exon microarrays of the

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present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or
5 include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in
10 turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in
15 EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon
20 microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST
25 microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional
30 presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the
35 present invention are also quite different from *in situ*

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synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

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In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

5 A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe
10 basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays
15 from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al.,
20 *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent
25 use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence
30 drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred
35 embodiments, the methods and apparatus of the present

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invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

5 After the physical substrate is prepared, experimental verification of predicted function is performed.

 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental
10 verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon
15 microarrays prepared as above- described.

 Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the
20 microarray art, *Reviewed in* Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous,
25 as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

 mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-
30 transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the
35 reference source is reverse transcribed in the presence of

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a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial
5 purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a
10 Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the
15 genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support
20 substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention
25 provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is
30 disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates
35 having 384, 864, 1536, 3456, 6144, or 9600 wells, and

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although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

5 In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such
10 as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting,
15 in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers,
20 etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together
25 with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

30 In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable
35 media can be packaged with the microarray, with the ordered

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probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then
5 separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification
10 sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted
15 to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than,
20 or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

25 Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and
30 more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query – including information on identical sequences and
35 information on nonidentical sequences that have diffuse or

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focal regions of sequence homology to the query sequence – can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

5 Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully
10 relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are
15 well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present
20 invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

25 FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

30 Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual
35 nucleotides would rarely be readable in hard copy output of

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display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the
5 first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a
10 convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any
15 point within rectangle 89 readily to be viewed, either automatically – for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 – or through user intervention, as by clicking a mouse or other pointing device at a point
20 in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned
25 into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the
30 sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to
35 computerized data, additional control over the first and

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last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the

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results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select

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a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs
5 (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with
10 the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

15 Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display
20 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the
25 probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As
30 noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of
35 bioinformatic assay of the genomic sequence. For example,

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where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

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Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof.

5 As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked
10 information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

15 Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

20 Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the
25 degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for
30 respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute
35 expression (signal intensity) can be expressed using

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normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay
5 is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing
10 gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene
15 predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as
20 white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of
25 sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

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The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present
35 invention rapidly identify and confirm the expression of

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portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from
5 previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic
10 acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human
15 genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 9,980 of these ORFs in heart.

As would immediately be appreciated by one of
20 skill in the art, each single exon probe having demonstrable expression in heart is currently available for use in measuring the level of its ORF's expression in heart.

Diseases of the heart and vascular system are a
25 significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as
30 causative, these disorders are for the most part believed to have polygenic etiologies.

For example, cardiovascular disease (CVD), which includes coronary heart disease, stroke, and peripheral arterial vascular disease, is the leading cause of death in
35 the United States and other developed countries. In

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developing regions, coronary heart disease and stroke are ranked second and third, respectively, as causes of mortality. In the United States alone, about 1 million deaths (about 42% of total deaths per year) result from CVD each year. CVD is also a significant cause of morbidity, with about 1.5 million people suffering myocardial infarction, and about 500,000 suffering strokes in the United States each year. With risk for CVD increasing with age, and an increasingly aging population, CVD will continue to be a major health problem into the future.

CVD is caused by arterial lesions that begin as fatty streaks, which consist of lipid-laden foam cells, and develop into fibrous plaques. The atherosclerotic plaque may grow slowly, and over several decades may produce a severe stenosis or result in arterial occlusion. Some plaques are stable, but other, more unstable, ones may rupture and induce thrombosis. The thrombi may embolize, rapidly occluding the lumen and leading to myocardial infarction or acute ischemic syndrome.

Risk factors for CVD include age and gender. In addition, a family history of CVD significantly increases risk, indicating a genetic basis for development of this disease complex. Obesity, especially truncal obesity, the cause of which is suspected to be genetic, is yet another risk factor for CVD. Familial disorders such as hyperlipidemia, hypoalphalipoproteinemia, hypertriglyceridemia, hypercholesterolemia, hyperinsulinemia, homocystinuria, and dysbetalipoproteinemia, all of which lead to lipid or lipoprotein abnormalities, can predispose one to the development of CVD. Both insulin-dependent and non-insulin-dependent diabetes mellitus, both of which have genetic components, have been also linked to the development of atherosclerosis.

The literature is replete with evidence for

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genetic causes of cardiovascular diseases. For example, studies by Allayee et al., Am. J. Hum. Genet. 63:577-585(1998), indicated a genetic association between familial combined hyperlipidemia (FCHL) and small dense LDL particles. The studies also concluded that the genetic determinants for LDL particle size are shared, at least in part, among FCHL families and the more general population at risk for CVD. Juo et al., Am. J. Hum. Genet. 63: 586-594 (1998) demonstrated that small, dense LDL particles and elevated apolipoprotein B levels, both of which are commonly found in members of FCHL families, share a common major gene plus individual polygenic components.

The common major gene was estimated to explain 37% of the variants of adjusted LDL particle size and 23% of the variants of adjusted apoB levels.

The atherogenic lipoprotein phenotype (ALP) is a common heritable trait, symptoms of which include a prevalence of small, dense LDL particles, increased levels of triglyceride-rich lipoproteins, reduced levels of high density lipoprotein, and increased risk of CVD, particularly myocardial infarction. Both Nishina et al., Proc. Nat. Acad. Sci. 89: 708-712 (1992) and Rotter et al., Am. J. Hum. Genet. 58: 585-594(1996) demonstrated linkage between ALP and the LDLR locus. Rotter et al., supra, also reported linkage to the CETP locus on chromosome 16 and to the SOD1 locus on chromosome 6, and possibly also to the APOA1/APOC3/APOA4 cluster on chromosome 11.

Mutations in genes identified as components of lipid metabolism, e.g., apolipoprotein E (apoE) and LDL receptor (LDLR), have been shown to be associated with predisposition to the development of CVD. For example, several apoE variants had been found to be associated with familial dysbetalipoproteinemia, characterized by elevated plasma cholesterol and triglyceride levels and an increased risk for atherosclerosis (de Knijff et al., Mutat 4: 178-

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194 (1994)). Mutations in the LDLR gene have been associated with the familial hypercholesterolemia, an autosomal dominant disorder characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL),
5 that can lead to increased susceptibility to CVD.

To date, mutations in numerous genes have been shown to be associated with increased CVD susceptibility. However, the identified genetic associations are believed not to account for all genetic contributions to CVD.

10 As yet another example, hypertension is a major health problem because of its high prevalence and its association with increased risk of CVD. Approximately 25% of all adults and over 60% of persons older than 60 years in the United States have high blood pressure.

15 Arterial or systemic hypertension is diagnosed when the average of two or more diastolic BP measurements on at least two subsequent visits is 90 mm Hg or more, or when the average of multiple systolic BP readings on two or more subsequent visits is consistently greater than 140 mm
20 Hg. Pulmonary hypertension is defined as pressure within the pulmonary arterial system elevated above the normal range; pulmonary hypertension may lead to right ventricle (RV) failure.

Hypertension, together with other cardiovascular
25 risk factors, leads to atherosclerosis and other forms of CVD, primarily by damaging the vascular endothelium. In more than 40% of the U.S. population, hypertension is accompanied by hyperlipidemia and leads to the development of atherosclerotic plaques. In the absence of
30 hyperlipidemia, intimal thickening occurs. Non-atherosclerotic hypertension-induced vascular damage can lead to stroke or heart failure.

Familial diseases associated with secondary hypertension include familial renal disease, polycystic
35 kidney disease, medullary thyroid cancer, pheochromocytoma,

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and hyperparathyroidism. Hypertension is also twice as common in patients with diabetes mellitus.

More than 95% of all hypertension cases are essential hypertension, that is, lack identifiable
5 antecedent clinical cause. Essential hypertension shows clustering in families and can result from a variety of genetic diseases. In most cases, high blood pressure results from a complex interaction of factors with both
10 genetic and environmental components. The recent search for genes that contribute to the development of essential hypertension has shown that the disorder is polygenic in origin. However, with several exceptions (such as angiotensinogen, angiotensin receptor-1, beta-3 subunit of guanine nucleotide-binding protein, tumor necrosis factor
15 receptor-2, and "-adducin), the particular genes involved are still being sought.

Susceptibility loci for essential hypertension have been mapped to chromosomes 17 and 15q. Hasstedt et al., Am. J. Hum. Genet. 43: 14-22 (1988) measured red cell
20 sodium in 1,800 normotensive members of 16 Utah pedigrees ascertained through hypertensive or normotensive probands, siblings with early stroke death, or brothers with early coronary disease, and suggested that red blood cell sodium was determined by 4 alleles at a single locus. This major
25 locus was thought to explain 29% of the variance in red cell sodium, and polygenic inheritance explained another 54.6%. A higher frequency of the high red blood cell sodium genotype in pedigrees in which the proband was hypertensive rather than normotensive provided evidence that this major
30 locus increases susceptibility to hypertension.

From a study of systolic blood pressure in 278 pedigrees, Perusse et al., Am. J. Hum. Genet. 49: 94-105 (1991) reported that variability in systolic blood pressure is likely influenced by allelic variation of a single gene,
35 with gender and age dependence. They also suggested that a

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single gene may be associated with a steeper increase of blood pressure with age among males and females.

There is strong evidence, however, for additional as yet uncharacterized, hypertension-associated loci on
5 other chromosomes.

For example, Xu et al., Am. J. Hum. Genet. 64: 1694-1701 (1999) carried out a systematic search for chromosomal regions containing genes that regulate blood pressure by scanning the entire autosomal genome using 367
10 polymorphic markers. Because of the sampling design, the number of sib pairs, and the availability of genotyped parents, this study represented one of the most powerful of its kind. Although no regions achieved a 5% genomewide significance level, maximum lod scores were greater than
15 2.0 for regions of chromosomes 3, 11, 15, 16, and 17.

As another example, cardiac arrhythmias account for several thousand deaths each year. Arrhythmias such as ventricular fibrillation, which causes more than 300,000 sudden deaths annually in the United States alone,
20 encompass a multitude of disorders. Another type of arrhythmia, idiopathic dilated cardiomyopathy, of which familial dilated cardiomyopathy accounts for 20-25%, is responsible for more than 10,000 deaths in the United States annually and is the predominant indication for
25 cardiac transplantation.

Cardiac arrhythmias can be divided into bradyarrhythmias (slowed rhythms) or tachyarrhythmias (speeded rhythms). Bradyarrhythmias result from abnormalities of intrinsic automatic behavior or
30 conduction, primarily within the atrioventricular node and the His-Purkinje's network. Tachyarrhythmias are caused by altered automaticity, reentry, or triggered automaticity.

Bradyarrhythmias arising from suspected polygenic disorders include Long QT syndrome 4, atrioventricular
35 block, familial sinus node disease, progressive cardiac

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conduction defect, and familial cardiomyopathy.

Tachyarrhythmias with possible underlying polygenic causes include familial ventricular tachycardia, Wolff-Parkinson-White syndrome, familial arrhythmogenic right ventricular dysplasia, heart-hand syndrome V, Mal de Meleda, familial ventricular fibrillation, and familial noncompaction of left ventricular myocardium.

For some of the arrhythmias, one or more of the causative genes have been identified.

For example, atrioventricular block has been associated with mutations in the SCN5A gene, as well as mutations in a locus mapped to 19q13. Studies have shown linkage of familial sinus node disease to a marker on 10q22-q24. Familial ventricular tachycardia has been linked to mutations in genes encoding the G protein subunit alpha-i2 (GNAI1), and/or related genes. Examination of families with Wolff-Parkinson-White syndrome suggest an autosomal dominant pattern of inheritance and evidence of linkage of the disorder to DNA markers on band 7q3. Linkage analysis shows strong evidence for localization of a gene for Mal de Meleda disease on 8qter. Familial ventricular fibrillation can be caused by mutations in the cardiac sodium channel gene SCN5A. Familial noncompaction of left ventricular myocardium has been linked to mutations in the gene encoding tafazzin (TAZ), or in the FK506-binding protein 1A gene (FKBP1A).

Familial dilated cardiomyopathy is characterized by an autosomal dominant pattern of inheritance with age-related penetrance. The linkage of familial dilated cardiomyopathy to several loci indicate that it is polygenic. These loci include CMD1A on 1p11-q11, CMD1B on 9q13, CMD1C on 10q21, CMD1D on 1q32, CMD1E on 3p, CMD1F on 6q, CMD1G on 2q31, CMD1H on 2q14-q22, and CMD1I, which results from mutation in the DES gene on 2q35.

In addition, cardiomyopathy can also be caused by

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mutations in the ACTC gene, the cardiac beta-myosin heavy chain gene (MYH7), or the cardiac troponin T gene.

Familial arrhythmogenic right ventricular dysplasia is inherited as an autosomal dominant with
5 reduced penetrance and is one of the major genetic causes of juvenile sudden death. It is estimated that the prevalence of familial arrhythmogenic right ventricular dysplasia ranges from 6 per 10,000 in the general population to 4.4 per 1,000 in some areas.

10 Several loci for familial arrhythmogenic right ventricular dysplasia have been mapped indicating that this disease is also polygenic in nature. These loci include ARVD1 on 14q23-q24, ARVD2 on 1q42-q43, ARVD3 on 14q12-q22, ARVD4 on 2q32.1-q32.3, ARVD5 on 3p23, and ARVD6 on 10p14-
15 p12.

Progressive cardiac conduction defect (PCCD), also called Lenegre-Lev disease, is one of the most common cardiac conduction diseases. It is characterized by progressive alteration of cardiac conduction through the
20 His-Purkinje system with right or left bundle branch block and widening of QRS complexes, leading to complete atrioventricular block and ultimately causing syncope and sudden death. It represents the major cause of pacemaker implantation in the world (0.15 implantations per 1,000
25 inhabitants per year in developed countries). The cause of PCCD is unknown but familial cases with right bundle branch block have been reported suggesting that at least some cases are of genetic origin. Reports have linked PCCD to HB1 on 19q13.3, and to mutations in the SCN5A gene (Schott
30 et al., Nature Genet. 23: 20-21 (1999)).

As yet a further example, congenital heart disease occurs at a rate of 8 per 1000 live births, which corresponds to approximately 32,000 infants with newly diagnosed congenital heart disease each year in the United
35 States. Twenty percent of infants with congenital heart

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disease die within the first year of life. Approximately 80% of the first-year survivors live to reach adulthood. Congenital heart disease also has economic impact due to the estimated 20,000 surgical procedures performed to
5 correct circulatory defects in these patients. The estimated number of adults with congenital heart disease in the United States is currently about 900,000.

In 90% of patients, congenital heart disease is attributable to multifactorial inheritance. Only 5-10% of
10 malformations are due to primary genetic factors, which are either chromosomal or a result of a single mutant gene.

The most common congenital heart disease found in adults is bicuspid aortic valve. This defect occurs in 2% of the general population and accounts for approximately
15 50% of operated cases of aortic stenosis in adults. Atrial septal defect is responsible for 30-40% of congenital heart disease seen in adults. The most common congenital cardiac defect observed in the pediatric population is ventricular septal defect, which accounts for 15-20% of all congenital
20 lesions. Tetralogy of Fallot is the most common cyanotic congenital anomaly observed in adults. Other congenital heart diseases include Eisenmenger's syndrome, patent ductus arteriosus, pulmonary stenosis, coarctation of the aorta, transposition of the great arteries, tricuspid
25 atresia, univentricular heart, Ebstein's anomaly, and double-outlet right ventricle.

A number of studies have identified putative genetic loci associated with one or more congenital heart diseases.

30 Congenital heart disease affects more than 40% of all Down syndrome patients. The candidate chromosomal region containing the putative gene or genes for congenital heart disease associated with Down syndrome is 21q22.2-q22.3, between ETS2 and MX1.

35 DiGeorge syndrome (DGS) is characterized by

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several symptoms including outflow tract defects of the heart such as teratology of Fallot. Most cases result from a deletion of chromosome 22q11.2 (the DiGeorge syndrome chromosome region, or DGCR). The 22q11 deletion is the second most common cause of congenital heart disease after Down syndrome. Several genes are lost in this deletion including the putative transcription factor TUPLE1. This deletion is associated with a variety of phenotypes, e.g., Shprintzen syndrome; conotruncal anomaly face (or Takao syndrome); and isolated outflow tract defects of the heart including Tetralogy of Fallot, truncus arteriosus, and interrupted aortic arch.

Whereas 90% of cases of DGS may now be attributed to a 22q11 deletion, other associated chromosome defects have been identified. For example, Greenberg et al., Am. J. Hum. Genet. 43:605-611 (1988), reported 1 case of DGS with del10p13 and one with a 18q21.33 deletion. Fukushima et al., Am. J. Hum. Genet. 51 (suppl.):A80 (1992) reported linkage with a deletion of 4q21.3-q25. Gottlieb et al., Am. J. Hum. Genet. 62: 495-498 (1998) concluded that the deletion of more than 1 region on 10p could be associated with the DGS phenotype. The association of the DiGeorge syndrome with at least 2 and possibly more chromosomal locations suggests strongly the involvement of several genes in this disease.

Digilio et al., J. Med. Genet. 34: 188-190 (1997), calculated empiric risk figures for recurrence of isolated Tetralogy of Fallot in families after exclusion of del(22q11), and concluded that gene(s) different from those located on 22q11 must be involved in causing familial aggregation of nonsyndromic Tetralogy of Fallot. Johnson et al., Am. J. Med. Genet. (1997) conducted a cytogenetic evaluation of 159 cases of Tetralogy of Fallot. They reported that a del(22q11) was identified in 14% who underwent fluorescence in situ hybridization (FISH) testing

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with the N25 cosmid probe.

Other congenital heart disease are also suspected to be of polygenic origin. For example, Holmes et al., Birth Defects Orig. Art. Ser. X(4): 228-230 (1974) described familial clustering of hypoplastic left heart syndrome in siblings consistent with multifactorial causation.

Other significant diseases of the heart and vascular system are also believed to have a genetic, typically polygenic, etiological component. These diseases include, for example, hypoplastic left heart syndrome, cardiac valvular dysplasia, Pfeiffer cardiocranial syndrome, oculofaciocardiodental syndrome, Kapur-Toriello syndrome, Sonoda syndrome, Ohdo Blepharophimosis syndrome, heart-hand syndrome, Pierre-Robin syndrome, Hirschsprung disease, Kousseff syndrome, Grange occlusive arterial syndrome, Kearns-Sayre syndrome, Kartagener syndrome, Alagille syndrome, Ritscher-Schinzel syndrome, Ivemark syndrome, Young-Simpson syndrome, hemochromatosis, Holzgreve syndrome, Barth syndrome, Smith-Lemli-Opitz syndrome, glycogen storage disease, Gaucher-like disease, Fabry disease, Lowry-Maclean syndrome, Rett syndrome, Opitz syndrome, Marfan syndrome, Miller-Dieker lissencephaly syndrome, mucopolysaccharidosis, Bruada syndrome, humerospinal dysostosis, Phaver syndrome, McDonough syndrome, Marfanoid hypermobility syndrome, atransferrinemia, Cornelia de Lange syndrome, Leopard syndrome, Diamond-Blackfan anemia, Steinfeld syndrome, progeria, and Williams-Beuren syndrome.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human heart and vascular system, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be

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expressed at detectable levels in human heart, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

5 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known
10 to be characteristic of a given heart or vascular disease, or to specific grades or stages thereof.

 In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
15 patient's heart or vascular tissues to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in heart or vascular tissue of individuals with
20 known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

 In another approach, the genome-derived single
25 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of heart or vascular disease to be assessed through the massively parallel
30 determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human heart. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

35 The utility is specific to the probe; at

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sufficiently high hybridization stringency, which stringencies are well known in the art – see Ausubel et al. and Maniatis et al. – each probe reports the level of expression of message specifically containing that ORF.

5 It should be appreciated, however, that the probes of the present invention, for which expression in the heart has been demonstrated are useful for both measurement in the heart and for survey of expression in other tissues.

10 Significant among such advantages is the presence of probes for novel genes.

 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
15 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
20 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
25 databases.

 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
30 that are currently available for achieving these utilities.

 The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
35 for surveying gene expression in the human.

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Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 5 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct 10 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for 15 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of 20 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. 25 Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell 30 Carcinoma Using Combination of cDNA Subtraction and

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Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);
Whitney et al., "Analysis of Gene Expression in Multiple
Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.*
46(3):425-8 (1999)), in drug discovery screens (see, for
5 example, Scherf et al., "A Gene Expression Database for the
Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44
(2000)) and in diagnosis to determine appropriate treatment
strategies (see, for example, Sgroi et al., "In vivo Gene
Expression Profile Analysis of Human Breast Cancer
10 Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of
pharmacological drug candidates upon cells, each probe
provides specific useful data. In particular, it should be
appreciated that even those probes that show no change in
15 expression are as informative as those that do change,
serving, in essence, as negative controls.

For example, where gene expression analysis is
used to assess toxicity of chemical agents on cells, the
failure of the agent to change a gene's expression level is
20 evidence that the drug likely does not affect the pathway
of which the gene's expressed protein is a part.
Analogously, where gene expression analysis is used to
assess side effects of pharmacological agents — whether in
lead compound discovery or in subsequent screening of lead
25 compound derivatives — the inability of the agent to alter
a gene's expression level is evidence that the drug does
not affect the pathway of which the gene's expressed
protein is a part.

WO 99/58720 provides methods for quantifying the
30 relatedness of a first and second gene expression profile
and for ordering the relatedness of a plurality of gene
expression profiles. The methods so described permit
useful information to be extracted from a greater
percentage of the individual gene expression measurements
35 from a microarray than methods previously used in the art.

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Other uses of microarrays are described in Gerhold *et al.*, *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena *et al.*

5 The invention particularly provides genome-derived single-exon probes known to be expressed in heart.

 The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity
10 sufficient to perform a hybridization reaction.

 Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA
15 complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes
20 can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

 Usefully, however, such probes are provided in a
25 form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known
30 amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
35 to be provided in a form suitable for amplification, the

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range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
5 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

10 Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
15 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
20 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
25 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
30 single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a
35 hybridization reaction in which the probe is not first

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bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

5 In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable
10 of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

15 Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 9,981 – 19,771, respectively, for probe SEQ ID NOS. 1 – 9,980. The minimum amount of ORF required to be
20 included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 9,981 – 19,771 individually by routine experimentation using standard high stringency
25 conditions.

 Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl
30 poly(dA), 0.2 µg/µl human c₀t1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high
35 stringency conditions can usefully be aqueous hybridization

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at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in
5 temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of
10 other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

15 Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are
20 maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly
25 translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further
30 be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have
35 sequence complementary to those described herein above and

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below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or
5 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution
10 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

15 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or
20 enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for
25 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

30 When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is
35 obtained using higher density arrays.

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If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human heart.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human heart. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 9,980.

When used for gene expression analysis, the

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genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue.

5 At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from

10 a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the

15 assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as

20 probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 9,980 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 9,981 - 19,771, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 9,980 can be

25 used, or that portion thereof in SEQ ID NOS. 9,981 - 19,771 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially

30 that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo

35 Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New

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England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 9,981 - 19,771. Such amino acid sequences are set out in SEQ ID NOS: 19,772 - 29,119. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from

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GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open
5 reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to
10 Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range
15 of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

20 The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by
25 all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window
30 were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

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PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of

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agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

5 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue
10 (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 \pm 25 bp, approximately 50% of the average PCR
15 amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR
20 failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene
25 finding algorithms.

 Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular
30 Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

 Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence
35 or the inclusion of vector and host contamination in some

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submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1 e^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1 e^{-5} to 1 e^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266

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(1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

5

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

10

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

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The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS.

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Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

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Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant
5 signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single
10 tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of
15 all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the
20 respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data — that is, presents the results returned by query of EST, NR and SwissProt databases using
25 the probe sequence. The legend for "bioinformatic expression" (*i.e.*, degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).
30

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were
35 identified; in heart, 150. The remaining tissues gave the

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following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since

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very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large
5 number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA
10 library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to
15 assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic
20 sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific
25 gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies,
30 Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two
35 sequences confirmed the tissue-specific gene expression as

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measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain
--

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Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca^{2+} binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

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AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon

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giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward *et al.*, *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi *et al.*, *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result
35

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duplicated with the array. Other highly expressed chip
 sequences included a translation elongation factor 1 α
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
 chromosome RNA-binding motif (Chai *et al.*, *Genomics*
 5 49(2):283-89 (1998))(AC007320-3). A low homology analog
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in
 trisomy 21 (Down's syndrome), showed high expression in
 both brain and heart, in agreement with the literature
 (Fuentes *et al.*, *Mol. Genet.* 4(10):1935-44 (1995)).

10 As a further validation of the approach, we
 selected the BAC AC006064 to be included on the array.
 This BAC was known to contain the GAPDH gene, and thus
 could be used as a control for the ORF selection process.
 The gene finding and exon selection algorithms resulted in
 15 choosing 25 exons from BAC AC006064 for spotting onto the
 array, of which four were drawn from the GAPDH gene. Table
 3 shows the comparison of the average expression ratio for
 the 4 exons from BAC006064 compared with the average
 expression ratio for 5 different dilutions of a
 20 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm

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Lung	-4.95 \pm 0.93	-3.75 \pm 0.21
Placenta	-3.56 \pm 0.25	-3.52 \pm 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

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exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION
5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene
10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the
15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease
20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,
25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

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EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

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The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be
10 expressed at significant levels in heart tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 9,980 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 9,980 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 9,980. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons
30 present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 9,981 - 19,771, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

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demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are

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presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be
5 useful for measuring expression of their cognate genes in human heart tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 9,981 - 19,771 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to
10 identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

15 The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as
20 "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the
25 SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of
30 the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is
35 found ("Top Hit Database Source").

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Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The
5 peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each
10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs
15 in an exhaustive process based on the following criteria:
1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for
20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as
25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

30 Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for
35 analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

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Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ – which is probative evidence that the query sequence has previously been shown to be expressed – the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 – 9,980) and probe exon (SEQ ID NOs.: 9,981 – 19,771, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

. . (a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

WO 01/57274**PCT/US01/00666**

Expression of Genes in Human Heart

Table 4 (413 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human heart.

WO 01/57274

PCT/US01/00666

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
442	10386	20209	4.41				
871	10797	20647	17.08				
1029	10947		2.14				
1280	11188	21039	7.97				
1597	11501	21361	1.87				
1619	11523	21381	4.97				
1684	11596	21467	1.01				
1715	11616	21485	0.95				
1721	11622	21491	7.45				
1848	11744	21620	0.98				
1935	11830	21713	3.03				
2119	12008	21907	2.62				
2233	12118	22020	2.34				
3149	13074	22875	3.7				
3403	13320	23121	1.52				
3471	13387	23192	8.97				
3513	13429		0.87				
3607	13521	23309	0.99				
4102	14002	23781	1.71				
4164	14064	23838	5.94				
4184	14084	23858	0.89				
4184	14084	23859	0.89				
4242	14141		1.03				
4730	14616	24402	1.76				
4779	14663		0.78				
4976	14851	24617	5.08				
4988	14863		2.07				
5217	15140	24834	1.92				
5217	15140	24835	1.92				
5328	15248		5				
5436	15356		5.89				
5483	15248		4.9				
5509	15427	25490	2.9				
5668	19451	25678	1.6				

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5690	15599	25700	1.41				
5863	15769		1.84				
6382	16244	26404	1.61				
6382	16244	26405	1.61				
6697	16577	26769	1.29				
6942	16820	27012	1.3				
7494	17364	27569	3.58				
7684	17534	27758	1.26				
8070	17961		3.7				
8219	18472	28355	2.31				
8390	18266		2.84				
8666	18555	28840	2.91				
8757	17906	28150	1.73				
8757	17906	28151	1.73				
8792	18606		2.19				
9464	18094		1.62				
9760	19280	25230	2.11				
5691	15600	25701	13.31	9.9E+00	AJ233028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
6669	16549	26745	1.54	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
7955	17805	28046	1.32	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1IH polypeptide 2 (Gtf2h2) genes, complete cds
7955	17805	28047	1.32	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1IH polypeptide 2 (Gtf2h2) genes, complete cds
2631	12499	22389	2.72	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2631	12499	22390	2.72	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2893	12820	22612	5.91	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
7206	17083	27271	2.97	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5239	15163	24932	2.07	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5239	15163	24933	2.07	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5678	15587	25687	5.51	8.9E+00	BE971806.1	EST_HUMAN	601651036R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5848	15754	25871	1.71	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
5848	15754	25872	1.71	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
433	10378	20199	1.75	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
7439	16452	26642	3.68	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
8509	18381		2.31	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
6346	16209		2.07	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
6868	16747	26940	1.53	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
6868	16747	26941	1.53	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5544	15460	25531	2.58	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
7085	18962	27155	3.83	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
7085	18962	27156	3.83	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2947	12874	22671	4.2	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
2947	12874	22672	4.2	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
6239	16105	26254	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
6239	16105	26255	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7535	17386		8.48	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
8690	18577	28860	3.26	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
7735	17585	27809	2.98	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
8575	18443	28712	1.85	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
6818	16697	26889	2.72	6.9E+00	P35679	SWISSPROT	80S RIBOSOMAL PROTEIN L4 (L2)
7925	17775	28015	1.3	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
6614	16494	26680	1.45	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291860 5'
6614	16494	26681	1.45	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291860 5'
							OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS:
7277	17154		1.47	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEINS VP5 AND VP8]
7863	17713	27957	3.82	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
7796	17646	27881	2.1	6.6E+00	Q92E07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
7796	17646	27882	2.1	6.6E+00	Q92E07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
8471	18344		2.17	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C
7296	17172	27372	8.32	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
7616	17467	27686	1.44	6.2E+00	AY010901.1	NT	Schizoplyllum commune unknown mRNA
5928	15833	25956	7.16	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
3479	13395		0.81	5.8E+00	7661557	NT	Homo sapiens DESC1 protein (DESC1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8770	17919	28166	2.44	5.6E+00	Q56276	SWISSPROT	LYCOPENE BETA CYCLASE
8769	17918	28165	2.65	5.5E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
8967	18773		1.94	5.5E+00	AL161571.2	NT	Ara bidopsis thaliana DNA chromosome 4, config fragment No. 67
6593	16473		1.62	5.4E+00	Q91082	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
7769	17619	27849	1.44	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
7769	17619	27850	1.44	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4675	14561	24354	1.54	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6710	16590		4.04	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8899	18708	29003	3.21	5.3E+00	Q27905	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYMERIN PRECURSOR
7655	17505	27730	1.21	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
7959	17809	28050	3.06	5.0E+00	AF162444.2	NT	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
8610	18477	28749	10.53	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
3972	13879		9.43	4.8E+00	AF185255.1	NT	Eunice australis histone H3 (H3) gene, partial cds
6970	19847		5.01	4.8E+00	AW750067.1	EST_HUMAN	PMO-BT0547-310700-002-504 BT0547 Homo sapiens cDNA
286	10251	20071	2.03	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
287	10251	20071	1.92	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3236	13160	22958	4.01	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6576	16434	28617	1.48	4.6E+00	U67569.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
8881	18693	28986	1.99	4.5E+00	AEO01044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
3003	12931	22723	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'
3003	12931	22724	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'
5764	15671		1.55	4.4E+00	I13414.1	NT	Murine I gene for MHC class II(a) associated invariant chain
6398	16259	26420	2.01	4.3E+00	Y13402.1	NT	Plasmodium falciparum R29R+var1 gene, exon 1
8235	18116	28368	7.49	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5387	15306		2.92	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
6060	16043	26186	1.57	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6060	16043	26187	1.57	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
7182	17059	27249	5.45	4.2E+00	A1809013.1	EST_HUMAN	wf67g03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
6517	16376	26553	7.65	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
6577	16435	26618	3.31	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
6577	16435	26619	3.31	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
6617	16497	26634	2.95	4.1E+00	NT	Pan. troglodytes novel repetitive solo LTR element in the RNU2 locus
7576	17427	27641	2.31	4.1E+00	EST_HUMAN	602247938F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
8259	18139		2.89	4.1E+00	SWISSPROT	HYPOTHETICAL PROTEIN HVLF1
8339	18216		12.46	4.1E+00	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3609051 5'
9672	19231	25241	1.86	4.1E+00	SWISSPROT	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IGF-BINDING PROTEIN 1)
6266	16131	26285	1.37	4.0E+00	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
8768	17917	28164	2.17	4.0E+00	SWISSPROT	CYTCHROME C OXIDASE POLYPEPTIDE III
8835	18648	28934	3.34	4.0E+00	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
8835	18648	28935	3.34	4.0E+00	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3459	13375	23181	3.89	3.9E+00	NT	N. tabacum chitinase gene 50 for class I chitinase C
4228	14124		0.99	3.9E+00	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5471	15391	25454	2.47	3.9E+00	EST_HUMAN	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5471	15391	25455	2.47	3.9E+00	EST_HUMAN	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
6108	16002	26140	4.46	3.9E+00	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
6355	16218	26379	4.68	3.9E+00	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
6840	16719	26913	2.32	3.9E+00	NT	X. laevis mRNA for M4 muscarinic receptor
8695	17879	28120	3.09	3.9E+00	NT	Homo sapiens NF2 gene
8715	18532	28816	5.58	3.9E+00	EST_HUMAN	nr18a12.st NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416
2588	12459		2.4	3.8E+00	NT	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN);
6911	16789	26982	1.18	3.8E+00	EST_HUMAN	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
3696	13845	23622	10.09	3.7E+00	NT	HUMSUPY13s Human brain cDNA Homo sapiens cDNA clone 148
8730	18586	28872	2.13	3.7E+00	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
8730	18586	28873	2.13	3.7E+00	EST_HUMAN	602120561F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
578	10516	20322	2.1	3.6E+00	EST_HUMAN	602120561F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
7022	16899	27090	3.66	3.6E+00	NT	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
7022	16899	27091	3.66	3.6E+00	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
7022	16899	27091	3.66	3.6E+00	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8228	18110		3.76	3.6E+00	M95795.1	NT	Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds; and the translation start site has been verified (glpE), the translation start site has been verified (glpG), and repressor protein (glpR) genes, complete cds
3209	13133	22334	1.04	3.5E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
1496	11400	21260	3.57	3.4E+00	AF254577.1	NT	Brassica napus RPB5d mRNA, complete cds
2532	12406	22298	1.02	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6354	16217	26378	2.41	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7889	17739	27982	3.17	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
8818	18631	28919	1.92	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
5036	14908	24679	1.41	3.3E+00	7662155	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
5036	14908	24680	1.41	3.3E+00	7662155	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
492	10435	20248	1.39	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
3938	10435	20248	0.79	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
5439	15359	25415	2.66	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5439	15359	25416	2.66	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5808	15713	25825	2.06	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
5808	15713	25826	2.06	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
5569	16427	26809	2.35	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
5569	16427	26910	2.35	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7221	17098		6.33	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
7491	17361	27567	1.17	3.2E+00	M35363.1	NT	S. cerevisiae threonine deaminase (ILV1) gene, complete cds
7837	17687	27932	1.69	3.2E+00	AB016081.2	NT	Oryzias latipes OIG06 gene for guanylyl cyclase C, complete cds
9089	18863		4.32	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5582	15497	25574	2.42	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7000	18877	27067	4.35	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
7000	18877	27068	4.35	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
							GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
7334	17238		3.8	3.1E+00	Q14957	SWISSPROT	DEOXYHYPPUSINE SYNTHASE (DHS)
7920	17770	28009	4.78	3.1E+00	P49365	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
8759	17908		3.78	3.1E+00	P33515	SWISSPROT	retinoic acid nuclear receptor isoform beta 2 [ntcra, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2871 nt]
8774	18591		3.35	3.1E+00	S56680.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2807	12737	22836	1.06	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5273	15195	24970	1.63	3.0E+00	X53096.1	NT	S. aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease
5245	18111		9.5	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7164	17041		1.45	3.0E+00	X67838.1	NT	B. napus DNA for myrosinase
							RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
8374	18251	28501	6.51	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
8374	18251	28502	6.51	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
1964	11858	21747	2.56	2.9E+00	AE002225.2	NT	Chlamydomonas reinhardtii AR39, section 53 of 94 of the complete genome
6129	15976	26112	1.63	2.9E+00	Z36879.1	NT	F. pringlei gdcSP gene for P-protein of the glycine cleavage system
6282	16146	26300	4.47	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6282	16146	26301	4.47	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6410	16271	26433	5.19	2.9E+00	P46539	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
1441	11346	21212	5.79	2.8E+00	AF189398.1	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product
1615	11519		3.12	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
6325	16188	26350	4.78	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
230	10199	20012	4.63	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
230	10199	20013	4.63	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
5408	15327	25377	1.75	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
7185	17062		2.21	2.7E+00	AL119459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7996	17846		2.16	2.7E+00	BE063527.1	EST_HUMAN	CMD-BT0281-031199-087-H04 BT0281 Homo sapiens cDNA
4576	14467	24263	4.35	2.6E+00	AF068749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5405	15324	25373	1.97	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5405	15324	25374	1.97	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
							Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
6533	16391		5.42	2.6E+00	AF235502.1	NT	fab bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
6696	16576	26767	1.2	2.6E+00	AJ132180.1	NT	fab bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
6696	16576	26768	1.2	2.6E+00	AJ132180.1	NT	fab bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
7567	17418	27634	2.95	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7927	17777		1.52	2.6E+00	9055193	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cps3), mRNA
9711	19649		2.31	2.6E+00	11419220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1448	11353	21216	2.08	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor	
1448	11353	21217	2.08	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5552	15468	25537	2.33	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5552	15468	25538	2.33	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5886	15468	25537	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5886	15468	25538	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6561	16419	26598	1.34	2.5E+00	AW949158.1	EST_HUMAN	QV4-F70005-110500-205-g07 FT0005 Homo sapiens cDNA
7264	17141	27334	1.75	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9086	18851		2.26	2.5E+00	AF239595.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
2980	12907	22707	0.86	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4816	14699	24485	7.62	2.4E+00		NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
5657	15569	25664	4.19	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
6733	16613	26802	2.14	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
6733	16613	26803	2.14	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
6780	16559		2.63	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
7026	16903		1.71	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
7125	17002	27194	9.45	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
7771	17621	27853	2.5	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
7771	17621	27854	2.5	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
7820	17670	27911	2.18	2.4E+00	X92511.1	NT	H.sapiens CTGF gene and promoter region
7881	17731		6.49	2.4E+00	P09099	SWISSPROT	XYLULOSE KINASE (XYLUKINASE)
7914	17764	28002	1.67	2.4E+00	BE326702.1	EST_HUMAN	h63f06.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
7914	17764	28003	1.67	2.4E+00	BE326702.1	EST_HUMAN	h63f06.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
8428	18302	28558	1.77	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPKD operon and downstream
8665	18554	28839	2.52	2.4E+00	AF158652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1233	11140	20992	9.36	2.3E+00	Z46724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4031	13934		1.28	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
6408	16269	26431	2.22	2.3E+00		NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
6479	19765		2.3	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
6573	16431	26613	1.53	2.3E+00	X60265.1	NT	M.mazei dnaK and dnaJ genes homologues coding for DnaK and DnaJ
7289	17165	27364	1.81	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
8988	18793	29063	2.6	2.3E+00	BF541987.1	EST_HUMAN	(FUCOSYLTRANSFERASE 4) (FUCT-IV)
8988	18793	29084	2.6	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9304	19002	25333	4	2.3E+00	BE985237.1	EST_HUMAN	501433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
9936	19405		1.37	2.3E+00	AF281862.1	NT	Neurospora crassa G protein alpha subunit GNA-3 (gna-3) gene, complete cds
4216	14114	23891	3.82	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4216	14114	23892	3.82	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
							SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5276	15198	24973	10.08	2.2E+00	O98307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5276	15198	24974	10.08	2.2E+00	O98307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5696	15605	25707	9.06	2.2E+00	BE250383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2859777 3'
5835	15741	25853	3.3	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
5978	15882	26005	2.89	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
6155	15113		3.14	2.2E+00	AA594574.1	EST_HUMAN	n195b02.st NCJ_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1058379 3'
6486	16344	26514	51.56	2.2E+00	AA449012.1	EST_HUMAN	2x05g10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785634 5'
7381	17250		11.83	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
7518	19468		2.1	2.2E+00	Q04706	SWISSPROT	TRANSPOSON TY1 PROTEIN A
7783	17633	27865	1.56	2.2E+00	A1290373.1	EST_HUMAN	qm69a03.x1 Soares_placenta_8tc9weeks_2NbHP8tc9w Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
7783	17633	27866	1.56	2.2E+00	A1290373.1	EST_HUMAN	qm69a03.x1 Soares_placenta_8tc9weeks_2NbHP8tc9w Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
7812	17662	27902	2.28	2.2E+00	BF246782.1	EST_HUMAN	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
7975	17825	28066	2.88	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
8739	17888	28132	4.5	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
8899	18700	28995	4.67	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
557	12670	20304	6.81	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3539	13455	AW449366.1	1.19	2.1E+00	AW449366.1	EST_HUMAN	UI-H-B13-akt-e-08-0-U1.s1 NCJ_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6074	16057	26206	3.72	2.1E+00	O70159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
6195	15955	26087	4.7	2.1E+00	N29575.1	EST_HUMAN	yy08a10.s1 Soares_melanocyte_2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
6948	16826		1.99	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
1178	11089	20934	1.23	2.0E+00	AF180527.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2/20000671 5'
							Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1178	11089	20935	1.23	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1313	11219	21076	1.43	2.0E+00	AF204927.1	NT	Oryctolagus cuniculus Na ⁺ K ⁺ -ATPase beta 1 subunit mRNA, complete cds
1557	11462		3.13	2.0E+00	P25582	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2102	11991	21890	4.6	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2102	11991	21891	4.6	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4011	13917	23692	2.09	2.0E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
4011	13917	23693	2.09	2.0E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
6678	16558	26751	3.8	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6678	16558	26752	3.8	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6678	16558	26753	3.8	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
7170	17047	27237	3.3	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
9629	19613	24998	5.81	2.0E+00	58348.43	NT	Gallus gallus mitochondrion, complete genome
5437	15357	25412	4.67	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
5437	15357	25413	4.67	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
6047	15950		2.27	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
6927	16805	26999	2.58	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
6927	16805	27000	2.58	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
7032	16909		3.36	1.9E+00	BF360206.1	EST_HUMAN	GM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
7156	17033		1.86	1.9E+00	Q51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
3054	12981	22773	1.71	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3082	13009	22799	4.48	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3082	13009	22800	4.48	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5577	15492		2.22	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
5712	15620	25723	1.9	1.8E+00	BF311999.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6043	15046	26078	1.3	1.8E+00	BF305652.1	EST_HUMAN	601893499F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7140	17017	27210	2.09	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
7293	17169	27399	1.21	1.8E+00	R31042.1	EST_HUMAN	yh7208.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
7899	17749		3.29	1.8E+00	AF111849.1	NT	Homo sapiens PRO630 mRNA, complete cds
8998	18901		3.76	1.8E+00	P36062	SWISSPROT	HYPOTHETICAL 75.5 KD PROTEIN IN SDH1-CIM5/YTA3 INTERGENIC REGION

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9428	19684		4.01	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
9504	19119		2.4	1.9E+00	9506404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA
9968	19429		1.34	1.8E+00	BF316805.1	EST_HUMAN	601903309F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135586 5'
1092	11008	20849	1.92	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2225	12110	22013	3.25	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2321	12202	22101	1.02	1.7E+00	AI141067.1	EST_HUMAN	oz43h05.x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4356	14252	24037	0.84	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5448	15369	25424	1.48	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5448	15369	25425	1.48	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5664	15575	25673	3.58	1.7E+00	Q9JTT8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1)(COUP-TF I)
7014	16891		1.29	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
7282	19467	27355	2.15	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
7282	19467	27356	2.15	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
8874	18686	28977	1.78	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
9384	19044	25306	1.37	1.7E+00	AI678443.1	EST_HUMAN	tu82407.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.t1 MSR1 repetitive element;
9860	19351	25185	2.26	1.7E+00	AI198573.1	EST_HUMAN	qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.t1 L1 repetitive element;
1989	11882	21775	16.73	1.9E+00	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
1997	11891	21783	3.61	1.9E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2003	11896	21788	1.96	1.9E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
2238	12122		1.48	1.9E+00	X98373.1	NT	B.napus gene encoding endo-polygalacturonase
2931	12858	22658	2.52	1.9E+00	W58426.1	EST_HUMAN	z42501.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29805 N-ACETYL LACTOSAMINE SYNTHASE (HUMAN);
3946	13854		5.14	1.9E+00	BF570077.1	EST_HUMAN	60218005T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4255	14154	23928	1.44	1.9E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4255	14154	23929	1.44	1.9E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5016	14890	24657	3.14	1.9E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5016	14890	24658	3.14	1.9E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5558	15474	25546	2.19	1.9E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2'01 gene, 3' end
6296	16160	26317	2.64	1.9E+00	BE697287.1	EST_HUMAN	RC0-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
6681	16661		1.21	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
6881	16760	26958	3.56	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
7444	19465	26946	1.3	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
7444	19465	26947	1.3	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
7611	17462	27679	1.29	1.6E+00	T41290.1	EST_HUMAN	ph6b6_19/1TV Outward Alu-priated hmcDNA library Homo sapiens cDNA clone ph6b6_19/1TV
7852	17702	27946	1.25	1.6E+00	AW835644.1	EST_HUMAN	QV4-L T0016-090200-100-d07 LT0016 Homo sapiens cDNA
7852	17702	27947	1.25	1.6E+00	AW835644.1	EST_HUMAN	QV4-L T0016-090200-100-d07 LT0016 Homo sapiens cDNA
8217	18520	25901	5.86	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
8944	18762	29047	3.25	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
9902	19379		1.65	1.6E+00	AV764043.1	EST_HUMAN	AV764043 MDS Homo sapiens cDNA clone MDSDAH08 5'
30	10017	19812	4.29	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
231	10200	20014	1.76	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AR39, section 32 of 94 of the complete genome
605	10541		1.79	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagridin) (Adam15), mRNA
2359	12239	22135	2.46	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2468	12344	22237	2.02	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3099	12239	22135	2.22	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3329	13249	23054	0.82	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5856	15762	25980	2.71	1.5E+00	R17879.1	EST_HUMAN	yg10e02.r1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:31693 5'
6230	16096		1.42	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
6250	16116	26268	29.13	1.5E+00	P47179	SWISSPROT	HYPOTHEICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
6250	16116	26269	29.13	1.5E+00	P47179	SWISSPROT	HYPOTHEICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7671	17521	27747	7.56	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
7782	17632		1.71	1.5E+00	BF337944.1	EST_HUMAN	602035771F1 NCL_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4183865 5'
7856	17706	27951	1.96	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b44HR Homo sapiens cDNA clone IMAGE:361306 5'
7856	17706	27952	1.96	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b44HR Homo sapiens cDNA clone IMAGE:361306 5'
8702	18520	28802	3.91	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243.s1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P243 3'
8828	18641		10.73	1.5E+00	X07380.1	NT	Maize mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
9223	18946		1.5	1.5E+00	6753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
9596	19178		2.89	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
9690	19243		1.42	1.5E+00	6978492	NT	Rattus norvegicus 5 - Lipoxigenase (Alox5), mRNA
27	10014	19808	1.28	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
27	10014	19809	1.28	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2231	12116		0.95	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2286	12169		9.38	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2634	12501	22394	1.63	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2746	12608	22500	3.29	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2746	12608	22501	3.29	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3034	12962	22755	1.01	1.4E+00	AE002324.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3034	12962	22756	1.01	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
3291	13213		0.87	1.4E+00	5453733	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
4162	14062	23835	1.09	1.4E+00	AW900455.1	EST_HUMAN	Homo sapiens Mad4 homolog (MAD4) mRNA
4162	14062	23836	1.09	1.4E+00	AW900456.1	EST_HUMAN	CMV-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4482	14376		1.53	1.4E+00	BF681547.1	EST_HUMAN	CV0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
5137	15004		0.8	1.4E+00	Q07869	SWISSPROT	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5301	15222	25026	1.51	1.4E+00	AW054976.1	EST_HUMAN	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5394	15313		5.17	1.4E+00	AB032983.1	NT	w45g07 x1 NCI_OGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5796	15702	25812	2.39	1.4E+00	Q13472	SWISSPROT	Homo sapiens mRNA for KIAA1157 protein, partial cds
5802	19765		4.9	1.4E+00	AB020712.1	NT	DNA TOPOISOMERASE III ALPHA
5860	15766	25884	2.71	1.4E+00	Q92777	SWISSPROT	Homo sapiens mRNA for KIAA0905 protein, complete cds
5860	15766	25885	2.71	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6318	16181	26341	1.86	1.4E+00	AJ133269.1	NT	SYNAPSIN II
7107	16984		5.21	1.4E+00	AJ271735.1	NT	Homo sapiens cavolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7256	17133	27325	1.88	1.4E+00	R20459.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
7303	17179	27381	3.37	1.4E+00	BE064667.1	EST_HUMAN	yg33f12.1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:34345 5'
8420	18294	28548	1.94	1.4E+00	AA195528.1	EST_HUMAN	RC1-BT0313-301299-012-f05 BT0313 Homo sapiens cDNA
8556	18426	28695	4.97	1.4E+00	AB006682.1	NT	z36e09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element
8709	18526	28808	5.15	1.4E+00	BE962107.2	EST_HUMAN	MER22 repetitive element;
8709	18526	28809	5.15	1.4E+00	BE962107.2	EST_HUMAN	Homo sapiens APECE2 mRNA for AIRE-1, complete cds
8727	18583	28867	2.68	1.4E+00	U30790.1	NT	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
8727	18583	28868	2.68	1.4E+00	U30790.1	NT	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
9221	19604		1.34	1.4E+00	AL161500.2	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds
							Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
558	10498		1.67	1.3E+00	Z73640.1	NT	Mucedo gene encoding 4-Dihydropyrimidin-5-carboxylate dehydrogenase
884	10810	20659	2.74	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1113	11028		16.5	1.3E+00	Y19213.1	NT	Homo sapiens putative pslHbA pseudogene for hair keratin, exons 2 to 7
1275	11183	21033	10.9	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1275	11183	21034	10.9	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1334	11241		1.62	1.3E+00	U61730.2	NT	Coix lacryma-jobi dihydroadipicinate synthase (dapA) gene, complete cds
1593	11497		2.09	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2196	12083		2.1	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP)
2503	12378		2.19	1.3E+00	BE966735.2	EST_HUMAN	and MASP-related protein, complete cds
2909	12835	22632	1.12	1.3E+00	6755621	NT	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
							Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
3547	13463	23258	1.03	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
4502	12835	22632	0.82	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
4964	14839	24607	0.98	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
4964	14839	24608	0.98	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5665	15576	25674	7.76	1.3E+00	AW362834.1	EST_HUMAN	PM0-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA
5665	15576	25675	7.76	1.3E+00	AW362834.1	EST_HUMAN	PM0-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA
5864	15770	25889	1.33	1.3E+00	M33496.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6828	16707	26901	1.25	1.3E+00	AJ009912.1	NT	Sus scrofa pip gene
6917	16795	26988	3.06	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38668195 3'
7054	16931		1.55	1.3E+00	9910247	NT	Homo sapiens GL004 protein (GL004), mRNA
7480	17350		5.44	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
7487	17357	27560	2.31	1.3E+00	X72019.1	NT	S.alba pht-1 mRNA for photolase
7487	17357	27561	2.31	1.3E+00	X72019.1	NT	S.alba pht-1 mRNA for photolase
							LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMN)
7574	17425	27639	1.45	1.3E+00	OC00754	SWISSPROT	wo85a07.x1 NC1_CGAP_K1111 Homo sapiens cDNA clone IMAGE:2462100 3'
7620	17471	27690	1.27	1.3E+00	A1927629.1	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38668195 3'
7675	17525	27751	4.9	1.3E+00	BE963379.2	EST_HUMAN	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
7868	17716	27961	1.6	1.3E+00	AE004392.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
7874	17724	27968	1.39	1.3E+00	M29963.1	NT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
8078	17969		4.3	1.3E+00	Q14117	SWISSPROT	Mfna 3-endo processing protein RNA15
8277	18157	28398	2.34	1.3E+00	P25299	SWISSPROT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8299	18178	28424	2.23	1.3E+00	Z18992.2	NT	Mus musculus desmin gene
8646	18510		1.81	1.3E+00	AW274791.1	EST_HUMAN	xp09e03.x1 NCL CGAP_HIN9 Homo sapiens cDNA clone IMAGE:2739868 3'
8826	18639	28923	2.82	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
8895	18705	28959	2.71	1.3E+00	Z98882.1	NT	Bacillus subtilis genomic DNA 23.9kB fragment
9362	19033		2.35	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
9533	19139	25263	3.24	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCL CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4158452 5'
9544	19499		2.68	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
634	10571	20384	8.14	1.2E+00	AA676246.1	EST_HUMAN	z122d08.s1 Soares fetal_liver spleen 1NFLS S1 Homo sapiens cDNA clone IMAGE:431535 3'
806	10735	20578	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
806	10735	20579	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
806	10735	20580	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
860	10786		2.19	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1145	11058	20901	5.53	1.2E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1187	11097	20943	1.77	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1187	11097	20944	1.77	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1963	11857	21746	1.05	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3072	12999	22789	0.95	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3128	13053	22851	5.41	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3128	13053	22852	5.41	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3249	13172		2.9	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3311	13232	23038	0.78	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3312	13233		0.99	1.2E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds
3650	13564	23350	7.28	1.2E+00	U75802.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3904	13814	23598	1.49	1.2E+00	BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4201	13232	23038	1.09	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4298	14196	23981	1.39	1.2E+00		NT	Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neonatal) (Glr2), mRNA
4371	14267		1.64	1.2E+00	M87060.1	NT	Rattus rattus cardiac AEC3 gene, exons 1-23
4422	14316	24102	1.26	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4460	14354	24145	1.82	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4485	14379		5.44	1.2E+00	Y09200.1	NT	T.pinnatum chloroplast rbcL gene, partial
4584	13233		0.94	1.2E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds
5409	15329	25379	1.96	1.2E+00	AW183276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5739	15647	25763	2.47	1.2E+00	X74885.1	NT	D.hydrel ayl repeat cluster DNA, fragment D
5769	15676	25783	3.28	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5798	15704	25815	1.87	1.2E+00	X89084.1	NT	C.glutamicum pla gene and ackA gene
5798	15704	25816	1.87	1.2E+00	X89084.1	NT	C.glutamicum pla gene and ackA gene
5823	15729	25841	32.83	1.2E+00	AA759254.1	EST_HUMAN	ah84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3'
5918	15823	25949	1.82	1.2E+00	AW813276.1	EST_HUMAN	MF3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6139	15986	26121	2.55	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
6369	19463	26392	1.9	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cda Homo sapiens cDNA clone cdAAFH03 5'
6508	16367	26544	2.4	1.2E+00	X74207.1	NT	L.lactis pyrD and pyrF genes
6984	16861	27055	3.45	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
7218	17095	27285	1.74	1.2E+00	AW377210.1	EST_HUMAN	MF2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
7407	17274	27480	3.08	1.2E+00	Z32850.1	NT	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
7540	17391	27601	1.8	1.2E+00	D11745.1	EST_HUMAN	HUMHM01A01 Liver HepG2 cell line: Homo sapiens cDNA clone hm01a01
7711	17561	27786	3.28	1.2E+00	X56832.1	NT	H.sapiens ENO3 gene for muscle specific enolase
8653	18542	28826	2.03	1.2E+00	AW817817.1	EST_HUMAN	PM0-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA
8689	18576		23.47	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
8752	17901	28145	4.87	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
9114	18877	28787	2.5	1.2E+00	AF065398.1	NT	Mus musculus 60 kDa ribonucleoprotein SSA/Ro gene, complete cds
9330	19572	25067	15.4	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9349	19025		1.49	1.2E+00	AF001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
456	10400	20217	1.13	1.1E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1726	11627	21496	1.39	1.1E+00	AW995393.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1857	11753	21628	0.92	1.1E+00	AW575889.1	EST_HUMAN	U1HF-BR0p-alk-f02-0-UI.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'
3288	13209	23009	6.61	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3288	13209	23010	6.61	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3441	13558	23165	0.93	1.1E+00		NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3510	13426		1.26	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
3531	13447	23244	0.99	1.1E+00	AI808360.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3657	13571	23357	1.16	1.1E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3657	13571	23358	1.16	1.1E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3678	13592	23378	17.81	1.1E+00		NT	Homo sapiens calpain 9 (nCL-4) (CAPN9) mRNA
3862	13773	23565	0.99	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4122	14022		5.89	1.1E+00	5835331	NT	R.unicornis complete mitochondrial genome
4860	14740	24520	1.18	1.1E+00	L23195.1	NT	Drosophila melanogaster cytoplasmic dynein heavy chain mRNA, complete cds
4921	14900	24573	2.92	1.1E+00	U18466.1	NT	African swine fever virus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4999	14874	24638	1.16	1.1E+00	X78425.1	NT	E.faecalis pbp5 gene
5249	15172	24945	1.57	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5449	15370	25426	12.04	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3825835 3'
5460	15380	25440	1.29	1.1E+00	AI138582.1	EST_HUMAN	qd85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6422	16283	26444	1.93	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6422	16283	26445	1.93	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6435	16296	26458	7.53	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6728	16608	26799	3.22	1.1E+00	BF693996.1	EST_HUMAN	602032582F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4246628 5'
7658	17508	27733	1.66	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
7715	17565	27791	4.39	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7744	17594	27815	20.08	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
8043	17934	28182	2.66	1.1E+00	11087364	NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
8090	17991		3.41	1.1E+00	AF068942.1	NT	Klebsormidium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
8447	13426		5.73	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
8450	18323	28581	4.41	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
8450	18323	28582	4.41	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
8662	18551	28835	4.73	1.1E+00	AI809899.1	EST_HUMAN	wf76e1.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
9300	18999		4	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
9402	19056	25310	2.13	1.1E+00	AF216696.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
9523	19570		1.54	1.1E+00	AF234169.1	NT	Dictyostelium discoideum isopentenyl pyrophosphate isomerase (DipI) mRNA, complete cds
92	10077		3.49	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
108	10089	19904	1.14	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
412	10358		2.16	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA and 26S rRNA
562	10502	20308	1.14	1.0E+00	AJ251690.1	NT	Giardia tigrina mRNA for homeodomain transcription factor (so gene)
661	10595	20413	4.51	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
663	10597		0.95	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1364	12692		1.04	1.0E+00	X80416.1	NT	V.cariel Algal-CAM mRNA
1722	11623	21492	1.32	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2435	12312	22208	1.4	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2435	12312	22209	1.4	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2651	12518	22408	1.09	1.0E+00	AF131205.1	NT	Mus musculus Serf1, protein (Serf1), survival of motor neuron protein (Snm), neuronal apoptosis inhibitory protein-rs6 (Naip-rs6), and neuronal apoptosis inhibitory protein-rs3 (Naip-rs3) genes, complete cds
2846	12774	22561	3.48	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2846	12774	22562	3.48	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2938	12865		0.99	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME 1
3162	13087	22891	1.17	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Soares_t0tal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP: C42D8.3 CE04204 :contains element MER22 MER22 repetitive element :
3327	13247		0.81	1.0E+00	AF222761.1	NT	Rattus norvegicus neuromedin U precursor (NmU) gene, exons 5 and 6
3548	10077		1.15	1.0E+00	U23806.1	NT	Xenopus laevis rhodopsin gene, complete cds
3627	13541	23328	1.44	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase
3978	13885	23660	0.86	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4178	14078		0.79	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4815	14698		0.88	1.0E+00	U75741.1	NT	Taenia ovis 45W antigen (ToW4) gene, complete cds
4951	14828		0.88	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5139	15006	24777	0.87	1.0E+00	AJ229978.1	NT	Bacillus subtilis 42.7kB DNA fragment from ysaA to ysaA
5228	15152	24919	2.49	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5568	15484	25557	4.31	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5568	15484	25558	4.31	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5719	15626	25729	4.82	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
5720	15627	25730	1.39	1.0E+00	AW452782.1	EST_HUMAN	UI-H-B13-alk-d-09-0-UJ.s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
5908	15814	25839	2.21	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6417	16279		8.43	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
6537	16395	26574	1.34	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
6546	16404	26583	5.99	1.0E+00	AA775191.1	EST_HUMAN	ec79b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868791 3'
6641	16521	26713	1.71	1.0E+00	BE668267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
6641	16521	26714	1.71	1.0E+00	BE668267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
6734	14828		1.38	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6861	16740	26932	2.7	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE)(MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
6861	16740	26933	2.7	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE)(MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
6967	19466		2.01	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0229-181099-011-e06 HT0229 Homo sapiens cDNA
7064	16941	27133	1.9	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
7339	17207	27405	1.76	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
7460	17320	27526	1.28	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
7460	17320	27527	1.28	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
7544	17395	27607	2.03	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GK Homo sapiens cDNA clone GKCCYA11 5'
7546	17397	27609	1.2	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
7546	17397	27610	1.2	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
7916	17766	28005	2.83	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAWC04 5'
7985	17835	28075	17.08	1.0E+00	AA004992.1	EST_HUMAN	zh94a02.r1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
7985	17835	28076	17.08	1.0E+00	AA004992.1	EST_HUMAN	zh94a02.r1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
9193	18928		2.05	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
9513	19126		1.51	1.0E+00	AW976184.1	EST_HUMAN	EST388293 IMAGE resequences, MAGN Homo sapiens cDNA
9859	19350		1.67	1.0E+00	AB040950.1	NT	Homo sapiens mRNA for KIAA1517 protein, partial cds
1553	11458	21315	0.84	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
1553	11458	21316	0.84	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
2598	12487	22360	0.9	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3553	13468		1.18	9.9E-01	AF174595.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5461	15381	25441	9.22	9.9E-01	P49957	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
7336	17204		1.38	9.9E-01	U65667.1	NT	Lycopodium esculentum putative M1 copy 1 nematode-resistance gene
7510	17298		2.43	9.9E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
8097	17988	28237	2.92	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
512	10454	20265	2.32	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
3732	13644	23429	0.82	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3732	13644	23430	0.82	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
6272	16137	26292	4.61	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983

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6272	16137	26293	4.61	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
8362	18239	28487	4.43	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350760 5'
8362	18239	28488	4.43	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350760 5'
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
9408	19061		1.62	9.8E-01	U52111.2	NT	we62e04.x1 Soares thymus NHFTh Homo sapiens cDNA clone IMAGE:2345694.3'
5106	14974		1.01	9.7E-01	AI660384.1	EST_HUMAN	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
6248	16114	26266	2.37	9.7E-01	U26716.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
6952	16830	27023	1.86	9.7E-01	AF149112.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
6954	16832	27026	1.74	9.7E-01	M90544.1	NT	UI-H-B14-aei-e-07-0-JJ.s1 NCI_QGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
8510	18382		4.52	9.7E-01	BF511209.1	EST_HUMAN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9956	19419		1.39	9.7E-01	AL114281.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4337	14234	24016	6.8	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4337	14234	24017	6.8	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4355	14251	24036	1.3	9.6E-01	AW799674.1	EST_HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5083	14953	24729	0.92	9.6E-01	7682375	NT	Homo sapiens KIAA0914 gene product (KIAA0914), mRNA
5517	15435	25498	3.46	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5517	15435	25499	3.46	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6890	16769		1.37	9.6E-01	X96275.1	NT	P.falciparum complete gene map of plasid-like DNA (IR-A)
8908	18622	28912	4.15	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG08 5'
8808	18622	28913	4.15	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG08 5'
9709	19646	24989	1.52	9.6E-01	U91423.1	NT	Spizura tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
3715	13627	23410	1.6	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3715	13627	23411	1.6	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
7266	17143	27336	1.17	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0295-241199-011-b02 CT0295 Homo sapiens cDNA
3165	13090		3.37	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3181	13106		1.67	9.4E-01	AF080595.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
9354	19029		1.64	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869929 5'
9708	19564		1.43	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1700	11601		1.11	9.3E-01	AF242382.1	NT	Homo sapiens phytyl-CoA hydroxylase (PHYH) gene, exon 5

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2594	12464	22357	1.13	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
3949	13857	23630	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
3949	13857	23631	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5155	15022		1.54	9.3E-01	AF075615.1	NT	Equus caballus microsatellite LEX013
5434	15354	25410	1.62	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5482	15402	25465	3.84	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
6701	16581	26771	1.88	9.3E-01	AA847040.1	EST_HUMAN	oe09603.s1 NCI_CGAP_Cv2 Homo sapiens cDNA clone IMAGE:1385357
9822	19325		1.56	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl.34 mRNA, complete cds
9954	19418		1.38	9.3E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LIP
3201	13125	22930	3.04	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184.3'
5943	15556	25649	4.23	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661.5'
7618	17469	27698	1.38	9.2E-01	6671677	NT	Homo sapiens carbonic anhydrase 4 (Car4), mRNA
7890	17740	27983	3.63	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
7952	17802	28041	1.73	9.2E-01	BF593251.1	EST_HUMAN	7658e06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3576219.3' similar to SW-NU5M_TRYBB
8960	18767	29059	1.85	9.2E-01	BF132402.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;
9006	18809	29101	2.01	9.2E-01	BF680047.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018.5'
2077	11967		1.43	9.1E-01	8923056	NT	602164769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296896.5'
3169	13094	22898	0.97	9.1E-01	T26418.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3169	13094	22899	0.97	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LAB200G8.5'
4310	14207	23991	0.86	9.1E-01	U68172.1	NT	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LAB200G8.5'
5919	15824	25950	2.92	9.1E-01	Q61704	SWISSPROT	Rattus norvegicus mucin (MUC2) gene, partial cds
6472	16331	26498	15.99	9.1E-01	AA806623.1	EST_HUMAN	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
6551	16409	26587	2.2	9.1E-01	U72995.1	NT	ob71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862.3'
9445	19641		30.05	9.1E-01	AF050113.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
3170	13095	22900	0.89	9.0E-01	7661625	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
4282	14181	23959	2.37	9.0E-01	AF099810.1	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
4945	14822	24589	0.82	9.0E-01	AF017729.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
6388	16250		1.45	9.0E-01	D38621.1	NT	Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete cds
						NT	Xenopus laevis gene for aldolase, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
5494	15413	25476	2.08	8.9E-01	AF026198.1	NT	
5786	15682		1.32	8.9E-01	X60986.1	NT	Rabbit MHC fragment RLA-DF DNA
8990	18794	29085	3.47	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of the complete genome
9285	18987		4.74	8.9E-01	AE002186.2	NT	Chlamydomonas reinhardtii, section 21 of 94 of the complete genome
4442	14336	24126	3.28	8.8E-01	Q26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
8430	18304	28560	2.98	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
9108	19722		1.75	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
457	10401	20218	1.54	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2353	12233	22130	1.09	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2845	12773	22560	4.64	8.7E-01	AA595863.1	EST_HUMAN	nm05f11.s1 NCL CGAP_P14.1 Homo sapiens cDNA clone IMAGE:1076877
							Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and putative
4938	14816		2.51	8.7E-01	AF121970.1	NT	dioxygenase alpha-ISP protein OhbB (ohbB), and putative
7613	17464	27681	1.45	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
8206	18090	28343	5.47	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-003 NN1021 Homo sapiens cDNA
8970	18776	29067	4.16	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
8970	18776	29068	4.16	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
9488	19534		2.78	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLCGYG07 3'
466	10409		1.66	8.6E-01	X17012.1	NT	Rat IGFI gene for insulin-like growth factor II
840	10767	20618	3.62	8.6E-01	W69086.1	EST_HUMAN	zd44e03.r1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:343516 5'
							Homo sapiens cytochrome P450, subfamily XXV1A (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
2224	12109	22012	1.01	8.6E-01	4503210	NT	
3568	13482	23273	0.81	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3730	13642	23427	1.29	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
5595	15509	25586	11.82	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5595	15509	25587	11.82	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6030	15934	26065	2.14	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6030	15934	26066	2.14	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6626	16506		1.52	8.6E-01	AF001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
6443	16304	26469	2.75	8.5E-01	BE542612.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3435305 5'
7924	17774	28013	1.36	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
7924	17774	28014	1.36	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9430	19643		2.52	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVBP1), mRNA
9436	19075		2.63	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
9683	19238	25243	1.29	8.5E-01	AB030818.1	NT	Mus musculus mper1 gene for period1, complete cds
4108	14008	23785	0.84	8.4E-01	AF143509.1	NT	Mus musculus NK cell receptor 2B4 gene, promoter region and partial cds
5378	19443	25145	2.7	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5378	19443	25146	2.7	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7721	17571		3.13	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 516
724	10656	20486	2.31	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3056	12983	22774	2.64	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3739	13651	23434	1	8.3E-01	AB010879.1	NT	Nicotiana glauca mRNA for chloroplast ribosomal protein L10, complete cds
3930	13839	23619	3.11	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
4917	14796	24570	1.12	8.3E-01	U46916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
4917	14796	24571	1.12	8.3E-01	U46916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5177	14796	24570	0.95	8.3E-01	U46916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5177	14796	24571	0.95	8.3E-01	U46916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5222	15145	24839	2.13	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7673	17424		4.2	8.3E-01	AI791952.1	EST_HUMAN	nm011212.y5 NCI_CGAP_Gc9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.t1 THR repetitive element;
7822	17672	27914	1.23	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
7867	17717	27962	3.1	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
8062	17953	28204	2.46	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
8076	17967		2.46	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
8623	18488	28760	2.03	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
2006	11898	21789	2.99	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2043	11934		1.51	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2646	12513		1.14	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
5045	14917	24691	1	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
6122	16016	26154	3.26	8.2E-01	AW376943.1	EST_HUMAN	CM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
6309	19462	26330	3.58	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
7788	17638	27871	1.53	8.2E-01	AF032659.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds
7937	17787	28028	6.66	8.2E-01	O9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7937	17787	28029	6.66	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN-BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
8909	18717	29011	2.81	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
8966	18772	29064	6	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
8971	18777	29069	6.65	8.2E-01	H87398.1	EST_HUMAN	YW14d02.r1 Soares_placenta_869weeks_2NbHP809W Homo sapiens cDNA clone IMAGE:252195 5'
9451	19083	25284	1.73	8.2E-01	AJ001261.1	NT	similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
2731	12593		1.29	8.1E-01	AF191839.1	NT	Mus musculus mRNA for NIPSNAP2 protein
3412	13329	23130	2.81	8.1E-01	AF055086.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3412	13329	23131	2.81	8.1E-01	AF055086.1	NT	Homo sapiens MHC class 1 region
5992	15897	26020	2.49	8.1E-01	Q13491	SWISSPROT	Homo sapiens MHC class 1 region
5992	15897	26021	2.49	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
8775	18592	28879	1.94	8.1E-01	BE938593.1	EST_HUMAN	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
8775	18592	28880	1.94	8.1E-01	BE938593.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
9166	18909	25343	1.84	8.1E-01	AE001711.1	NT	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
170	10142		3.02	8.0E-01	AJ271510.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
285	10250	20070	3.76	8.0E-01	AJ132772.1	NT	Staphylococcus aureus partial pta gene for phosphate acetyltransferase allele 15
1990	11884		1.83	8.0E-01	BF530982.1	EST_HUMAN	Bos taurus tubb and rtf genes
3039	12967	22761	2.73	8.0E-01	AF127897.1	NT	602072473F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215091 5'
3273	13194	22963	1.14	8.0E-01	AB006193.1	NT	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds
3643	13557		1.8	8.0E-01	AL162758.2	NT	Mus musculus gene for oviductal glycoprotein, complete cds
4432	14327	24115	5.65	8.0E-01	X83739.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 717
6661	16541		2.84	8.0E-01	AW901489.1	EST_HUMAN	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
446	10390	20211	3.78	7.9E-01	D11476.1	NT	RC0-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA
698	10631		1.16	7.9E-01	AE002130.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
1587	11491		65.97	7.9E-01	AB040885.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1634	11538		1.37	7.9E-01	U32739.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
2216	12102	22006	5.24	7.9E-01	AB004816.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2217	12103	22007	2.29	7.9E-01	AF130459.1	NT	Oryctolagus cuniculus mRNA for mitogenin29, complete cds
3472	13388	23193	2.75	7.9E-01	AF228694.1	NT	Danio rerio Ttp4-associated protein Tap1A (tap1A) mRNA, complete cds
4204	14103		0.92	7.9E-01	BE263612.1	EST_HUMAN	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4508	14401	24188	1.02	7.9E-01	6753745	NT	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4508	14401	24189	1.02	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5075	14945	24720	0.84	7.9E-01	Z47210.1	NT	Mus musculus dexB, cap3A, cap3B and cap3C genes and orfs
5075	14945	24721	0.84	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs

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5084	14954		1.01	7.9E-01	M29930.1	NT	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17
6721	16601	26790	2.43	7.9E-01	X90996.1	NT	P. sativum GR gene
7604	17373	27592	4.78	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
7781	17631	27864	3.95	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
8372	18249		2.36	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
8543	18415	28682	2.48	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
858	10784		1.75	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2229	12114	22016	3.2	7.8E-01	AW939567.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4803	14491	24278	0.79	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5698	15607	25709	2.32	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
7323	17199	27399	1.27	7.8E-01	Y10159.1	NT	D. discoideum recGAP gene
9424	19623		1.42	7.8E-01	L29260.1	NT	Arabidopsis thaliana 1-aminio-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
138	10112	19932	6.33	7.7E-01	AF184345.1	NT	Lycopodium hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
709	10641		1.85	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IaAlpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-lt>
2680	12645	22436	2.8	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3313	13234		0.8	7.7E-01	8988408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNAC-T7) (GALNAC-T7), mRNA
3549	13464	23259	4.45	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4297	14195	23979	2.88	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4297	14195	23980	2.88	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5415	15335	25386	1.44	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5415	15335	25387	1.44	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5626	15541	25630	1.95	7.7E-01	R08600.1	EST_HUMAN	yf24b02.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:127755 3'
9212	10112	19932	2.6	7.7E-01	AF184345.1	NT	Lycopodium hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
9311	19004		6.14	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
5710	15618	25720	4.04	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
5710	15618	25721	4.04	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds

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6999	16579	26770	1.41	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; fPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
6726	16806	26796	2.04	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
6726	16806	26797	2.04	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
7184	17061	27252	1.28	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
7347	17215	27414	7.52	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
7347	17215	27415	7.52	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
8664	18553	28837	2.31	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
8664	18553	28838	2.31	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
8948	18756		4.81	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
9073	18850		2.74	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
502	10444		1.52	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21, segment HS21C101
569	10508	20315	2.23	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3315	13236	23040	0.88	7.5E-01	C14203.1	EST_HUMAN	C14203 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-037E11 5'
4573	10083	19900	13.92	7.5E-01	8922672	NT	Homo sapiens hypothetical protein FLJ10793 (FLJ10793), mRNA
9381	19042		3.57	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
9828	19329	25209	1.87	7.5E-01	D90907.1	NT	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885
9884	19368	25190	1.42	7.5E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
1114	11029	20869	1.23	7.4E-01	AI598146.1	EST_HUMAN	tn14b09.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2295	12177	22076	0.97	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3665	13579	23366	1.22	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4213	14111	23889	4.43	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7258	17135	27328	7.23	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9041	18828		3.28	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1nh), mRNA
9150	18901		1.59	7.4E-01	AI472641.1	EST_HUMAN	ta13h01.x1 NCL_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4515	14408	24194	0.95	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 62 of 70) of the complete genome
4602	14490	24277	4.76	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5127	14994		1.1	7.3E-01	5360211	NT	Homo sapiens growth arrest-specific 7 (GAS7), transcript variant b, mRNA
5984	15889	26010	5.61	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
5984	15889	26011	5.61	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6454	16315	26480	7.42	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
6454	16315	26481	7.42	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
8729	18585	29870	3.29	7.3E-01	AA678019.1	EST_HUMAN	z125b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
8729	18585	28871	3.29	7.3E-01	AA678019.1	EST_HUMAN	z125b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
814	10742		2.54	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1914	11809	21687	3.68	7.2E-01	X79140.1	NT	N.tabacum NtEF-4A13 mRNA
2412	12289	22186	1.46	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3028	12956	22748	1.16	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3406	13323	23124	2.14	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I allele, complete cds
3795	13707	23494	1.31	7.2E-01	BF338350.1	EST_HUMAN	60203559F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183222 5'
4660	14546	24335	2.41	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
							Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
5064	14934	24706	1.16	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
5064	14934	24707	1.16	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
6923	16801	26994	1.21	7.2E-01	AF236061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
7922	17772	28011	2.22	7.2E-01	BF670061.1	EST_HUMAN	60211838F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276381 5'
8121	18009	28256	4.78	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
9570	19160		4.08	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 617
677	10610	20431	10.38	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3024	12952	22745	10.8	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4114	14014	23793	2.93	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4114	14014	23794	2.93	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
5623	15538	25625	1.56	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
5623	15538	25626	1.56	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6149	16022	26162	6.97	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvoyltetrahydropterin synthase (pr) gene, complete cds
7669	17519	27746	2.25	7.1E-01	BE904405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896495 5'
9363	19560		1.61	7.1E-01	AA421492.1	EST_HUMAN	z106h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1209	11118	20966	1.04	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0814 protein, partial cds
1209	11118	20967	1.04	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0814 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2399	12277	22173	1.4	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
2399	12277	22174	1.4	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
4989	14864		1.95	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6880	16759		8.1	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
8463	18336	28599	2	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
8463	18336	28600	2	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
954	10878	20725	15.73	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
954	10878	20726	15.73	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1288	11196	21049	2.21	6.9E-01	AA593530.1	EST_HUMAN	nm28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3182	13107	22911	1.63	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
3399	13316	23117	0.85	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811
6652	16532	26726	2.73	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
6652	16532	26727	2.73	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8582	18450	28719	3.56	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
8582	18450	28720	3.56	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
9016	19543		2.37	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKH-14)
941	10866	20713	1.03	6.8E-01	AF017794.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2639	12506		1.16	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2799	11502	21362	1.58	6.8E-01	AA854475.1	EST_HUMAN	aj75a05.s1 Soares_parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X56411_rna1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4469	14363	24153	1.26	6.8E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon III and flanks
4749	14634	24420	0.83	6.8E-01	4798521	NT	Homo sapiens hevin (HEVIN) mRNA
7556	17407	27622	1.52	6.8E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cde
8437	18311	28566	2.34	6.8E-01	AJ276675.1	NT	Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
8437	18311	28567	2.34	6.8E-01	AJ276675.1	NT	Stagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
8458	18331	28563	2.59	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
8458	18331	28594	2.59	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
8619	18485	28757	1.79	6.8E-01	AF184151.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C(1A) (eIF-4C) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
295	10259	20080	29.34	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
336	10295	20110	19.53	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2100	11989	21887	1.57	6.7E-01	AA451864.1	EST_HUMAN	zx12g12.s1 Soares_tet1 N52HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2120	12713	21908	3.59	6.7E-01	AF186073.1	NT	Drosophila melanogaster MeiB5C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2966	12893	22692	3.7	6.7E-01	6678580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4350	14246	24032	0.96	6.7E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
4881	14762	24538	0.85	6.7E-01	AW079110.1	EST_HUMAN	xa05g12.x1 NCI_OGAP_Cot17 Homo sapiens cDNA clone IMAGE:2574598 3'
5182	15046	24811	0.89	6.7E-01	AJ252942.1	NT	Dendrobium fimbriatum mRNA for phosphoenolpyruvate carboxylase, partial
5627	15542	25631	1.62	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
5817	15723	25836	1.42	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
5817	15723	25837	1.42	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6329	16192	26198	3.98	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
6342	16205	26367	1.46	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8323	18200	28449	2.23	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
8754	17903	28147	3.69	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
2452	12329	22227	0.87	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2667	12532	22422	1.29	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3445	13362	23168	1.04	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3608	13522	23310	3.05	6.6E-01	Y07669.1	NT	Calicivirus random DNA marker, 282bp
4020	13924			6.6E-01	U01328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RbRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5822	15728	25840	3.96	6.6E-01	6980577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
6525	16384	26563	3.63	6.6E-01	AV680506.1	EST_HUMAN	AV680506 GLC Homo sapiens cDNA clone GLCID04 3'
7571	17422		2.41	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9619	19197	25256	1.35	6.6E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
608	10544	20352	1.37	6.5E-01	MT5140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
608	10544	20353	1.37	6.5E-01	MT5140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3386	13304	23104	5.1	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
3951	13859	23633	1.08	6.5E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4185	14085	23860	4.17	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4215	14113	23890	0.86	6.5E-01	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
4994	14869	24632	2.27	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5175	15041		0.88	6.5E-01	U37258.1	NT	Acetobacter xylinum putative ATP binding protein delta-AceB gene, partial cds, and GDP-mannose:cellulobiose diphosphopyrenol alpha-mannosyltransferase gene, complete cds
6036	15939	26071	1.38	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7919	17769	28008	2	6.5E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
8030	17922	28168	3.24	6.5E-01	H87583.1	EST_HUMAN	yw17706.r1 Soares placenta_8to8weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:252515 5'
8073	17964	28215	4.03	6.5E-01	AA601287.1	EST_HUMAN	not15cd7.s1 NCI_CGAP_Phet Homo sapiens cDNA clone IMAGE:1100748 3'
8170	18058		4.27	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
8877	18689	28981	2.3	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
9419	19069		2.79	6.5E-01	BE465050.1	EST_HUMAN	hV74a10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
9651	19490		1.69	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
252	10218	20035	5.4	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3410	13327	23128	2.45	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3785	13697	23484	1.34	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4389	14285	24066	0.84	6.4E-01	Y12488.1	NT	M.musculus whn gene
4389	14285	24067	0.84	6.4E-01	Y12488.1	NT	M.musculus whn gene
7007	16884	27076	1.76	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
7807	17657	27895	13.62	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
7818	17688	27908	1.44	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126 5'
9528	19135		6.34	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCG09 5'
9951	19553		1.65	6.4E-01	9845300	NT	Rat cytomegalovirus Mastricht, complete genome
427	10372	20196	4.41	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
524	10466	20277	2.15	6.3E-01	U32699.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2116	12005	21903	3.87	6.3E-01	U81136.1	NT	Shigella flexneri multi-antibiotic resistance locus
2534	12408	22300	3.89	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2534	12408	22301	3.89	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2983	12911		0.93	6.3E-01	Y17275.1	NT	Lycopodium obscurum p68a gene, complete CDS

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3985	13892	23688	1.38	6.3E-01	X99675.1	NT	D.melanogaster mRNA for metabotropic glutamate receptor
6959	16837		3.17	6.3E-01	BE902044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
7150	17027	27223	1.67	6.3E-01	S62927.1	NT	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
7421	17288	27495	2.72	6.3E-01	9627521	NT	Varida virus, complete genome
7421	17288	27496	2.72	6.3E-01	9627521	NT	Varida virus, complete genome
8004	17864	28095	1.4	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
8413	18288	28543	2.27	6.3E-01	AA877715.1	EST_HUMAN	m09h06.s1 NCL_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 002916 HILARK.;
8847	18511	28791	11.72	6.3E-01	AI804160.1	EST_HUMAN	CM-BT043-090299-046 BT043 Homo sapiens cDNA
8725	18581	28865	1.94	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
8968	18680	28969	1.98	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
9128	19697	24899	9.21	6.3E-01	9910283	NT	Mus musculus keratin complex 2, gene 6g (Kt2-6g). mRNA
9220	18944		1.54	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
9435	19619		1.58	6.3E-01	X83528.1	NT	C.limicola pscD gene
5578	15493	25569	2.12	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
6426	16287		3.06	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
6831	16710	26903	5.45	6.2E-01	H72255.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'
7435	16448	26638	1.71	6.2E-01	BE562887.1	EST_HUMAN	601338146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
7476	17336		2.56	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
7799	17649	27886	7.14	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
8007	17857	28099	5.02	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
8007	17857	28100	5.02	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2345	12225		4.5	6.1E-01	6678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc). mRNA
4831	14809	24577	0.99	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxypolyphenylbenzoate methyltransferase mRNA, complete cds
4931	14809	24578	0.99	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxypolyphenylbenzoate methyltransferase mRNA, complete cds
6104	15998	26134	3.78	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6104	15998	26135	3.78	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6792	16671	28863	3.72	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
7108	16985	27175	1.75	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4). mRNA
7108	16985	27176	1.75	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4). mRNA
7419	17286	27492	19.47	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
7419	17286	27493	19.47	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7778	17628	27860	1.59	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
486	10429	20243	0.92	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
549	10490		2.64	6.0E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1339	11245	21103	1.76	6.0E-01	AF065253.1	NT	Homo sapiens respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3744	13656	23438	1.02	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
5227	15151	24918	1.56	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5339	15260	25086	2.58	6.0E-01	AW139713.1	EST_HUMAN	UI-H-B1-aeh-a-10-0-UJ.st NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619.3'
5940	15845	25968	2.61	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6350	16213	26375	6.2	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
6725	16605	26794	4.19	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
6725	16605	26795	4.19	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
7653	17503	27727	1.69	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
7894	17744		1.43	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
8411	18286	28541	1.78	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
8411	18286	28542	1.78	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
8838	18651	28939	2.74	6.0E-01	AK20623.1	EST_HUMAN	tf08i07.x1 NCL_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2095621.3'
9900	19115	25291	1.64	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
9787	19554	25065	2.1	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
9809	19484		2.18	6.0E-01	BE167617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
984	10907	20752	1.25	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3232	13156	22954	4.85	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3232	13156	22955	4.85	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4129	14029		4.12	5.9E-01	AF162756.1	NT	Rattus norvegicus connexin 2 mRNA, partial cds
5889	15795	25917	2.1	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
8061	17952	28203	2.67	5.9E-01	Q9X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
8328	18205	28454	3.1	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA
8529	18401	28669	2.36	5.9E-01	AF084626.1	NT	Mus spretus strain SPRET/Ei CD48 antigen (Cd48) gene, partial cds
9165	18908	28342	1.91	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
9404	19057		2.18	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for oridine-5'-phosphate decarboxylase, complete cds
9614	19193		4.15	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1867	11763	21637	1.44	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3902	13812	23596	0.96	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4413	14307	24090	2.81	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4690	14376		1.04	5.8E-01	AF110846.1	NT	Megascelia scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products
5753	15661	25768	1.29	5.8E-01	D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (TFujivara) Homo sapiens cDNA clone GEN-500E06 5'
6077	16060		2.3	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
6604	16484		2.62	5.8E-01	H41571.1	EST_HUMAN	ynr1b03.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
6764	16643	26830	2.23	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
6764	16643	26831	2.23	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
7153	17030	27224	8.64	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
8358	18235	28483	8.47	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
8396	18272		3.23	5.8E-01	BF700092.1	EST_HUMAN	602127377F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
8482	18355		1.78	5.8E-01	BF700092.1	EST_HUMAN	602127377F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3186	13111	22915	1.48	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3460	13376		2.43	5.7E-01	AB038503.1	NT	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3829	13741	23533	1.65	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV6S72-BJ1S1) mRNA, partial cds
5201	15064	24827	2.24	5.7E-01	U78517.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor II (cAMP-GEFII) mRNA, partial cds
5836	15742	25854	3.72	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'
6100	15110	24874	1.41	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6564	18422	26803	2.12	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
9124	18883		1.68	5.7E-01	BE716051.1	EST_HUMAN	MR3-HT0736-180700-003-002 HT0736 Homo sapiens cDNA
3318	13239	23043	1.21	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3318	13239	23044	1.21	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3808	13720	23509	0.83	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4146	14046	23818	0.83	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
7111	16888	27180	4.16	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
7111	16888	27181	4.16	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9023	18817		2.46	5.6E-01	BE886280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
9137	18893	28794	1.73	5.6E-01	AA493535.1	EST_HUMAN	ng75g10.s1 NCJ_CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element;
9624	19133		1.32	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
9919	19392		3.09	5.6E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'

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Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1193	11103	20949	1.09	5.5E-01	8393912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2668	12533	22423	2.88	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2668	12533	22424	2.88	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2888	12815	22608	1.34	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3027	12955		1.39	5.5E-01	H46219.1	EST_HUMAN	yo18at0.s1 Scores adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3196	13121	22926	3.1	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3634	13548	23335	1.29	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
139	10113	19933	3.74	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
139	10113	19934	3.74	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
570	10509	20316	2.61	5.4E-01	AF232005.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
570	10509	20317	2.61	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
1250	11157	21006	2.24	5.4E-01	AW896087.1	EST_HUMAN	GV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2059	11949		2.78	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of the complete genome
2208	12095	21998	2.23	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
7738	17588		2.01	5.4E-01	BF572536.1	EST_HUMAN	602076546F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
8427	18301	28557	2.87	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
8892	18702	28966	4.51	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
8892	18702	28997	4.51	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
9087	18862		2.12	5.4E-01	A1858398.1	EST_HUMAN	w37g04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
505	10447	20260					Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2093	11982	21877	2.02	5.3E-01	AF019413.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2093	11982	21878	0.91	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2765	12617	22508	8.24	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2755	12617	22509	8.24	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3205	13129	22931	2.92	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds

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4117	14017		1.29	5.3E-01	U39887.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5350	15270	25098	1.75	5.3E-01	AI820921.1	EST_HUMAN	zu42h12.y6 Soares ovary/tumor N8HOT Homo sapiens cDNA clone IMAGE:740711 5'
5350	15270	25099	1.75	5.3E-01	AI820921.1	EST_HUMAN	zu42h12.y6 Soares ovary/tumor N8HOT Homo sapiens cDNA clone IMAGE:740711 5'
5467	15387	25447	1.91	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb.J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5467	15387	25448	1.91	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb.J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
7161	17038		2.15	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for chloroplast product
8846	18658	28946	5.62	5.3E-01	BE566291.1	EST_HUMAN	601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
9015	19551		2.46	5.3E-01	AA916053.1	EST_HUMAN	og30e05.s1 NCI_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb.J02611 APOLOPROTEIN D PRECURSOR (HUMAN);
799	10728	20568	11.31	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1148	11061	20904	7.69	5.2E-01	Q9WV30	SW/SSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT6)
1174	11086	20930	2.83	5.2E-01	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
1843	11739		5.04	5.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2099	11988	21886	2.75	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3081	13008	22798	1.9	5.2E-01	U65942.1	NT	Chlamydomonas abortus strain S26/3 POMVP91A and POMVP90A precursor, genes, complete cds
3199	13124		1.22	5.2E-01	D73443.1	NT	Azotobacter vinelandii icd gene for isocitrate dehydrogenase, complete cds
3359	13278		1.76	5.2E-01	AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3397	13314	23114	1.9	5.2E-01	AA984165.1	EST_HUMAN	am77g05.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3560	13494		1.13	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
3582	13496	23287	1.06	5.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), celltrectin (CAL T), NAD(P)H dehydrogenase-like protein (NSDHL), and Li>
4949	14826		1.29	5.2E-01	7106444	NT	Mus musculus vanilloid receptor-like protein 1 (Vr1), mRNA
7761	17611	27837	1.28	5.2E-01	AF143932.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
9719	19260	25221	2.46	5.2E-01	AW137066.1	EST_HUMAN	UI-H-B11-acp-a-08-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714799 3'
9887	19370		3.43	5.2E-01	P18516	SW/SSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
601	10537	20347	1.89	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
632	10569	20381	3.28	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene

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632	10669	20382	3.28	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI v1) 16S rRNA gene
1632	11536		1.06	5.1E-01	X87885.1	NT	R.norvegicus mRNA for mammalian fusca protein
1977	11870		1.44	5.1E-01	BF683096.1	EST_HUMAN	602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298117 5'
3984	13891	23667	3.84	5.1E-01	AI858495.1	EST_HUMAN	w39b12.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2427263 3'
4094	13994	23771	2.86	5.1E-01	P96380	SWISSPROT	TRANSORPTION-REPAIR COUPLING FACTOR (TRCF)
6133	15980	26116	1.57	5.1E-01	R80873.1	EST_HUMAN	y94a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
7584	17435	27650	4.54	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
7586	17437	27653	3.57	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
9230	19478		3.62	5.1E-01	BF030207.1	EST_HUMAN	601558863F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3828767 5'
9473	19100		2.03	5.1E-01	BF439982.1	EST_HUMAN	nac51f10.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element:
2087	11977	21871	1.37	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
2087	11977	21872	1.37	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
2097	11986	21882	1.32	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2097	11986	21883	1.32	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3688	13601	23388	0.84	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3797	13709	23495	3.44	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6961	16839		5.62	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
7442	16455	26844	3.61	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
7550	17401	27614	2.25	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
7550	17401	27615	2.25	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
7941	17791		1.27	5.0E-01	BE869218.1	EST_HUMAN	601446024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
9003	18806	29099	9.32	5.0E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
9170	18913		2.26	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
9858	19349		2.02	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
9869	19358		2.94	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
772	10702	20541	1.98	4.9E-01	BF571482.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1864	11760	21634	1.39	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5679	15588	25688	2.46	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
5679	15588	25689	2.46	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6406	16267	26429	1.76	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7197	17074		1.41	4.9E-01	BF209791.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
7359	19768		2.2	4.9E-01	10946863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
9065	18846		1.43	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
9851	19733		3.55	4.9E-01	AA613562.1	EST_HUMAN	nd22e11.s1 NCL_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1144652 3'
4577	14136		1.12	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5381	15300	25153	8.94	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6018	15922		3.94	4.8E-01	AA659878.1	EST_HUMAN	nu85f09.s1 NCL_CGAP_A1M1 Homo sapiens cDNA clone IMAGE:1217513
6330	16193		1.96	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (D8S22298E) mRNA
6563	16421	26601	3.82	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6563	16421	26602	3.82	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6613	16493	26679	1.16	4.8E-01	AI820744.1	EST_HUMAN	yj7f10.y5 Soares breast 2Nbl-Hst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER6 repetitive element ;
8111	18001		2.04	4.8E-01	X83502.1	NT	S.cerevisiae ORFs from chromosome X
9369	19511		2.52	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon V1P II SIRE repeat region
9870	19359		2.26	4.8E-01	BE790632.1	EST_HUMAN	601584324F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938909 5'
5925	15830	25953	8.36	4.7E-01	BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
8221	18103		5.77	4.7E-01	AF102673.1	NT	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds
8434	18308	28564	2.06	4.7E-01	U41069.1	NT	Human collagen alpha2(X) (COL11A2) gene, exons 6 through 16, and partial cds
8682	18570	28853	2.43	4.7E-01	AW880448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
9390	19049		1.36	4.7E-01	AW341561.1	EST_HUMAN	hdf11c08.x1 Soares, NFL T. GBC S1 Homo sapiens cDNA clone IMAGE:2909198 3'
3674	13588	23375	1.27	4.6E-01	AW818638.1	EST_HUMAN	RC1-ST0278-040400-018-b06 ST0278 Homo sapiens cDNA
3683	13597	23383	1.28	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3683	13597	23384	1.28	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5087	14957		0.97	4.6E-01	Mt11267.1	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
5360	15280	25111	3.38	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5360	15280	25112	3.38	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5404	15323	25372	1.78	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5414	15334	25384	3.29	4.6E-01	AI247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN;
5414	15334	25385	3.29	4.6E-01	AI247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN;
5418	15339	25393	1.58	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
6057	16040	26181	1.47	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6057	16040	26182	1.47	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6643	16722	26916	13.48	4.6E-01	BF697399.1	EST_HUMAN	602130963F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
7363	17230	27430	26.48	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
7363	17230	27431	26.48	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
7730	17580	27802	1.33	4.6E-01	AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
7730	17580	27803	1.33	4.6E-01	AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
8359	18236		2.86	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
8368	18245	28495	4.78	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
8368	18245	28496	4.78	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
8766	17915	28160	5.45	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
8766	17915	28161	5.45	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
9313	19005		1.43	4.6E-01	D53316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-105F03 5'
9978	19491					NT	Linanthus jamaicensis maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
1869	11765	21639	1.73	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1869	11765	21640	1.73	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2841	12769	22558	4.87	4.5E-01	AA677086.1	EST_HUMAN	zif5402.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3275	13196	22996	3.97	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3331	13251	23056	1.05	4.5E-01	AF126373.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
3942	13850		1.41	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN
3982	13889	23665	1.1	4.5E-01	AI708908.1	EST_HUMAN	as96e09.x1 Barstead_aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2363480 3'
4085	15079		4.02	4.5E-01	AW873495.1	EST_HUMAN	hc80g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4862	14742	24522	0.94	4.5E-01	BE983445.2	EST_HUMAN	601657228R1 NIH_MGC.67 Homo sapiens cDNA clone IMAGE:3666023 3'
5406	15325	25375	1.45	4.5E-01	AW608814.1	EST_HUMAN	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
5983	15888		1.47	4.5E-01	Q00956	SWISSPROT	COAT PROTEIN
6488	16346	26515	2.49	4.5E-01	AI858849.1	EST_HUMAN	w32e02.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
6897	16776	26970	3.14	4.5E-01	AI648596.1	EST_HUMAN	SWISNFX COMPLEX 170 KDA SUBUNIT ;
7100	16977		1.54	4.5E-01	11444786	NT	ts56g11.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282844 3'
7991	17841	28082	25.09	4.5E-01	MB6006.1	EST_HUMAN	Homo sapiens hypothetical protein DKF7p547G183 (DKF7p547G183), mRNA
7991	17841	28083	25.09	4.5E-01	MB6006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
8237	18117	28369	2.42	4.5E-01	AW591271.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
9036	19724		2.25	4.5E-01	BE871461.1	EST_HUMAN	x014h01.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
9694	19245		1.44	4.5E-01	BF337531.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
9763	19283		2.15	4.5E-01	11422099	NT	601449201F1 NIH_MGC.65 Homo sapiens cDNA clone IMAGE:3852961 5'
9974	19652	24987	1.83	4.5E-01	AF238234.2	NT	602033276F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183290 5'
1991	11895		2.47	4.4E-01	6680503	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2340	12220	22118	3.59	4.4E-01	P49765	SWISSPROT	Entamoeba histolytica diaphanous protein (dia) gene, partial cds
3274	13195	22994	0.99	4.4E-01	AF058790.1	NT	Mus musculus integral membrane-associated protein 1 (lmap1), mRNA
3274	13195	22995	0.99	4.4E-01	AF058790.1	NT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3277	13198	22998	1.87	4.4E-01	BF056726.1	EST_HUMAN	Rattus norvegicus SynGAP-b mRNA, complete cds
4141	14041		1.33	4.4E-01	BE378707.1	EST_HUMAN	Rattus norvegicus SynGAP-b mRNA, complete cds
4924	14803		0.93	4.4E-01	BE141396.1	EST_HUMAN	791402.y1 NCL_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
5326	15246	25050	1.99	4.4E-01	P04929	SWISSPROT	601237139F1 NIH_MGC.44 Homo sapiens cDNA clone IMAGE:3609393 5'
5326	15246	25051	1.99	4.4E-01	P04929	SWISSPROT	MR0-HT0078-131299-007-g05 HT0078 Homo sapiens cDNA
5490	15409	25474	1.3	4.4E-01	SG6019.1	NT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5499	15418	25481	1.98	4.4E-01	AV720408.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5624	15539	25627	1.6	4.4E-01	AI198413.1	EST_HUMAN	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5624	15539	25628	1.6	4.4E-01	AI198413.1	EST_HUMAN	AV720408 GLO Homo sapiens cDNA clone GLCC5C12 5'
5782	15688	25798	1.79	4.4E-01	AW080795.1	EST_HUMAN	qi62h11.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6532	16462		10.84	4.4E-01	Z11679.1	NT	UNKNOWN PROTEIN ;
							qi62h11.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
							UNKNOWN PROTEIN ;
							xc27e08.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:Q95154 Q95154
							AFLATOXIN B1-ALDEHYDE REDUCTASE ;
							S.tuberosum mRNA for induced stolon lip protein (partial)

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7354	17222	27422	1.29	4.4E-01	O62836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
7723	17573	27798	1.99	4.4E-01	A1268650.1	EST_HUMAN	gc39f09.x1 NCL CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1910921 3'
7724	17574		2.45	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
7813	17863	27903	4.67	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
7935	17785	28025	1.33	4.4E-01	S76404.1	NT	beta-HKA=H-K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
7935	17785	28026	1.33	4.4E-01	S76404.1	NT	beta-HKA=H-K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
9296	18996	25329	2.29	4.4E-01	6677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
9306	19663		3.29	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
9731	19267	25224	5.34	4.4E-01	9627742	NT	Autographa californica nucleopolyhedrovirus, complete genome
9824	19326		1.75	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A (HHR23A)
405	10351	20178	1.98	4.3E-01	AF155218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
405	10351	20179	1.98	4.3E-01	AF155218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
1585	11489	21350	1.1	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2843	12771		0.96	4.3E-01	AW935269.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3022	12950	22742	0.93	4.3E-01	AW999477.1	EST_HUMAN	MR0-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
3221	13145		1.53	4.3E-01	AE000698.1	NT	Aquifex aeolicus section 30 of 109 of the complete genome
4059	13961	23737	1.15	4.3E-01	J00306.1	NT	Human somatostatin I gene and flanks
4306	10351	20178	1.02	4.3E-01	AF155218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
4306	10351	20179	1.02	4.3E-01	AF155218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
4875	14755		1.11	4.3E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 14
5059	14929		1.06	4.3E-01	9635250	NT	Xestia c-nigrum granulovirus, complete genome
5600	15514	25592	3.04	4.3E-01	AF179825.1	NT	Salmix scitireus olfactory receptor (SSC186) gene, partial cds
6029	15933	26084	3.86	4.3E-01	AJ001678.1	NT	Coturnix coturnix japonica ifnG gene
6102	15996		4.01	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
6393	16255		2.54	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158296 5'
6909	16787		2.83	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-I (flaC-fla) genes, complete cds
7608	17459	27674	1.65	4.3E-01	AW630048.1	EST_HUMAN	hh74et0.yt NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
7608	17459	27675	1.65	4.3E-01	AW630048.1	EST_HUMAN	hh74et0.yt NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
							xn63e05.x1 Scores_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
7872	17722	27967	1.27	4.3E-01	AW170559.1	EST_HUMAN	TR-O00189 O00189 MU-ADAPTIN-RELATED PROTEIN 2 ;
8302	18049	26195	2.64	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
8537	18409	28673	1.98	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
8537	18409	28674	1.98	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
9916	19390		2.02	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1335	12691	21099	1.04	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1904	11800		0.89	4.2E-01	AA761653.1	EST_HUMAN	nc24a09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'
3558	13472	23263	4.78	4.2E-01	AE003947.1	NT	Xyella fastidiosa, section 93 of 229 of the complete genome
3585	13499	23288	1.09	4.2E-01	AI280338.1	EST_HUMAN	q194b01.x1 Soares_NihMP.u. S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3803	13715	23503	0.96	4.2E-01	AW835527.1	EST_HUMAN	QV0-L.T0015-180200-127-h01.LT0015 Homo sapiens cDNA
3900	13810	23595	1	4.2E-01	Q04886	SWISSPROT	SOX-8 PROTEIN
4545	14438		3.63	4.2E-01	BE073574.1	EST_HUMAN	RC5-BT0559-020300-013-E06 BT0559 Homo sapiens cDNA
4599	14487	24273	4.96	4.2E-01	AA534093.1	EST_HUMAN	ni69h01.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4671	14557	24350	3.13	4.2E-01	R13467.1	EST_HUMAN	yf77a01.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5503	15422	25484	1.5	4.2E-01	BF242055.1	EST_HUMAN	601879721F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4108493 5'
5533	15450	25518	1.56	4.2E-01	AW854162.1	EST_HUMAN	RC3-CT0254-060400-029-g04.CT0254 Homo sapiens cDNA
6151	16024	26164	9.1	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6151	16024	26165	9.1	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6184	19461	26219	2.1	4.2E-01	S82504.1	NT	Brcal=breast cancer gene [rats, W.F., spleen, Genomic, 419 nt, segment 2 of 2]
6217	16083	26233	5.91	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
6663	16543	26739	2.1	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
6663	16543	26740	2.1	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
6776	16655	26844	1.19	4.2E-01	4756039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
7992	17842	28084	1.48	4.2E-01	AW863666.1	EST_HUMAN	MF3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
8400	18276	28528	2.2	4.2E-01	AB023439.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
8699	18517	28799	2.04	4.2E-01	BE966485.2	EST_HUMAN	601660352R1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3906085 3'
9863	19353		1.66	4.2E-01	AV731815.1	EST_HUMAN	AV731815 HTF Homo sapiens cDNA clone HTFBH05 5'
1078	10994	20835	1.88	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210199-142 BT091 Homo sapiens cDNA
1087	11003	20844	2.4	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1087	11003	20845	2.4	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1592	11496	21356	1.03	4.1E-01	AI905949.1	EST_HUMAN	PM-BT103-270499-684 BT103 Homo sapiens cDNA
2678	12543	22434	1.52	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2910	12836	22633	1.76	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2910	12836	22634	1.76	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3263	13186	22985	1.13	4.1E-01	AA906344.1	EST_HUMAN	q194b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
4177	14077	23852	2.59	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE, isoAF, isoAG, isoAH, isoAI, isoAJ, isoAK, isoAL, isoAM, isoAN, isoAO, isoAP, isoAQ, isoAR, isoAS, isoAT, isoAU, isoAV, isoAW, isoAX, isoAY, isoAZ, isoBA, isoBB, isoBC, isoBD, isoBE, isoBF, isoBG, isoBH, isoBI, isoBJ, isoBK, isoBL, isoBM, isoBN, isoBO, isoBP, isoBQ, isoBR, isoBS, isoBT, isoBU, isoBV, isoBW, isoBX, isoBY, isoBZ, isoCA, isoCB, isoCC, isoCD, isoCE, isoCF, isoCG, isoCH, isoCI, isoCJ, isoCK, isoCL, isoCM, isoCN, isoCO, isoCP, isoCQ, isoCR, isoCS, isoCT, isoCU, isoCV, isoCW, isoCX, isoCY, isoCZ, isoDA, isoDB, isoDC, isoDD, isoDE, isoDF, isoDG, isoDH, isoDI, isoDJ, isoDK, isoDL, isoDM, isoDN, isoDO, isoDP, isoDQ, isoDR, isoDS, isoDT, isoDU, isoDV, isoDW, isoDX, isoDY, isoDZ, isoEA, isoEB, isoEC, isoED, isoEE, isoEF, isoEG, isoEH, isoEI, isoEJ, isoEK, isoEL, isoEM, isoEN, isoEO, isoEP, isoEQ, isoER, isoES, isoET, isoEU, isoEV, isoEW, isoEX, isoEY, isoEZ, isoFA, isoFB, isoFC, isoFD, isoFE, isoFF, isoFG, isoFH, isoFI, isoFJ, isoFK, isoFL, isoFM, isoFN, isoFO, isoFP, isoFQ, isoFR, isoFS, isoFT, isoFU, isoFV, isoFW, isoFX, isoFY, isoFZ, isoGA, isoGB, isoGC, isoGD, isoGE, isoGF, isoGG, isoGH, isoGI, isoGJ, isoGK, isoGL, isoGM, isoGN, isoGO, isoGP, isoGQ, isoGR, isoGS, isoGT, isoGU, isoGV, isoGW, isoGX, isoGY, isoGZ, isoHA, isoHB, isoHC, isoHD, isoHE, isoHF, isoHG, isoHH, isoHI, isoHJ, isoHK, isoHL, isoHM, isoHN, isoHO, isoHP, isoHQ, isoHR, isoHS, isoHT, isoHU, isoHV, isoHW, isoHX, isoHY, isoHZ, isoIA, isoIB, isoIC, isoID, isoIE, isoIF, isoIG, isoIH, isoII, isoIJ, isoIK, isoIL, isoIM, isoIN, isoIO, isoIP, isoIQ, isoIR, isoIS, isoIT, isoIU, isoIV, isoIW, isoIX, isoIY, isoIZ, isoJA, isoJB, isoJC, isoJD, isoJE, isoJF, isoJG, isoJH, isoJI, isoJJ, isoJK, isoJL, isoJM, isoJN, isoJO, isoJP, isoJQ, isoJR, isoJS, isoJT, isoJU, isoJV, isoJW, isoJX, isoJY, isoJZ, isoKA, isoKB, isoKC, isoKD, isoKE, isoKF, isoKG, isoKH, isoKI, isoKJ, isoKK, isoKL, isoKM, isoKN, isoKO, isoKP, isoKQ, isoKR, isoKS, isoKT, isoKU, isoKV, isoKW, isoKX, isoKY, isoKZ, isoLA, isoLB, isoLC, isoLD, isoLE, isoLF, isoLG, isoLH, isoLI, isoLJ, isoLK, isoLL, isoLM, isoLN, isoLO, isoLP, isoLQ, isoLR, isoLS, isoLT, isoLU, isoLV, isoLW, isoLX, isoLY, isoLZ, isoMA, isoMB, isoMC, isoMD, isoME, isoMF, isoMG, isoMH, isoMI, isoMJ, isoMK, isoML, isoMN, isoMO, isoMP, isoMQ, isoMR, isoMS, isoMT, isoMU, isoMV, isoMW, isoMX, isoMY, isoMZ, isoNA, isoNB, isoNC, isoND, isoNE, isoNF, isoNG, isoNH, isoNI, isoNJ, isoNK, isoNL, isoNM, isoNO, isoNP, isoNQ, isoNR, isoNS, isoNT, isoNU, isoNV, isoNW, isoNX, isoNY, isoNZ, isoOA, isoOB, isoOC, isoOD, isoOE, isoOF, isoOG, isoOH, isoOI, isoOJ, isoOK, isoOL, isoOM, isoON, isoOO, isoOP, isoOQ, isoOR, isoOS, isoOT, isoOU, isoOV, isoOW, isoOX, isoOY, isoOZ, isoPA, isoPB, isoPC, isoPD, isoPE, isoPF, isoPG, isoPH, isoPI, isoPJ, isoPK, isoPL, isoPM, isoPN, isoPO, isoPP, isoPQ, isoPR, isoPS, isoPT, isoPU, isoPV, isoPW, isoPX, isoPY, isoPZ, isoQA, isoQB, isoQC, isoQD, isoQE, isoQF, isoQG, isoQH, isoQI, isoQJ, isoQK, isoQL, isoQM, isoQN, isoQO, isoQP, isoQQ, isoQR, isoQS, isoQT, isoQU, isoQV, isoQW, isoQX, isoQY, isoQZ, isoRA, isoRB, isoRC, isoRD, isoRE, isoRF, isoRG, isoRH, isoRI, isoRJ, isoRK, isoRL, isoRM, isoRN, isoRO, isoRP, isoRQ, isoRR, isoRS, isoRT, isoRU, isoRV, isoRW, isoRX, isoRY, isoRZ, isoSA, isoSB, isoSC, isoSD, isoSE, isoSF, isoSG, isoSH, isoSI, isoSJ, isoSK, isoSL, isoSM, isoSN, isoSO, isoSP, isoSQ, isoSR, isoSS, isoST, isoSU, isoSV, isoSW, isoSX, isoSY, isoSZ, isoTA, isoTB, isoTC, isoTD, isoTE, isoTF, isoTG, isoTH, isoTI, isoTJ, isoTK, isoTL, isoTM, isoTN, isoTO, isoTP, isoTQ, isoTR, isoTS, isoTT, isoTU, isoTV, isoTW, isoTX, isoTY, isoTZ, isoUA, isoUB, isoUC, isoUD, isoUE, isoUF, isoUG, isoUH, isoUI, isoUJ, isoUK, isoUL, isoUM, isoUN, isoUO, isoUP, isoUQ, isoUR, isoUS, isoUT, isoUU, isoUV, isoUW, isoUX, isoUY, isoUZ, isoVA, isoVB, isoVC, isoVD, isoVE, isoVF, isoVG, isoVH, isoVI, isoVJ, isoVK, isoVL, isoVM, isoVN, isoVO, isoVP, isoVQ, isoVR, isoVS, isoVT, isoVU, isoVV, isoVW, isoVX, isoVY, isoVZ, isoWA, isoWB, isoWC, isoWD, isoWE, isoWF, isoWG, isoWH, isoWI, isoWJ, isoWK, isoWL, isoWM, isoWN, isoWO, isoWP, isoWQ, isoWR, isoWS, isoWT, isoWU, isoWV, isoWW, isoWX, isoWY, isoWZ, isoXA, isoXB, isoXC, isoXD, isoXE, isoXF, isoXG, isoXH, isoXI, isoXJ, isoXK, isoXL, isoXM, isoXN, isoXO, isoXP, isoXQ, isoXR, isoXS, isoXT, isoXU, isoXV, isoXW, isoXX, isoXY, isoXZ, isoYA, isoYB, isoYC, isoYD, isoYE, isoYF, isoYG, isoYH, isoYI, isoYJ, isoYK, isoYL, isoYM, isoYN, isoYO, isoYP, isoYQ, isoYR, isoYS, isoYT, isoYU, isoYV, isoYW, isoYX, isoYY, isoYZ, isoZA, isoZB, isoZC, isoZD, isoZE, isoZF, isoZG, isoZH, isoZI, isoZJ, isoZK, isoZL, isoZM, isoZN, isoZO, isoZP, isoZQ, isoZR, isoZS, isoZT, isoZU, isoZV, isoZW, isoZX, isoZY, isoZZ

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Accession No.	Top Hit Descriptor
4373	14289		0.83	4.1E-01	EST_HUMAN	R41726.1	yg11b03.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31814 3'
4567	14459	24247	1.26	4.1E-01	EST_HUMAN	AV747880.1	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
5185	15049		0.87	4.1E-01	NT	Z99124.1	Bacillus subtilis complete genome (section 21 of 21): from 3969281 to 4214814
5844	15657	26650	4.13	4.1E-01	EST_HUMAN	BF681383.1	602156590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6395	16257	26418	2.91	4.1E-01	NT	U67535.1	Methanococcus jannaschii section 77 of 150 of the complete genome
6683	16663	26757	1.3	4.1E-01	EST_HUMAN	BF574604.1	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
7253	17130	27323	1.23	4.1E-01	NT	6755521	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Sitpec-pending), mRNA
7888	17738		1.3	4.1E-01	NT	AL139076.2	Campylobacter jejuni NCTC11168 complete genome; segment 3/6
8018	17868		1.58	4.1E-01	EST_HUMAN	BF349382.1	GM2-HT0137-200999-010-e08 HT0137 Homo sapiens cDNA
8213	18097	28349	164	4.1E-01	NT	X58700.1	Zea mays ZMPM52 gene for 19 kDa zein protein
8696	17880	28121	2.79	4.1E-01	SWISSPROT	Q09470	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
9624	19702		1.72	4.1E-01	NT	D87675.1	Homo sapiens DNA for amyloid precursor protein, complete cds
1023	10940	20763	1.27	4.0E-01	NT	8404656	Laqueus rubellus mitochondrion, complete genome
1316	11223	21079	0.96	4.0E-01	NT	AF203478.1	Drosophila melanogaster Dalmation (dmt) mRNA, complete cds
1469	11374		4.06	4.0E-01	NT	6679258	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
1960	12709	21742	1.17	4.0E-01	NT	Z96933.1	Ascobolus immersus masc2 gene
1960	12709	21743	1.17	4.0E-01	NT	Z96933.1	Ascobolus immersus masc2 gene
2774	10110	19931	1.09	4.0E-01	NT	6678490	Mus musculus ubiquitin-protein ligase e3 component n-recoglin (Ubr1), mRNA
2939	12866	22665	2.24	4.0E-01	NT	AL163280.2	Homo sapiens chromosome 21 segment HS21C080
2939	12866	22666	2.24	4.0E-01	NT	AL163280.2	Homo sapiens chromosome 21 segment HS21C080
3637	13551	23339	1.61	4.0E-01	NT	AF068903.1	Streptococcus pneumoniae Y1C (Y1C), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3755	13668	23451	3.24	4.0E-01	NT	AJ277511.1	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3755	13668	23452	3.24	4.0E-01	NT	AJ277511.1	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4712	14598		7.34	4.0E-01	SWISSPROT	Q31849	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
5803	15517	25596	1.31	4.0E-01	EST_HUMAN	AW970810.1	EST382691 IMAGE resequences, MAGK Homo sapiens cDNA
8959	18766		3.24	4.0E-01	NT	L76080.1	Synechocystis sp. PCC 9413 transposase gene, complete cds
9312	19507		2.22	4.0E-01	NT	AL163300.2	Homo sapiens chromosome 21 segment HS21C100
9825	19327		1.33	4.0E-01	SWISSPROT	P36049	HYPOTHEICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
9910	19387		1.4	4.0E-01	NT	AL139075.2	Campylobacter jejuni NCTC11168 complete genome; segment 2/6
227	10196	20007	1.59	3.9E-01	EST_HUMAN	AW352188.1	GM4-HT0136-150999-014-f09 HT0136 Homo sapiens cDNA
1356	11262	21119	2.1	3.9E-01	NT	AF206618.1	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2605	12473	22367	3.54	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2673	12538	22427	5.98	3.9E-01	X82032.1	NT	H.sapiens B-myb gene
2673	12538	22428	5.98	3.9E-01	X82032.1	NT	H.sapiens B-myb gene
3058	12885	22776	3.63	3.9E-01	AJ225896.1	NT	Sinorhizobium meliloti egl, syrB2, cys3 genes and ori3
3988	13895	23672	1.47	3.9E-01	BF592611.1	EST_HUMAN	7161d01.x1 NCI CGAP Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
4919	14798	24572	1.48	3.9E-01	BE728687.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
5613	15628	25611	3.53	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
7324	17200	27400	1.5	3.9E-01	AW196888.1	EST_HUMAN	xn86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:O94821 O94821 KIAA0713 PROTEIN ;
7503	17372	27581	1.4	3.9E-01	AI937337.1	EST_HUMAN	wp76a02.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFX5_HUMAN P48382 BINDING REGULATORY FACTOR. ;
7680	17630	27755	2.97	3.9E-01	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
8195	18080		2.22	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCBOC11 5'
9091	19642		2.49	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
9209	18940		2.38	3.9E-01	Q61670	SWISSPROT	HOMEBOX PROTEIN HLX1
9288	18990	25328	1.26	3.9E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
154	10128		7.44	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1827	11724		1.22	3.8E-01	AE003870.1	NT	Xylella fastidiosa, section 16 of 229 of the complete genome
2524	12398	22289	2.44	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2591	12726	22352	4.41	3.8E-01	6878002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
2972	12899		0.92	3.8E-01	AJ261057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3010	12938	22732	2	3.8E-01	AF043383.1	NT	Pleurocetes americanus aminopeptidase N (ampN) gene, partial cds
3438	13355	23160	7.77	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3494	13410		0.79	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3506	13410		0.91	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3841	13752	23545	0.84	3.8E-01	6754095	NT	Mus musculus general transcription factor II I (Gtf2), mRNA
5046	14918	24692	0.98	3.8E-01	BE544653.1	EST_HUMAN	60107410F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460154 5'
5445	15366	25422	1.62	3.8E-01	Q04988	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
5994	15899	25023	4.47	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA ta54f11.x1 Soares_total_tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element
6053	16036	26177	3.81	3.8E-01	AI374601.1	EST_HUMAN	M.musculus gene for kallikrein-binding protein
6438	16299		4.83	3.8E-01	X61597.1	NT	
6980	16857	27052	3.07	3.8E-01	AB046881.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							ye43h05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element;contains PTR5 repetitive element' ;
7516	17304		4.11	3.8E-01	T954413.1	EST_HUMAN	
8820	18633		2.82	3.8E-01	BE719219.1	EST_HUMAN	RC0-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
8939	18747	29041	2.57	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
8939	18747	29042	2.57	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
9297	18997		2.38	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
9422	19661		1.34	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
9530	19137		2.21	3.8E-01	BE29256.1	EST_HUMAN	QV3-ET0053-190700-271-a05 ET0053 Homo sapiens cDNA
9917	19638		1.84	3.8E-01	AF291483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds
9921	19675	24993	1.37	3.8E-01	T54787.1	EST_HUMAN	yb42b11.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:73821 3' similar to similar to gb:A06977 SERUM ALBUMIN PRECURSOR (HUMAN)
9937	19406	25180	1.3	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
9970	19430	25151	1.33	3.8E-01	AA776820.1	EST_HUMAN	ah37b01.s1 Soares testis_NHT Homo sapiens cDNA clone 1291657 3' similar to TR:Q15288 Q15288 NO DISTINCTIVE PROTEIN MOTIFS. ;
2431	12308	22203	9.85	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3414	13331	23133	9.48	3.7E-01	AF056836.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4136	14036	23812	6.63	3.7E-01	A1218707.1	EST_HUMAN	ok39c07.x1 Soares NSF_F8_9W_OT_PA_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4225	14123	23998	1.53	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4292	14190	23974	3.32	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
6235	16101	26250	2.73	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6392	16254	26415	4.51	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
6392	16254	26416	4.51	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
6848	16727	26921	2.34	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
6848	16727	26922	2.34	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7307	17183		1.46	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
7864	17714	27958	3.93	3.7E-01	A1336411.1	EST_HUMAN	q46b07.x1 Soares fetal_lung_Nb-HL19W Homo sapiens cDNA clone IMAGE:1950997 3'
8232	18113	28365	1.81	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
8392	18268	28518	2.66	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
8392	18268	28519	2.66	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
8762	17911	28155	4.23	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
8979	18784		2.76	3.7E-01	6677678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
9008	19303		1.87	3.7E-01	J04992.1	NT	Human heart/skeletal muscle A1PIADP translocator (ANT1) gene, complete cds
9176	18917		1.94	3.7E-01	AJ243525.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
9272	18976		2.41	3.7E-01	D86976.1	NT	Human mRNA for KIAA0223 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9634	19206		2.18	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
9701	19251	25217	1.52	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
9964	19746		1.31	3.7E-01	AJ237934.1	NT	Bos taurus partial stat5B gene, exons 2-15 and joined CDS
979	10902		7.17	3.6E-01	U89241.1	NT	Human mibp gene, partial cds
1292	11199	21054	2.59	3.6E-01	T80255.1	EST_HUMAN	y03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1292	11199	21055	2.59	3.6E-01	T80255.1	EST_HUMAN	y03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1874	11770	21645	6.05	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1874	11770	21646	6.05	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1908	11803	21682	6.18	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2007	11899		1.08	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2223	12108		1.04	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2341	12221		2.39	3.6E-01	X76725.1	NT	P.irregular (P3804) gene for actin
2437	12314	22211	1.63	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-01.1-g07 ST0171 Homo sapiens cDNA
2589	12460	22350	2.28	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE)
2899	15077		8.9	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3424	13341	23145	1.85	3.6E-01	X76758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
3424	13341	23146	1.85	3.6E-01	X76758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
4308	14205	23988	1.16	3.6E-01	BE707833.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4835	14523	24312	0.85	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4984	14570	24367	1.23	3.6E-01	AJ229237.1	NT	Bacteria from anoxic bulk soil 16S rRNA gene (strain XB45)
4941	14819	24587	2.01	3.6E-01	AW338933.1	EST_HUMAN	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5899	15805	25928	1.6	3.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
6238	16104		5.49	3.6E-01	R94090.1	EST_HUMAN	y174a06.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:275987 5'
6317	16180	26340	1.66	3.6E-01	AW027174.1	EST_HUMAN	w172c10.x1 Soares thymus_NHFTn Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
6816	16695	26886	13.42	3.6E-01	AL161583.2	NT	O15117 FYN BINDING PROTEIN. [1]; Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
7205	17082	27269	3.37	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7205	17082	27270	3.37	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7302	17178	27380	1.4	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
7674	17524	27750	15.34	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8314	18191	28440	1.94	3.6E-01	BE002300.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
8453	18326	28585	3.69	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
8741	17890	28134	3.56	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
9044	19761		1.81	3.6E-01	Y19210.1	NT	Homo sapiens HRB5 gene for hair keratin, exons 1 to 9
9127	18886		3.05	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1685 section 225 of 400 of the complete genome
9281	18983		3.03	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
9889	19704		1.58	3.6E-01	AW190229.1	EST_HUMAN	x160e11.x1 NQ1_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
202	10174	19990	2.18	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
662	10596	20414	0.97	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
708	10640	20466	1.24	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
708	10640	20457	1.24	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
763	10694	20531	3.17	3.5E-01	BF129796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1603	11508	21370	1.17	3.5E-01	BF310688.1	EST_HUMAN	601894633F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1622	11526	21384	1.05	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2563	12725	22327	1.85	3.5E-01	AA223252.1	EST_HUMAN	zr08a09.s1 Stragagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
2672	12637		0.86	3.5E-01	U05897.1	NT	Fibroblast succinogenes S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
4165	14065	23839	1.92	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
4379	14275	24056	1.29	3.5E-01	BE146585.1	EST_HUMAN	RC5-HT0218-181099-011-g02 HT0218 Homo sapiens cDNA
4790	14675	24462	0.84	3.5E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE 1-K similar to R07879, Z40498
4849	14730	24513	3.84	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
6199	15959		3.47	3.5E-01	X98505.1	NT	S.scrofa mRNA for OD31 protein (PECAM-1)
6704	16584		1.88	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
7171	17048	27238	3.21	3.5E-01	4507670	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
7612	17463	27680	1.51	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL II) (BII)
7888	17538	27764	5	3.5E-01	Z26825.1	NT	X.laevis gene for albumin including HP1 enhancer
8116	18005	28251	2.99	3.5E-01	X61084.1	NT	C.griseus rhodopsin gene for opsin protein
8396	18263	28513	2.34	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
8396	18263	28514	2.34	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8951	18758	29052	3.34	3.5E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
9206	18937		2.12	3.5E-01	X64565.1	NT	B. taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
9941	19616	24999	2.25	3.5E-01	H80814.1	EST_HUMAN	ys64f11.1.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
9941	19616	25000	2.25	3.5E-01	H80814.1	EST_HUMAN	ys64f11.1.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
691	10624		1.9	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
960	10883	20731	4.53	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, ccsS genes, of222 and partial inaA gene
1304	11211	21066	1.73	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2852	12232	22129	2.81	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
2842	12509	22400	1.46	3.4E-01	AL161516.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
2971	12898	22697	0.81	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2871	12898	22698	0.81	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3124	13049	22846	5.41	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3488	13404	23209	3.48	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3722	13634		2.33	3.4E-01	BF449010.1	EST_HUMAN	7n94a01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
3965	13872		1.16	3.4E-01	AA594196.1	EST_HUMAN	Q9UJ15 DJ18C9.1 ;
4394	14290	24074	0.78	3.4E-01	AF166341.1	NT	not1b10.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4544	14437	24221	1.82	3.4E-01	BE069912.1	EST_HUMAN	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4828	14710	24494	0.93	3.4E-01	BE463761.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
4870	14750		3.57	3.4E-01	AI240973.1	EST_HUMAN	hyt7d09.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3197585 3' similar to contains L1 t3 L1 repetitive element;
4970	14845	24614	1.2	3.4E-01	X16544.1	NT	qj95c05.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element;
5487	15406	25469	2.85	3.4E-01	AL161594.2	NT	Sea urchin hsp70 gene II for heat shock protein 70
5551	15467		4.71	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5654	15566		2.06	3.4E-01	U02971.1	NT	zn12d11.s1 Stratagene hNT neuron: (#937233) Homo sapiens cDNA clone IMAGE:547221 3'
5715	15623	25724	2.57	3.4E-01	AW204505.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
5780	15687	25796	1.47	3.4E-01	AL120544.1	EST_HUMAN	UI-H-B1-a-ei-e-12-Q-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6045	15948		1.52	3.4E-01	NG5225.1	EST_HUMAN	DKFp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
						EST_HUMAN	zb53e12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6148	16021	26161	1.41	3.4E-01	AI468082.1	EST_HUMAN	tm63g05.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
6943	16821		1.77	3.4E-01	AA337063.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN);
7139	17016	27209	1.62	3.4E-01	9633624	NT	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
7313	17189	27390	3.88	3.4E-01	P26013	SWISSPROT	Bovine enterovirus strain K2577, complete genome
7313	17189	27391	3.88	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
7433	16446	26635	4.17	3.4E-01	U19492.1	NT	INTEGRIN BETA-8 PRECURSOR
7433	16446	26636	4.17	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7690	17540	27766	2.22	3.4E-01	AJ225084.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
8390	18257		4.09	3.4E-01	AE000881.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
8407	18293	28536	2.2	3.4E-01	P06925	SWISSPROT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
8440	18314	28572	2.26	3.4E-01	AF045981.1	NT	PROBABLE E4 PROTEIN
8604	18471	28742	1.77	3.4E-01	M25856.1	NT	Ruditius arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
8604	18471	28743	1.77	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
8790	18605	28896	1.8	3.4E-01	AB035507.1	NT	Human von Willebrand factor gene, exons 36 and 37
8814	18627	28916	4.03	3.4E-01	AL161515.2	NT	Rattus norvegicus mRNA for s-glycerin/MUC18, complete cds
9020	18814		2.01	3.4E-01	U93604.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9130	18887		1.3	3.4E-01	Z21821.1	NT	Citrus variegation virus putative replicase gene, partial cds
9229	19508		1.82	3.4E-01	AF254351.1	NT	S.cerevisiae RIB5 gene encoding Riboflavin synthase
9347	19024		4.9	3.4E-01	L26339.1	NT	Schizosaccharomyces pombe Cwf8p (cwf8) gene, complete cds
9378	19538		2.49	3.4E-01	BE218652.1	EST_HUMAN	Human autoantigen mRNA, complete cds
9432	19639		2.13	3.4E-01	9838361	NT	hvi2h08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.f3
9637	19140	26264	1.79	3.4E-01	AJ207131.1	NT	P TR5 repetitive element ;
						NT	Beta vulgaris mitochondrion, complete genome
						NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
						NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-
						NT	hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B
9829	19330		1.79	3.4E-01	AF019413.1	NT	(Bf), and complement component C2 (C2) genes,>
14	10000	19791	7.91	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
100	10000	19791	3.92	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
440	10384	20208	1.16	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
617	10554	20366	1.41	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1182	11093	20940	3.05	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1285	11193	21046	4.82	3.3E-01	BF588890.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1388	11492	21352	1.11	3.3E-01	6753665	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1704	11605		1.05	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week Homo sapiens cDNA 5' end
2355	12235		4.74	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'- decarboxylase) (UMPS) mRNA
2919	12846	22648	2	3.3E-01	AJ251805.1	NT	Bacteriophage phi-Ye03-12 complete genome
2982	12910		1.12	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P36)
3016	12944	22737	1.01	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mithramycin biosynthetic genes
3450	13367	23173	1.14	3.3E-01	AB012922.1	NT	Homo sapiens MTAT-L1 gene, complete cds
3738	13650	23433	2.17	3.3E-01	O84945	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3884	13795	23582	1.59	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3920	13829	23609	1.92	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4271	14170		2.74	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4589	14477		1.48	3.3E-01	AI639114.1	EST_HUMAN	tp78b12.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb.X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
5263	15185	24960	2.68	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5263	15185	24961	2.68	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5622	15537	25623	2.71	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
5622	15537	25624	2.71	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6117	16011	26148	3.64	3.3E-01	AI628131.1	EST_HUMAN	ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
6117	16011	26149	3.64	3.3E-01	AI628131.1	EST_HUMAN	ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
6575	16433	26616	1.5	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
6981	16858	27053	19.46	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
7477	17337	27542	3.26	3.3E-01	N89866.1	EST_HUMAN	za87h01.s1 Soares fetal_lung NBHL19W Homo sapiens cDNA clone IMAGE:297649 3'
7507	17295	27504	2.81	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
7739	17589		2.07	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMG1-C) gene, exons 1-3, complete cds
8104	17994	28242	2.71	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
8104	17994	28243	2.71	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
8389	18265		1.82	3.3E-01	BF526499.1	EST_HUMAN	602070802F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4213585 5'
8561	18431	28700	12.76	3.3E-01	BE219351.1	EST_HUMAN	hw51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
8652	18541	28825	3.94	3.3E-01	P47953	SWISSPROT	ob71g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
8956	18763		4.79	3.3E-01	AA806821.1	EST_HUMAN	Rhizobium leguminosarum syn plasmid pRL5J nodX gene
8972	10000	19791	1.88	3.3E-01	X07990.1	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
9119	18881	28789	1.63	3.3E-01	6598319	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
9817	19323		6.05	3.3E-01	AP000002.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
449	10393		1.98	3.2E-01	AF018261.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
701	10634		2.05	3.2E-01	AL1161501.2	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1146	11059	20902	18.99	3.2E-01	AF047013.1	NT	P. vulgaris arc5-1 gene
1261	11168	21019	1.04	3.2E-01	Z50202.1	NT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1368	11274	21130	6.25	3.2E-01	Q48624	SWISSPROT	S. cerevisiae chromosome II reading frame ORF YBR172c
1737	11638	21506	1.22	3.2E-01	Z36041.1	NT	EST369264 IMAGE resequences, MAGD Homo sapiens cDNA
1744	11645	21513	5.5	3.2E-01	AW957194.1	EST_HUMAN	EST369264 IMAGE resequences, MAGD Homo sapiens cDNA
1744	11645	21514	5.5	3.2E-01	AW957194.1	EST_HUMAN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1800	11698	21574	1.16	3.2E-01	AL111655.1	NT	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2114	12003	21901	2.89	3.2E-01	BF203817.1	EST_HUMAN	Mus musculus Pbx/knotted 1 homeobox (Pknxt1), mRNA
2494	12368		2.9	3.2E-01	7710079	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2677	12542	22433	1.55	3.2E-01	AF060588.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
3556	13470		0.96	3.2E-01	D10872.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
3868	13779		0.97	3.2E-01	AL161546.2	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4295	14193	23977	1.35	3.2E-01	M18318.1	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4375	14271	24052	0.81	3.2E-01	AF111167.2	NT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4397	14293	24077	1.33	3.2E-01	Q10288	SWISSPROT	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4632	14520		5.86	3.2E-01	BF083617.1	EST_HUMAN	Mouse renin (Ren-1-d) gene, complete cds
4907	15081		1.18	3.2E-01	M32352.1	NT	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5133	15000	24771	0.98	3.2E-01	AY008847.1	NT	CM0-HT0569-060300-269-f10 HT0569 Homo sapiens cDNA
5223	15146	24913	2.82	3.2E-01	BE173954.1	EST_HUMAN	Rat ISO-atrial natriuretic factor gene, complete cds
6752	16631	28819	1.42	3.2E-01	M60266.1	NT	H. sapiens gene fragment for acetylcholine receptor (ACHR) alpha subunit exons 8, 9 and 3' flanking region
6872	16751	28946	13.32	3.2E-01	X02508.1	NT	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
6875	16754	28951	14.29	3.2E-01	BF311635.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6929	16807		1.35	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
6986	16863	27056	1.5	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
7247	17124		2.19	3.2E-01	W86611.1	NT	Human monocytic antigen CD14 (CD14) mRNA, complete cds
7741	17591	27812	3	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, epc and epd genes, complete cds; and unknown genes
7910	17760		3.25	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
8058	17949	28199	2.7	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBD221
9152	19662		3.28	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
9669	19228		2.97	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
9801	19313		1.58	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
9855	19696	24898	1.57	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2636	12503	22397	3.73	3.1E-01	R18051.1	EST_HUMAN	ye90106.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to
2665	12655	22419	3.45	3.1E-01	7661971	NT	gb:M64241 QM PROTEIN (HUMAN);
2665	12655	22420	3.45	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2827	12756		1.01	3.1E-01	AW629036.1	EST_HUMAN	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
3136	13061		2.78	3.1E-01	AB029089.1	NT	h46h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2976391 3'
3832	13744	23536	1.15	3.1E-01	AJ251586.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
5073	14943	24717	0.99	3.1E-01	AA576308.1	EST_HUMAN	Daucus carota mRNA for transcription factor E2F (E2F gene)
5365	15285	25119	8.66	3.1E-01	AF176111.1	NT	nm61h05.s1 NCI_CGAP_Br3 Homo sapiens cDNA clone IMAGE:1072761 3'
5447	15368		45.03	3.1E-01	Y13278.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5527	15444	25510	1.94	3.1E-01	AF184122.1	NT	Mus musculus mRNA for polycystin
5890	15796	25918	1.34	3.1E-01	AW983549.1	EST_HUMAN	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6160	19438	24861	2.4	3.1E-01	BE737392.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
7023	16900	27092	1.87	3.1E-01	R45318.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7791	17641	27874	7.76	3.1E-01	BF696639.1	EST_HUMAN	y946f01.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35639 3'
7791	17641	27875	7.76	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
7832	17682	27926	1.96	3.1E-01	A1244001.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
8211	18095	28348	1.95	3.1E-01	BF216117.1	EST_HUMAN	q161e11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700
8823	18636	28920	1.99	3.1E-01	7662291	NT	HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
9279	18982		1.63	3.1E-01	AF294308.1	NT	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4098814 5'
9315	19007		1.64	3.1E-01	AF304162.1	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
9457	19089		2.45	3.1E-01	AF195983.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
						NT	Sitostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
						NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9806	19318						Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
66	12635	19866	3.11	3.1E-01	AF196779.1	NT	Homo sapiens protein kinase C, epsilon (Pkcε), mRNA
254	10220	20037	1.58	3.0E-01	6755083	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1204	11114	20960	1.12	3.0E-01	AJ271735.1	NT	xs63f08.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1491	11396	21266	1.89	3.0E-01	AJ006755.1	EST_HUMAN	Balaenoptera physalus gene encoding atrial natriuretic peptide
2089	11978	21873	6.26	3.0E-01		NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3175	13100		0.86	3.0E-01	AF237778.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polygluturonate lyase, complete cds
3789	13701	23488	0.98	3.0E-01	AB030481.1	NT	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
4412	14306	24089	1.34	3.0E-01	AB017785.1	EST_HUMAN	Balaenoptera physalus gene encoding atrial natriuretic peptide
5283	15205	24981	1.91	3.0E-01	AJ006755.1	NT	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5379	15298	25147	5.34	3.0E-01	BE741629.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5379	15298	25148	3.18	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5401	16320	25368	3.18	3.0E-01	BE693575.1	EST_HUMAN	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6086	16031	26171	3.51	3.0E-01	U01247.1	NT	Mouse cyokeratin 15 gene, complete cds
6335	16198	26358	2.61	3.0E-01	D16313.1	NT	Mus musculus midnolin (Midn-pending), mRNA
6429	16290	26451	2.57	3.0E-01	10847007	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
6625	16505	26693	1.35	3.0E-01	AF071810.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
6877	16756		1.25	3.0E-01	AE001755.1	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec3f9), mRNA
6937	16815	27007	4.67	3.0E-01	9910161	NT	601339070F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
7944	17794	28034	1.27	3.0E-01	BE566083.1	EST_HUMAN	Aspergillus oryzae btpA gene for ER chaperone BP, complete cds
8980	18785	29074	1.89	3.0E-01	AB030231.1	NT	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
8980	18785	29075	2.89	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
9564	19647		2.89	3.0E-01	H51029.1	EST_HUMAN	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
9636	19690		1.43	3.0E-01	AJ297631.1	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1978	18171	21762	2.76	3.0E-01	6677766	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2201	12088	21989	1.6	2.9E-01	AE000736.1	NT	Chrysodidymus synuroideus mitochondrion, complete genome
3147	13072	22873	0.99	2.9E-01	AF222718.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
3213	13137	22939	1.03	2.9E-01	AF078111.1	NT	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3213	13137	22940	2.29	2.9E-01	AW764239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3821	13733	23522	1.28	2.9E-01	AI610836.1	EST_HUMAN	tp21a11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
3994	13901		0.82	2.9E-01	AW002902.1	EST_HUMAN	wr02f10.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480395 3'
4384	14280	24059	1.01	2.9E-01	AA284468.1	EST_HUMAN	zs57d12.r1 NCL_CGAP_GOB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4388	14284	24064	0.78	2.9E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
4388	14284	24065	0.78	2.9E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
4729	14815	24401	0.92	2.9E-01	AB019029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5218	15141		1.49	2.9E-01	R37485.1	EST_HUMAN	y77e12.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5522	15440	25504	4.45	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5522	15440	25505	4.45	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5529	15446	25513	5.83	2.9E-01	U03420.1	NT	Mus musculus Eph receptor A8 (EphA8), mRNA
5818	15724	25838	2.24	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6171	15128	24847	1.51	2.9E-01	AF142329.1	NT	Mus musculus Filih protein (Filih) gene, complete cds; and Ligih protein (Ligih) gene, partial cds
6218	16084	26234	2.52	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR508C
6249	16115	26267	1.74	2.9E-01	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), lapasin (lapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr-
6619	16499	26686	1.76	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
6619	16499	26687	1.76	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8267	18147	28387	1.96	2.9E-01	AF12843.1	NT	Typanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
8502	18375	28639	2.69	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
8502	18375	28640	2.69	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
8864	18676	28965	1.77	2.9E-01	AA935373.1	EST_HUMAN	ny95h02.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element;
8866	18678	28967	4.54	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
9514	19127	25260	1.53	2.9E-01	AW005671.1	EST_HUMAN	wz88f05.x1 NCL_CGAP_Brn25: Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element MER29 repetitive element;
9802	19184	25248	2.74	2.9E-01	AF092453.1	NT	Homo sapiens TNF- α -inducible RNA binding protein (TRIP) gene, complete cds
9644	19212		1.33	2.9E-01	BE788199.1	EST_HUMAN	601482059F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884559 5'
9883	19367	25189	4.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
9883	19367	25189	4.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
556	10497		1.84	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP160 mRNA, complete cds
1067	10983	20828	2.47	2.8E-01	AF168050.1	NT	Guirra guira oocyte maturation factor Mos (c-mos) gene, partial cds
1256	11163	21013	1.1	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1256	11163	21014	1.1	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1269	11176	21025	1.01	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1696	11598	21470	1.55	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0364-120200-065-b05 CT0364 Homo sapiens cDNA
1966	11860	21750	1.77	2.8E-01	AL047620.1	EST_HUMAN	DKFZp586i2321_1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586i2321
2084	11974	21869	1.47	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2423	12300	22197	2.94	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2423	12300	22198	2.94	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2500	12375		2.47	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2630	12498	22388	1.37	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2940	12867		1.49	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2941	12868	22667	2.48	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
2941	12868	22668	2.48	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3332	13252	23057	1.1	2.8E-01	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (4/7)
3915	13824	23604	1.75	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4103	14003		2.21	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
4352	14248	24034	0.98	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4357	14253	24038	2.2	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4673	14559	24352	1.03	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4673	14559	24353	1.03	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4722	14608	24394	2.8	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4755	14640	24427	1.54	2.8E-01	BF528185.1	EST_HUMAN	802042601F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4180129 5'
4787	14672	24459	1.7	2.8E-01	AI272669.1	EST_HUMAN	ql59c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element ;
5252	19440	24948	21.36	2.8E-01	AA349997.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5443	15363	25419	2.33	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
5770	15677	25784	1.44	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
5770	15677	25785	1.44	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6038	15941	26073	7.67	2.8E-01	BF511215.1	EST_HUMAN	UI-H-BI4-aci-F04-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6713	16593	26781	1.24	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
6713	16593	26782	1.24	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
6778	16657	26847	2.39	2.8E-01	U51688.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
6994	16871		7.25	2.8E-01	BF347847.1	EST_HUMAN	602022987F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158525 5'
7311	17187	27388	1.35	2.8E-01	AF080592.1	NT	Mus musculus centrin (Cetn2) gene, complete cds
7900	17451		1.15	2.8E-01	L13654.1	NT	Lycopodium esculentum peroxidase (TPX1) mRNA, complete cds
7789	17639	27872	2.79	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
8126	18014	28261	2.27	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
8126	18014	28262	2.27	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
8153	18041	28291	3.01	2.8E-01	BF695970.1	EST_HUMAN	601882148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
8254	18134	28382	2.62	2.8E-01	AF051662.1	NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
8599	18466		3.49	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
9552	19150		6.37	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
9857	19219	25236	3.11	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA
9826	19851		1.69	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
468	10411	20230	2.33	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
597	10533	20341	3.14	2.7E-01	AA450061.1	EST_HUMAN	zx39b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1240	11147	20996	1.49	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1604	11509		1.73	2.7E-01	X79816.1	NT	G.lambia SR2 gene
1698	11600	21471	2.96	2.7E-01	W58097.1	EST_HUMAN	z422h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1738	11639	21507	1.25	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2088	12712		2.38	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2316	12197	22094	8.78	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M89), partial
2406	12283	22180	3.51	2.7E-01	A1310858.1	EST_HUMAN	ta43c11.x2 NCL_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
2956	12883		1.25	2.7E-01	BF088284.1	EST_HUMAN	GM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3929	13838	23618	1.88	2.7E-01	A1928015.1	EST_HUMAN	wo92e11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
3943	13851	23626	2.31	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4796	14881	24488	0.89	2.7E-01	L27516.1	NT	Triticum aestivum (W cs66) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4973	14848		3.5	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
5221	15144	24838	3.49	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (CHOX-1.4)
6064	16047	26192	2.25	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6527	16386	26565	2.23	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6527	16386	26566	2.23	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7378	17247	27453	10.08	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRRS)
7378	17247	27454	10.08	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRRS)
7379	17248		2.24	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
7801	17651	27888	1.29	2.7E-01	AF091848.1	NT	Oryzobagrus curticulus calgranulin C mRNA, partial cds
7827	17677	27921	1.93	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-A1c isoform a (NF-A1c) mRNA, complete cds
8187	18073	28322	1.76	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
8187	18073	28323	1.76	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
8197	18082	28333	4.09	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
9398	19034		1.27	2.7E-01	X95267.1	NT	G.gallus mRNA for ryanodine receptor type 3
9810	19320		2.15	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
462	12667	20224	1.54	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
472	10416		1.39	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1371	11277	21133	2.23	2.6E-01	BE885087.1	EST_HUMAN	60'510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1418	11324	21188	0.97	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1854	11750	21624	8.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1854	11750	21625	8.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10 x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S
							RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2046	11937		9.9	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2106	11995	21895	1.2	2.6E-01	M11844.1	NT	B.maritimus rbcL gene
2424	12301		2.68	2.6E-01	Y12996.1	NT	60'1126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
2499	12374		9.68	2.6E-01	BE272440.1	EST_HUMAN	EST386035 IMAGE: ressequences, MAGM Homo sapiens cDNA
3053	12980		1.03	2.6E-01	AW974531.1	EST_HUMAN	h30c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3174914 3' similar to contains L1.t3 L1 repetitive element;
3485	13401		0.94	2.6E-01	BE217816.1	EST_HUMAN	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3532	13448	23245	1.12	2.6E-01	M22342.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
3591	13505	23295	1.7	2.6E-01	AF229118.1	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3651	13565	23351	0.9	2.6E-01	AB071446.1	Rattus norvegicus mRNA for organic anion transporter 3, complete cds
4010	13916	23691	1	2.6E-01	AW959510.1	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4062	13964	23742	13.13	2.6E-01	BE080598.1	QV1-BT0630-040-00-132-e03 BT0630 Homo sapiens cDNA
4259	14158	23935	0.95	2.6E-01	AF175293.1	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4393	14289	24072	0.84	2.6E-01	AB0211180.1	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4393	14289	24073	0.84	2.6E-01	AB0211180.1	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4448	14342	24134	1.17	2.6E-01	AA457617.1	aa89d07.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4548	14441	24224	1.63	2.6E-01	U01103.1	Arabidopsis thaliana PSI type III chlorophyll <i>alb</i> -binding protein (Lhca3*) mRNA, complete cds
4616	14504	24292	1.28	2.6E-01	AF142703.1	Ophresilia radiciosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4896	14776	24554	3.56	2.6E-01	H04858.1	yj51e05.r1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:152288 5'
5051	14923	24696	0.86	2.6E-01	P08503	ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR (MCAD)
5700	19764		2.03	2.6E-01	AE001811.1	Thermotoga maritima section 123 of 136 of the complete genome
5763	15670	25777	1.93	2.6E-01	AI582557.1	ts02e12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
5763	15670	25778	1.93	2.6E-01	AI582557.1	ts02e12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
6552	16410	26588	1.52	2.6E-01	R10365.1	yf37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
6585	16465	26656	1.27	2.6E-01	R02411.1	ye82a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
6852	16731	26925	3.01	2.6E-01	BF343588.1	602014422F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150396 5'
6900	16779	26973	2.04	2.6E-01	Q10199	HYPOTHETICAL 75.2 KD PROTEIN G11C11.02 IN CHROMOSOME II
7046	16923	27112	4.34	2.6E-01	BE830339.1	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
7046	16923	27113	4.34	2.6E-01	BE830339.1	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
7854	17704		1.16	2.6E-01	Q28295	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8812	18625		93.65	2.6E-01	X51755.1	Human lambda-immunoglobulin constant region complex (germline)
9136	18892		1.98	2.6E-01	10190655	Mus musculus Jerky (Jrk), mRNA
9328	19655		1.92	2.6E-01	BE883491.1	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
9365	19053	25309	2.6	2.6E-01	AF316896.1	Homo sapiens Na/K-ATPase gamma subunit (FXYD2) gene, complete cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
9833	19333		6.03	2.6E-01	AF141325.2	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
9999	19376		1.5	2.6E-01	Q01631	ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENLYL CYCLASE)
241	10209	20025	2.12	2.5E-01	4502296	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
242	10209	20025	1.86	2.5E-01	4502296	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
255	10221		3.24	2.5E-01	M2650.1	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
815	10743	20589	1.32	2.5E-01	U09964.1	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1044	10962		1.86	2.5E-01	AE002156.1	Ureaplasma urealyticum section 57 of 59 of the complete genome
1105	11021	20894	9.5	2.5E-01	T89837.1	ye11g07.r1 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1503	11407	21266	0.85	2.5E-01	AL115624.1	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1897	11599		5.43	2.5E-01	4885108	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1840	12706	21612	0.88	2.5E-01	BE69604.1	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1840	12706	21613	0.88	2.5E-01	BE69604.1	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
2357	12337		8.29	2.5E-01	AE000675.1	Aquifex aeolicus section 7 of 109 of the complete genome
2446	12323		1.35	2.5E-01	AA251987.1	zs11a12.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
2597	12466	22359	0.97	2.5E-01	X96310.1	B. taurus mRNA for D-aspartate oxidase
3366	13285		2.87	2.5E-01	AW973471.1	EST1385464 MAGE resequences, MAGM Homo sapiens cDNA
3490	13406	23211	0.86	2.5E-01	AF233875.1	Danio rerio peptide YY precursor gene, complete cds
3502	13419	23220	7.93	2.5E-01	AL161517.2	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3774	13686	23488	1.15	2.5E-01	AI741483.1	wg11c07.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3774	13686	23489	1.15	2.5E-01	AI741483.1	wg11c07.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3977	13884		0.83	2.5E-01	P32323	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4222	14120		1.2	2.5E-01	Q03314	RHIB PROTEIN
4514	14407	24193	0.96	2.5E-01	AF242431.1	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
4643	14531		1.14	2.5E-01	Q27225	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4649	14535	24324	3.78	2.5E-01	AF007768.1	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4872	14558	24351	2.19	2.5E-01	AE004416.1	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4698	14584		3.16	2.5E-01	AJ230113.1	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4726	14612	24398	0.79	2.5E-01	BE896785.1	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
4750	14635	24421	0.89	2.5E-01	AB011070.1	Mus musculus gene for uncoupling protein 3, 5'-flanking region and partial 5'UTR
5169	15035	24802	0.86	2.5E-01	AW663183.1	h175109.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968649 5' similar to contains TAR1.12 TAR1 repetitive element;
5169	15035	24803	0.86	2.5E-01	AW663183.1	h175109.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968649 5' similar to contains TAR1.12 TAR1 repetitive element;
5284	15186	24962	11.62	2.5E-01	S83390.1	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]
6366	16229		1.32	2.5E-01	AF134119.1	Mus musculus SKD1 (Skd1) gene, complete cds
6500	16359	26532	3.73	2.5E-01	AL163282.2	Homo sapiens chromosome 21 segment HS21C082
6583	16463	26655	2.99	2.5E-01	BF109040.1	7157a03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
6788	16667	26858	2.25	2.5E-01	BF038595.1	601459238F1 NIH_MGC_06 Homo sapiens cDNA clone IMAGE:3862809 5'
7020	16897	27087	3.95	2.5E-01	H53236.1	y48407.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202601 5'
7481	17351	27554	16.11	2.5E-01	U86651.2	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
7481	17351	27555	16.11	2.5E-01	U86651.2	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
7522	17341	27547	2.04	2.5E-01	AF085164.1	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
7522	17341	27548	2.04	2.5E-01	AF085164.1	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
7814	17664	27904	1.5	2.5E-01	AW581997.1	RC3-STO186-130100-015-a07 ST0186 Homo sapiens cDNA
8010	17860	28105	1.62	2.5E-01	AW152246.1	xg40c10.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
8011	17861	28106	1.68	2.5E-01	X58491.1	Mouse L1Md LINE DNA
8426	18300	28556	2.32	2.5E-01	D50914.1	Human mRNA for KIAA0124 gene, partial cds
9074	18851	29117	2.45	2.5E-01	AF200528.1	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
9100	19729		4.2	2.5E-01	AL161541.2	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
9559	19581	25072	1.28	2.5E-01	AF170072.1	Spodoptera frugiperda CALNUC mRNA, complete cds
541	10482	20292	1.53	2.4E-01	AA936316.1	on70d04.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
830	10757	20608	2.38	2.4E-01	BF576124.1	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1282	11190	21041	17.41	2.4E-01	AJ289880.1	Homo sapiens KIAA0851 gene (partial), X13 gene and LZ1FL1 gene
1282	11190	21042	17.41	2.4E-01	AJ289880.1	Homo sapiens KIAA0851 gene (partial), X13 gene and LZ1FL1 gene
1362	11268	21123	1.04	2.4E-01	Y17293.1	Homo sapiens FLI-1 gene, partial
1808	11705		24.08	2.4E-01	AF267753.1	Mesembryanthemum crystallinum putative potassium channel protein Mktip mRNA, complete cds
1858	11754	21629	1.41	2.4E-01	AF251708.1	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2091	11980	21875	0.88	2.4E-01	AF111168.2	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2122	12010		1.16	2.4E-01	P45384	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2215	12101	22005	2.01	2.4E-01	AE000680.1	Aquifex aeolicus section 12 of 109 of the complete genome

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2332	12213	22111	0.85	2.4E-01	BF002171.1	EST_HUMAN	7123d04.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2491	12366	22280	1.63	2.4E-01	Z36534.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A;
2734	12596	22491	2.14	2.4E-01	X71783.1	NT	D.discoideum (Ax3-K) ponA gene
2756	12618	22510	6.68	2.4E-01	AF030154.1	NT	S.pombe swi6 gene
							Bovine adenovirus 3 complete genome
3093	13020		2.82	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3109	13035	22831	1.85	2.4E-01	X74209.1	NT	H.sapiens AGT gene, Pet1 fragment of intron 4
4817	14700	24486	0.88	2.4E-01	BE160080.1	EST_HUMAN	QV1-HT0412-020400-136-b10 HT0412 Homo sapiens cDNA
4981	14856	24622	50.15	2.4E-01	D00944.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5469	15389	25451	7.53	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5469	15389	25452	7.53	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
							7154d04.x1 NCL_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
							Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ;contains element TAR1 TAR1 repetitive element
5593	15508	25583	2.13	2.4E-01	BF592336.1	EST_HUMAN	Drosophila melanogaster p38a MAP kinase gene, complete cds
5642	15555	25648	2.66	2.4E-01	AF035546.1	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
5705	15813	25714	2.15	2.4E-01	7681801	NT	wc82c11.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464
5937	15842	25966	1.79	2.4E-01	AI698989.1	EST_HUMAN	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
6345	16208	26371	8.87	2.4E-01	L43001.1	NT	Bos taurus guaranyl cyclase-activating protein 2 (guca2) mRNA, complete cds
6860	16739	26931	1.62	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
							wd43e02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains
7517	17305	27511	5.72	2.4E-01	AI693515.1	EST_HUMAN	MER22.b1 TAR1 repetitive element;
7965	17815	28056	1.93	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
8149	18037	28285	3.63	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
8209	18093	28347	1.99	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
8534	18406		2.42	2.4E-01	Z21647.1	NT	P.asiatica mosaic virus genomic RNA
9030	18821	29109	1.55	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
9162	19626		2.39	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
9222	18945		2.54	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
9439	19509		1.59	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
9650	19716		1.26	2.4E-01	BF229975.1	EST_HUMAN	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
9865	19355		3.35	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
383	10330	20153	0.9	2.3E-01	IS75898.1	NT	aromatase [P.oephila guttata=zebra finches, ovary, mRNA, 3188 nt]

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
621	10558		4.42	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
651	10587	20403	19.84	2.3E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
918	10842	20687	3.35	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508818 5'
1494	11398	21258	1.5	2.3E-01	6677980	NT	Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA
1546	11451		0.88	2.3E-01	U22837.2	NT	Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds
1586	11490	21351	1.38	2.3E-01	AJ245480.1	NT	Brassica napus slg gene for S-locus glycoprotein, cultivar T2
1614	11518	21378	2.75	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
1999	11892		1.3	2.3E-01	AJ235535.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/TEL gene
2396	12274	22169	1.56	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2615	12483	22372	1.02	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2794	11271	21127	0.88	2.3E-01	AB015033.1	NT	Marinibacteria agarovorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2834	12861	22661	1.29	2.3E-01	AA601379.1	EST_HUMAN	not6d06 s1 NCL_CGAP_Phet Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THR repetitive element ;
3045	12972		5.73	2.3E-01	R21732.1	EST_HUMAN	yf21b07 s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3324	13244	23051	1.09	2.3E-01	H69836.1	EST_HUMAN	yf97h10, r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3766	13679	23461	1.11	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3856	13767		3.72	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4253	14152	23926	0.85	2.3E-01	R82252.1	EST_HUMAN	yf17f01, r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4300	14198		3.35	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4349	14245	24031	1.02	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4386	14282	24061	2.08	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4454	14348	24140	5.1	2.3E-01	5031084	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4956	14668	24455	0.82	2.3E-01	J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5002	14877	24541	0.95	2.3E-01	BF316135.1	EST_HUMAN	601896136F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125368 5'
5101	14969	24745	0.98	2.3E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (hLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
5146	15013	24783	26.95	2.3E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5246	15169	24942	2.6	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5332	15252	25074	1.71	2.3E-01	BF058381.1	EST_HUMAN	7k30b06.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] ;

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5395	15314	25361	4.83	2.3E-01	X96587.1	NT	C.familiaris rom1 gene
5618	15533	25617	1.87	2.3E-01	A1708940.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
5618	15533	25618	1.87	2.3E-01	A1708940.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6111	16005	26142	3.93	2.3E-01	A1718148.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element;
6384	16246	26408	2.62	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
6487	16345		3.19	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
6491	16349	26519	1.59	2.3E-01	BE888071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
6560	16418		2.9	2.3E-01	N80983.1	EST_HUMAN	zat12e08.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:292358 5'
6664	16544	26741	2.28	2.3E-01	M68931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
7657	17607	27732	1.37	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
7712	17562	27787	2.54	2.3E-01	BE173060.1	EST_HUMAN	MR0-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
7740	17590	27811	2.26	2.3E-01	AJ293281.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
7974	17824		4.95	2.3E-01	BF133577.1	EST_HUMAN	601646156R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
8525	18397	28663	2.84	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
8525	18397	28664	2.84	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
8658	18547	28830	2.39	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome
9144	18898		2.53	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
9232	18951		20.46	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M6 Homo sapiens cDNA clone HCOE44 5'
9258	19477		1.65	2.3E-01	AA089819.1	EST_HUMAN	chn1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9266	18970		2.07	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA
9324	19665	24990	2.05	2.3E-01	AW303623.1	EST_HUMAN	xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175 Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2; contains PTR5.b2 TAR1 repetitive element;
9358	19708	24905	4.88	2.3E-01	BE882464.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3903689 5'
9407	19060		1.93	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
9456	19088		2.09	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9549	19088		4.54	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9793	19310		2.67	2.3E-01	BF475611.1	EST_HUMAN	nac39n12.x1 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element;

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
84	10068	19885	0.96	2.2E-01	AI052190.1	EST_HUMAN	oz14a10.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
1545	11450	21311	3.13	2.2E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region
1972	11865	-	0.91	2.2E-01	AF171901.1	NT	Trimeresurus malabaricus cytb gene, partial cds; mitochondrial gene for mitochondrial product
2042	11933	21829	2.78	2.2E-01	M34640.1	NT	Fresh-water sponge Em11 alpha collagen (COLF1) gene
2354	12234	22131	6.24	2.2E-01	BF677538.1	EST_HUMAN	60208608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248969 5'
2543	12417	22307	2.41	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2543	12417	22308	2.41	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2853	12781	22570	4.04	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2853	12781	22571	4.04	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2890	12817		1.59	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3346	13266		2.67	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3743	13655		1.05	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4007	13913	23688	0.81	2.2E-01	AF213391.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4118	14018		1.19	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4125	14025	23800	5.07	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Konk6) genes, complete cds
4166	14066	23840	1.97	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mek1) mRNA, complete cds
4166	14066	23841	1.97	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mek4) mRNA, complete cds
4258	14157	23933	1.16	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4258	14157	23934	1.16	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4399	14294	24078	1.09	2.2E-01	Z54148.1	NT	B.abortus bp26 gene
4719	14605		1.22	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4724	14610	24396	2.47	2.2E-01	AA211216.1	EST_HUMAN	zq87c05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648963 5'
4891	14771	24549	1.19	2.2E-01	M86524.1	NT	Human dystrophin gene
4975	14850		1.2	2.2E-01	L13299.1	NT	Mus musculus vinculin gene, exon 3
5513	15431	25495	1.71	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5518	15436		3.99	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6189	16074	26223	10.59	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
6319	16182	26342	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
6319	16182	26343	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
6676	16566		2.19	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
7157	17034	27227	4.27	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7217	17094		2.29	2.2E-01	AW855039.1	EST_HUMAN	PM3-CT0263-241209-009-b07 CT0263 Homo sapiens cDNA
7270	17147	27341	1.66	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
7304	17180	27382	1.39	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA
7353	17221	27421	1.4	2.2E-01	W02988.1	EST_HUMAN	za04f08.r1 Scars melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:291591 5'
7366	17344	27550	13.13	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
7397	17315	27522	3.98	2.2E-01	M89643.1	NT	Brachydanio rerio apendynin beta and gamma chains (Epd) gene, complete cds
7648	17498	27720	3.57	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds; nuclear gene for chloroplast product
7719	17569	27794	2.2	2.2E-01	BF206507.1	EST_HUMAN	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
8723	18540	28824	4.94	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
8766	17905	28149	2.91	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
9077	18854		2.2	2.2E-01	BE870959.1	EST_HUMAN	601448957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
9183	19720		3.72	2.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CAL T), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
9269	18973		2.34	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
9379	15093	24887	2.56	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
9875	19713		3.75	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GK6 Homo sapiens cDNA clone GKGAHB02 5'
955	10879	20727	1.74	2.1E-01	AA569289.1	EST_HUMAN	nm31e1.s1 NCI CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
958	10881	20729	0.9	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1108	11023		2.16	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1180	11091	20936	1.24	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1180	11091	20937	1.24	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1871	11767	21642	1.84	2.1E-01	AA906824.1	EST_HUMAN	ok73e02.s1 NCI CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765
2111	12000	21899	3.08	2.1E-01	BF605073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2894	12821	22613	1.65	2.1E-01	6912445	NT	602038129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
3736	13648		5.05	2.1E-01	9838361	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3967	13874	23651	1.01	2.1E-01	P11675	SWISSPROT	Beta vulgaris mitochondrion, complete genome
3967	13874	23652	1.01	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4279	14178		1.28	2.1E-01	AB033041.1	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4474	14368	24157	1.21	2.1E-01	AB010273.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4766	14651	24439	1.26	2.1E-01	AJ009794.1	NT	Homo sapiens pshsp47 gene, complete cds
							Homo sapiens hox11 proto-oncogene, exons 1 to 3 and hug-1 gene

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5134	15001	24772	0.99	2.1E-01	M8281.1	NT	Saccharomyces cerevisiae tau138 (TFC3) gene, complete cds
5243	15167	24938	5.99	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
6123	15970	26106	1.86	2.1E-01	U04642.1	NT	Human difactory receptor (OR17-2) gene, partial cds
6385	16247		1.97	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
6535	16393	26572	1.74	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
6559	16417	26596	1.35	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6559	16417	26597	1.35	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6705	16585		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1B), mRNA
6951	16829	27022	4.78	2.1E-01	U68399.1	NT	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
7224	17101	27289	5.88	2.1E-01	Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w
7479	17349	27553	2.36	2.1E-01	X97378.1	NT	A.thaliana mRNA for ARA1BP1b protein
7547	17398	27611	1.19	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
7917	17757	28006	2.49	2.1E-01	Z97067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
7929	17779	28018	1.49	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIACYLGLYCEROL KINASE)
8849	18661		2.31	2.1E-01	11036647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
8862	18674	28964	2.15	2.1E-01	BE180422.1	EST_HUMAN	RC3-HT0622-040500-013-b11 HT0622 Homo sapiens cDNA
9522	19132		1.6	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
9730	19534		1.4	2.1E-01	L32586.1	NT	Human granulin gene
9905	19382	25174	1.29	2.1E-01	BE672330.1	EST_HUMAN	7a59c02.x1 NCI_OGAP_GC6 Homo sapiens cDNA clone IMAGE:3223034 3'
9979	19436		1.29	2.1E-01	5835904	NT	Salvelinus alpinus mitochondrion, complete genome
193	10165	19983	1.72	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for aveta, complete cds
523	10455		2.39	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
684	10617	20440	1.19	2.0E-01	M77085.1	NT	O.cuniculus germline IgH heavy chain V-H pseudogene, allotype VH2
793	10722	20563	1.81	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
995	10915	20759	1.03	2.0E-01	D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915
1109	11024	20866	2.57	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1234	11141	20983	1.42	2.0E-01	AJ132695.5	NT	Homo sapiens tac1 gene
1286	11194	21047	1.29	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1471	11376	21241	13.51	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1534	11438	21295	2.51	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1538	11442	21300	1.59	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1688	11590		1.82	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1723	11624		1.64	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1847	11743	21618	1.33	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1847	11743	21619	1.33	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
2299	12181		1.67	2.0E-01	X82877.1	NT	H. sapiens Nat-D-glucose cotransport regulator gene
2861	12789		0.95	2.0E-01	AF074990.1	NT	Homo sapiens full length insert cDNA YH5A11
3442	13359	23166	0.8	2.0E-01	P46607	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3520	13436		0.89	2.0E-01	AW236005.1	EST_HUMAN	xp15b02.x1 NCI CGAP HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3646	13560	23346	0.81	2.0E-01	P34641	SWISSPROT	MER21 repetitive element;
3945	13853	23628	0.8	2.0E-01	X83997.1	NT	CED-11 PROTEIN
4464	14358		8.47	2.0E-01	BE826165.1	EST_HUMAN	C.parasitica capC gene
4859	14739	24519	1.07	2.0E-01	AF147083.1	NT	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
4972	14847	24616	6.07	2.0E-01	8922030	NT	Homo sapiens gamma-glutamyl hydrolase gene, exons 8 and 9 and complete cds
5041	14913	24687	1.1	2.0E-01	Y19216.1	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5342	15263	25039	2.55	2.0E-01	X56600.1	NT	Homo sapiens putative psbHbD pseudogene for hair keratin, exons 1 to 9
5510	15428	25491	2.13	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5694	15603	25705	5.29	2.0E-01	U15300.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5874	15780	25900	4.31	2.0E-01	X61033.1	NT	Saccharomyces cerevisiae HalpA (HAL5) mRNA, complete cds
5834	15839	25962	3.54	2.0E-01	AW360865.1	EST_HUMAN	M. auratus mu class glutathione transferase gene
6637	16517		6.95	2.0E-01	AF028026.1	NT	PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA
6772	16651	26839	4.18	2.0E-01	XG1151.1	NT	Andes virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
7511	17299		4.39	2.0E-01	AE001278.1	NT	M. musculus scp2 gene exon 14
7692	17542		2.07	2.0E-01	AF146692.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
7774	17624	27857	1.95	2.0E-01	AF086907.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
7774	17624	27858	1.95	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
8214	18098	28350	2.7	2.0E-01	D89088.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
8214	18098	28351	2.7	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
9503	19118		1.37	2.0E-01	AF206637.2	NT	Salvelinus pluvius mRNA for transferrin, complete cds
9747	19308	25202	3.22	2.0E-01	AI023592.1	EST_HUMAN	Pimephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
9769	19288		6.61	2.0E-01	AF078164.2	NT	ov80a10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
							Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9897	19374	25193	1.5	2.0E-01	11528496	NT	Mus musculus fructosamine 3 kinase (Fn3k), mRNA
105	10086		10.35	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
349	10308	20126	6	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
640	10577	20392	1.31	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
640	10577	20393	1.31	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
647	10584	20400	5.37	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
648	10584	20400	7.32	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
970	10893		1.61	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA
1088	11004	20846	9.3	1.9E-01	AA358813.1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 5' end
1348	11254	21110	2.3	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1416	11322		3.91	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2330	12211	22109	3.31	1.9E-01	8922593	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2892	12819	22611	3.91	1.9E-01	U66086.1	NT	Sigmodon hispidus p53 gene, partial cds
2908	12834		5.55	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3349	13269	23072	3.4	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3434	13351	23156	4.63	1.9E-01	R16487.1	EST_HUMAN	yf42f10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'
3735	13647	23432	0.93	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
3762	13675	23457	0.96	1.9E-01	P39788	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
3910	13820	23600	3.02	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
3992	13899	23676	1.89	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4138	14038	23813	1.06	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-230700-007-c04 FN0010 Homo sapiens cDNA
4369	14265	24049	0.89	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
4662	14548	24338	0.84	1.9E-01	Z93780.1	NT	Fugu rubripes genes encoding carbamoyl phosphate synthetase III, myosin light chain, MAP2
4912	14791	24566	0.86	1.9E-01	AW849203.1	EST_HUMAN	IL3-CT0215-180200-087-D02 CT0215 Homo sapiens cDNA
4943	14821		1.04	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
4962	14837	24605	1.11	1.9E-01	O95239	SWISSPROT	KINESIN-LIKE PROTEIN KIF4
5031	14903	24676	1.03	1.9E-01	AJ251176.1	NT	Phoca vitulina partial aar2B gene for alpha adrenergic receptor 2B
5113	14981	24755	0.99	1.9E-01	Z70296.1	NT	S.mansoni elastase HP1 gene
5123	14991		1.19	1.9E-01	AI631199.1	EST_HUMAN	ts93g12.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2238886 3' similar to gb:M21574 ALPHA
5163	15020	24789	0.99	1.9E-01	8679095	NT	PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);
5441	15361		4.28	1.9E-01	AW130149.1	EST_HUMAN	Mus musculus Notch gene homolog 3, (Drosophila) (Notch3), mRNA
5466	15386	25446	7.67	1.9E-01	AF127937.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
							Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5588	15503		2.26	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6162	15119	24863	1.7	1.9E-01	R43212.1	EST_HUMAN	yg09a12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element
6423	16284	26446	1.43	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
6449	16310	26476	3.06	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
6658	16538	26735	1.62	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
7041	16918	27109	12.89	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
8038	17930	28176	2.16	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
8038	17930	28177	2.16	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
8137	18025	28271	1.75	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8961	18788	29060	2.61	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9546	19146		1.67	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
9880	19546		1.26	1.9E-01	AF001168.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds
29	10016	19811	2.26	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
260	12663	20041	1.22	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
366	10322	20145	2.41	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
729	10661	20493	2.15	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
966	10889	20735	0.85	1.8E-01	AI912212.1	EST_HUMAN	wd71f02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1075	10990	20832	1.21	1.8E-01	AF000580.1	NT	Dictyostelium discoideum plasmid Ddp5, complete genome
1267	11174	21024	5.28	1.8E-01	AL111789.1	NT	Yersinia pestis plasmid pCD1
1487	11392	21252	1.29	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1) mRNA
1487	11392	21253	1.29	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1) mRNA
1803	11700		0.92	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1823	11720		1.93	1.8E-01	AI733708.1	EST_HUMAN	qg22d10.x5 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:176181 3' similar to TR.O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE
1873	11769	21844	1.6	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya6, Scya6-ps, Scya6 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2680	12527		2.99	1.8E-01	AF935728.1	EST_HUMAN	QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA
2868	12796		1.61	1.8E-01	AF184589.1	NT	Jonopsidium aculea LEAFY protein (LEAFY2) gene, partial cds
2873	12800	22595	1.09	1.8E-01	AW182300.1	EST_HUMAN	xj41a03.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3085	13012	22803	1.28	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3570	13484	23275	1.07	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704.3' similar to contains Alu repetitive element;
3570	13484	23276	1.07	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704.3' similar to contains Alu repetitive element;
4154	14054	23928	0.8	1.8E-01	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
4238	14137		1.73	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DOB), complete cds
4456	14350	24141	5.12	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4663	14549	24339	2.36	1.8E-01	AB051897.1	NT	Mus musculus Soyab, Soyab, Soyab16-ps, Soyab5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Soyab16 pseudogene, small inducible cytokine A5 precursor, complete cds
4700	14586	24377	0.93	1.8E-01	X92179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
4977	14852	24618	1.77	1.8E-01	AW814270.1	EST_HUMAN	MF3-S.T0203-151299-112-g06 ST0203 Homo sapiens cDNA
5027	14900	24670	4.17	1.8E-01	AF181258.1	NT	Mesorhizobium lotus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5053	14925	24697	1.28	1.8E-01	AI439891.1	EST_HUMAN	t57e04.x1 NC1 CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134690.3'
5117	14985		1.03	1.8E-01	AJ00742.1	NT	Homo Sapiens histH1 gene, 5' UTR
5549	15465	25535	1.41	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5922	15927	25952	1.29	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
5948	15853		2.5	1.8E-01	N04853.1	EST_HUMAN	y62h02.11 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:278163.5'
6179	16065	26214	1.38	1.8E-01	AB018561.1	NT	Citrus latifolia mRNA for wsvs, complete cds
6179	16065	26215	1.38	1.8E-01	AB018561.1	NT	Citrus latifolia mRNA for wsvs, complete cds
7382	17251	27456	1.72	1.8E-01	MF73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
7396	17314	27521	1.22	1.8E-01	9626232	NT	Bacteriophage like, complete genome
7933	17783	28022	1.19	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
8033	17925	28172	3.19	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
8065	17956	28205	6.65	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysis genes, complete cds
8118	16065	26214	2.9	1.8E-01	AB018561.1	NT	Citrus latifolia mRNA for wsvs, complete cds
8118	16065	26215	2.9	1.8E-01	AB018561.1	NT	Citrus latifolia mRNA for wsvs, complete cds
8119	18007	28254	3.88	1.8E-01	AF019107.1	NT	Dicystosium discoideum unknown (DG1041) gene, complete cds
8381	18258	28507	2.64	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
8752	17907	28152	3.99	1.8E-01	X37033.1	NT	B.taurus mRNA for potassium channel
8976	18781	29073	2.83	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbxa2r), mRNA
9169	18912	25344	1.65	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NC1 CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156318.5'
9625	19200		2.05	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9738	19272		7.94	1.8E-01	R24494.1	EST_HUMAN	yf48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
9779	19294		1.63	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hxx1)
563	10503	20309	1.8	1.7E-01	BE385184.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
788	10717	20559	2.04	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
945	10870		1.89	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1042	10960	20802	1.6	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1042	10960	20803	1.6	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1938	11833		3.8	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2829	12758	22548	1.93	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2829	12758	22549	1.93	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2896	12823	22616	1.74	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2967	12894	22693	1.35	1.7E-01	AJ238736.1	NT	Naja naja atra ctk-1 gene, exons 1-3
2967	12894	22694	1.35	1.7E-01	AJ238736.1	NT	Naja naja atra ctk-1 gene, exons 1-3
3067	12994	22785	1.89	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
							Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3401	13318	23119	1.96	1.7E-01	AJ269505.1	NT	Homo sapiens hap1 gene, complete CDS
3557	13471	23262	1	1.7E-01	AJ224877.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL-IRX gene fused to intron 5 of the AF-4/FEL gene
3859	13770	23562	4.41	1.7E-01	AJ235377.1	NT	5 of the AF-4/FEL gene
4459	14353		1.88	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
							qh57e09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element ;
4732	14617	24403	1.4	1.7E-01	AJ247635.1	EST_HUMAN	Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds
4986	14861		1.16	1.7E-01	U28376.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5067	14937		1.18	1.7E-01	AF072725.1	NT	ne13a02.st1 NCL_CGAP_Cc8 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5321	15241	25046	1.76	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.st1 NCL_CGAP_Cc8 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5321	15241	25047	1.76	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.st1 NCL_CGAP_Cc8 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5820	15726	25839	12.31	1.7E-01	H72118.1	EST_HUMAN	ys02g06.st1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213688 3'
6112	18006		2.15	1.7E-01	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds

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6320	16183	26344	7.96	1.7E-01	BE734179.1	EST_HUMAN	601566022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
6588	16468	26658	1.2	1.7E-01	AF0000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
6814	16693	26882	7.03	1.7E-01	7709428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
6814	16693	26883	7.03	1.7E-01	7709428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
7066	16943	27135	2.46	1.7E-01	D00394.1	NT	Rat (SHR strain) SX1 gene
7531	17382	27593	7.38	1.7E-01	AF001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
7601	17452	27666	2.06	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
7875	17725		2.42	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C094
7942	17792	28032	1.48	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
7943	17793	28033	1.57	1.7E-01	AA627972.1	EST_HUMAN	h960e07.s1 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb.L25081 TRANSFORMING PROTEIN RHOC (HUMAN);
8067	17958	28208	9.13	1.7E-01	BE390835.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
8192	18068	28317	2.47	1.7E-01	AA814617.1	EST_HUMAN	af43a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
8456	18329	28589	7.88	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
8456	18329	28590	7.88	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
8949	18757		1.92	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9012	18811	29107	4.38	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
9139	19666		1.5	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9420	19513		1.28	1.7E-01	AB24404.1	EST_HUMAN	tx69g05.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb.M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
9705	19263	25218	5.79	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
120	10097	19917	1.88	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
664	12641	20416	1.53	1.6E-01	R31497.1	EST_HUMAN	yh75f12.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:135599 5'
1505	11409	21268	4.05	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1882	11778	21653	2.4	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
1941	11836		1	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2335	12719	22115	0.96	1.6E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2443	12320	22218	2.19	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2863	12791	22583	8.9	1.6E-01	AF185599.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2863	12791	22584	8.9	1.6E-01	AF185599.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3581	13495	23285	1.31	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3581	13495	23286	1.31	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3919	13828		2.61	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome

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4234	14132	23608	7.92	1.6E-01	AF179680.1	NT	Homo sapiens apelin gene, complete cds
4353	14249		2.44	1.6E-01	AW988601.1	EST_HUMAN	EST380677 MAGE sequences, MAGJ Homo sapiens cDNA
4361	14257		4.01	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4781	14665	24451	0.86	1.6E-01	Z28330.1	NT	S.cerevisiae chromosome XI reading frame ORF YKR105c
4781	14665	24452	0.86	1.6E-01	Z28330.1	NT	S.cerevisiae chromosome XI reading frame ORF YKR105c
4865	14745	24524	1.14	1.6E-01	AA088343.1	EST_HUMAN	z84h09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
4889	14769	24546	1.92	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV.;
4889	14769	24547	1.92	1.6E-01	AJ006356.1	NT	Lycopodium esculentum RsaI fragment 2, satellite region
4958	14833	24801	1.09	1.6E-01	BE018707.1	EST_HUMAN	Lycopodium esculentum RsaI fragment 2, satellite region
5390	15309	25162	3.12	1.6E-01	AW197496.1	EST_HUMAN	bb83h08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049023 5' similar to gb:M61715
5390	15309	25163	3.12	1.6E-01	AW197496.1	EST_HUMAN	TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X69657 M.musculus (MOUSE);
5398	15317	25364	2.07	1.6E-01	AF034716.1	NT	xm43f01.x1 NCL_CGAP_GG6 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
5873	15779	25898	2.24	1.6E-01	AL161588.2	NT	HYPOTHETICAL 127.6 KD PROTEIN;
5873	15779	25899	2.24	1.6E-01	AL161588.2	NT	HYPOTHETICAL 127.6 KD PROTEIN;
6157	15115	24858	3.7	1.6E-01	AW291215.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN;
6571	16429	26612	1.84	1.6E-01	AW246359.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN;
6592	16472	26962	1.42	1.6E-01	L49349.1	NT	HYPOTHETICAL 127.6 KD PROTEIN;
7187	17064	27254	1.89	1.6E-01	Z49501.1	NT	HYPOTHETICAL 127.6 KD PROTEIN;
7564	17415		1.7	1.6E-01	BF375171.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN;
7565	17416	27631	1.91	1.6E-01	Z49501.1	NT	HYPOTHETICAL 127.6 KD PROTEIN;
8049	17940	28190	2.71	1.6E-01	AW850853.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN;
8364	18241	28490	1.78	1.6E-01	O14647	SWISSPROT	HYPOTHETICAL 127.6 KD PROTEIN;
8364	18241	28491	1.78	1.6E-01	O14647	SWISSPROT	HYPOTHETICAL 127.6 KD PROTEIN;
8459	18332		7.6	1.6E-01	AF100064.1	NT	HYPOTHETICAL 127.6 KD PROTEIN;
8713	18530	28814	10.07	1.6E-01	6671552	NT	HYPOTHETICAL 127.6 KD PROTEIN;
9001	18804	29097	2.69	1.6E-01	AW877127.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN;
9025	19678		2.17	1.6E-01	6679466	NT	HYPOTHETICAL 127.6 KD PROTEIN;
9141	19806	28795	2.33	1.6E-01	AV719685.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN;
9565	19493		6.33	1.6E-01	AB045310.1	NT	HYPOTHETICAL 127.6 KD PROTEIN;
9727	19265		2.84	1.6E-01	AK024496.1	NT	HYPOTHETICAL 127.6 KD PROTEIN;

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9807	19319		2.47	1.6E-01	AF287344.1	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
9827	19328	25208	1.27	1.6E-01	9508522	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Ospg5), mRNA
248	10214	20030	1.87	1.5E-01	BE710087.1	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
248	10214	20031	1.87	1.5E-01	BE710087.1	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
572	12840		2.28	1.5E-01	AV711696.1	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
766	10697	20534	1.4	1.5E-01	AL163284.2	Homo sapiens chromosome 21 segment HS21C084
1076	10992	20834	0.88	1.5E-01	AJ009735.1	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1081	10997	20838	1.87	1.5E-01	AJ251885.1	Homo sapiens partial SL C22A2 gene for organic cation transporter (OCT2), exon 1
1097	11013		1.82	1.5E-01	L36125.1	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1198	11108	20953	1.36	1.5E-01	AW195516.1	xn3sd11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2896086 3'
1254	11161	21010	2.81	1.5E-01	D26535.1	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1254	11161	21011	2.81	1.5E-01	D26535.1	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1466	11371	21238	1.49	1.5E-01	AF117340.1	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
1866	11762	21636	1.54	1.5E-01	AW444451.1	UI-H-B13-akb-b-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2679	12544	22435	1.12	1.5E-01	BF696381.1	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
2999	12927	22719	0.89	1.5E-01	M81441.1	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3308	13229	23034	4.22	1.5E-01	AA935049.1	cc68d05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3322	13242	23048	0.87	1.5E-01	Z23104.1	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
3322	13242	23049	0.87	1.5E-01	Z23104.1	L.stagnalis mRNA for G protein-coupled receptor
3380	13298	23097	0.96	1.5E-01	AW612237.1	hh29f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2956539 3' similar to contains element MER16 repetitive element ;
3696	13610	23394	1.34	1.5E-01	U09964.1	Mus musculus ICR/Swiss glycerinaldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3706	13619	23403	185.26	1.5E-01	7108358	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3791	13703	23490	2.35	1.5E-01	AW665983.1	hjt0706.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3806	13718	23506	0.8	1.5E-01	AJ003165.1	Populus trichocarpa cv. Trichobal ABI3 gene
3806	13718	23507	0.8	1.5E-01	AJ003165.1	Populus trichocarpa cv. Trichobal ABI3 gene
3964	13871	23649	0.96	1.5E-01	AW366659.1	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA
4006	13912	23687	0.97	1.5E-01	Z12628.1	B.napus mitochondrial DNA for ORF158
4091	13991	23768	8.36	1.5E-01	AL163284.2	Homo sapiens chromosome 21 segment HS21C084
4623	14511	24301	1.34	1.5E-01	BF687665.1	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'

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4945	12544	22435	2.18	1.5E-01	BF96581.1	EST_HUMAN	802083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4980	14566	24361	1.08	1.5E-01	BE173796.1	EST_HUMAN	CMD-H10565-280200-245-b10 HT0565 Homo sapiens cDNA
4980	14566	24362	1.08	1.5E-01	BE173796.1	EST_HUMAN	CMD-H10565-280200-245-b10 HT0565 Homo sapiens cDNA
4929	14508	24578	1.3	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5072	14942	24716	0.84	1.5E-01	AF003105.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds
5216	15139	24833	2.02	1.5E-01	P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5266	15188		5.67	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
5400	15319	25367	4.06	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5424	15345	25398	6.77	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5424	15345	25399	6.77	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5652	15664	25660	1.9	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2) mRNA
5652	15664	25661	1.9	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2) mRNA
5684	15693	25694	1.87	1.5E-01	AJ276605.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
5760	15668	25774	2.44	1.5E-01	BE2727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
5785	15691		1.66	1.5E-01	4506396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
5828	15734	25845	1.78	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
5917	19455	25948	1.96	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
5935	15840	25963	5.13	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (O5ORF3), mRNA
5942	15847	25971	1.81	1.5E-01	P48508	SWISSPROT	GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
5972	15876	26000	2.09	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6031	15935	26067	1.4	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
6166	15123	24866	5.63	1.5E-01	AW970295.1	EST_HUMAN	EST382376 MAGE sequences, MAGK Homo sapiens cDNA
6284	16148		1.77	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
6374	16236	26396	1.88	1.5E-01	AI973157.1	EST_HUMAN	wf52c08.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
6481	16340	26507	1.68	1.5E-01	AW500611.1	EST_HUMAN	U1HF-BN0-akk-d-05-Q-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6481	16340	26508	1.68	1.5E-01	AW500611.1	EST_HUMAN	U1HF-BN0-akk-d-05-Q-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
							cc85g12.s1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
6786	16665	26856	1.22	1.5E-01	AA970317.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
6895	16774		11.77	1.5E-01	C16800.1	EST_HUMAN	C16800 Clontech human aorta poly+ mRNA (#6572) Homo sapiens cDNA clone GEN-529H109 5'
6912	16790	26983	1.88	1.5E-01	L27835.1	NT	Pangasinodon gigas growth hormone (GH) mRNA, complete cds
6996	16873	27064	1.44	1.5E-01	D84476.1	NT	Homo sapiens mRNA for ASK1, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7130	17007	27200	1.71	1.5E-01	4501972	NT	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
7265	17142	27335	2.48	1.5E-01	N74226.1	EST_HUMAN	zaf9e06.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:296866 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
7306	17182		2.98	1.5E-01	AV754819.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
7438	16451	26641	6.6	1.5E-01	U00455.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
7706	17556	27781	7.02	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7706	17556	27782	7.02	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7860	17710	27955	2.86	1.5E-01	X98852.1	NT	P. leniusculus mRNA for integrin beta subunit
7908	17758	27998	2.45	1.5E-01	AI814046.1	EST_HUMAN	wk53ht12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb.M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7908	17758	27999	2.45	1.5E-01	AI814046.1	EST_HUMAN	wk53ht12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb.M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7939	17789	28031	1.54	1.5E-01	U4032.1	NT	Danio rerio transcription factor Pax6b (Pax6) mRNA, complete cds
8009	17859	28103	1.35	1.5E-01	AJ011954.1	NT	Claviceps purpurea ps1 gene
8009	17859	28104	1.35	1.5E-01	AJ011954.1	NT	Claviceps purpurea ps1 gene
8199	18084	28334	5.15	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21G080
8199	18084	28335	5.15	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21G080
8342	18219		1.74	1.5E-01	AB042975.1	NT	Sus scrofa CYP81 gene for lanosterol 14 alpha-demethylase, exon 1
8425	18299	28555	1.73	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
8506	16236	26396	2.17	1.5E-01	AI973157.1	EST_HUMAN	wr52c08.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
9099	19647		20.02	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
9331	19565		4.14	1.5E-01	R83077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:194430 5'
9621	19588		2.14	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDA0D04 5'
9726	19497	25133	3.99	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 11/6
9932	19402	25179	3.01	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
9972	19432		1.58	1.5E-01	AF020346.1	NT	Rattus norvegicus pyridoxal kinase mRNA, complete cds
296	10260		1.96	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85S6P to TCRBV21S2A2 region
892	10818		2.57	1.4E-01	ID78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1238	11145		1.62	1.4E-01	T91864.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:112032 3'
1714	11615		1.43	1.4E-01	6679980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1717	11618	21487	1.53	1.4E-01	AE001170.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1863	11759		0.94	1.4E-01	AA135741.1	EST_HUMAN	UI-H-B1-acfa-a-09-0.U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1942	11837		10.35	1.4E-01	AA720615.1	EST_HUMAN	nv72d07.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2426	12303	22199	0.97	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2762	12624	22517	3.07	1.4E-01	A1933496.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3823	13735	23524	1	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
3823	13735	23525	1	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4083	13985	23762	8.38	1.4E-01	A1690094.1	EST_HUMAN	b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4083	13985	23763	8.38	1.4E-01	A1690094.1	EST_HUMAN	b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4144	14044	23817	3.16	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
							z550b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:X01057.maf1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element;
4313	14210		0.8	1.4E-01	AA776287.1	EST_HUMAN	
5032	14904		0.91	1.4E-01	AW866022.1	EST_HUMAN	QV3-SN0022-100500-186-h09 SN0022 Homo sapiens cDNA
5116	14984	24759	1	1.4E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment: HS21C084
5147	15014	24784	0.81	1.4E-01	AJ005180.1	NT	Lycopodium esculentum genomic RAPD band 26
5248	15171	24944	4.5	1.4E-01	T90677.1	EST_HUMAN	ye15c11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5267	15189	24963	4.29	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5267	15189	24964	4.29	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5805	15710	25823	2.72	1.4E-01	BE329891.1	EST_HUMAN	hr67c02.x1 NCI_CGAP_K1d17 Homo sapiens cDNA clone IMAGE:3133538 3'
5903	15809	25934	5.64	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5903	15809	25935	5.64	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5959	15863	25985	3.07	1.4E-01	AW082796.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
5959	15874		1.56	1.4E-01	BE263536.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
5982	15887	26009	1.89	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM00336-080300-103-409 UM00336 Homo sapiens cDNA
6371	16233		1.62	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-aat-c-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
6936	16814		1.33	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'
7167	17044	27236	4.48	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
7300	17176	27377	8.05	1.4E-01	BF310959.1	EST_HUMAN	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
7343	17211	27410	1.36	1.4E-01	W93411.1	EST_HUMAN	zd9a04.r1 Soares_fetal_heart_NBH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element;
7387	17256	27461	1.56	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
7387	17256	27462	1.56	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
7436	18449	26639	2.03	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase 1a1 (IAL), and zinc finger protein (DNZ1) genes, complete cds
8091	17982		2.02	1.4E-01	AA811400.1	EST_HUMAN	oa99a03.s1 NCI_CGAP_GOB1 Homo sapiens cDNA clone IMAGE:1320364 3'
8216	18100	28352	3.28	1.4E-01	R53401.1	EST_HUMAN	y70c05.r1 Soares breast 2NB1Bst Homo sapiens cDNA clone IMAGE:154088 5'
8613	18480	28751	1.89	1.4E-01	X66092.1	NT	C.perfringens ORF for putative membrane transport protein

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8764	17913	28158	2.23	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
8813	18626		3.02	1.4E-01	X52102.1	NT	M. musculus p16K gene for 16 kDa protein
9365	19517	25138	1.48	1.4E-01	AB000890.1	NT	Ephydratia fluviatilis mRNA for aldolase, partial cds
9433	19065	25277	2.32	1.4E-01	X74773.1	NT	P. salina plastid gene secY
9427	19073		1.89	1.4E-01	11968117	NT	Rattus norvegicus desmin (Des), mRNA
9470	19734		1.82	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
9560	19156		3.01	1.4E-01	AF089221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transformylase (GART) genes, complete cds
9573	19163		2.29	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2866767-3002965
9646	19764		3.28	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
9762	19282		1.41	1.4E-01	BE782738.1	EST_HUMAN	60146575F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3668795 5'
9831	19332		1.42	1.4E-01	11425031	NT	Homo sapiens ephrin-B3 (EFNB3), mRNA
9850	19566		3.41	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
9926	19398		1.77	1.4E-01	AW377998.1	EST_HUMAN	MF0-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
319	10281	20098	2.69	1.3E-01	4759467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
319	10281	20099	2.69	1.3E-01	4759467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
518	10460	20271	1.86	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
620	10557	20369	0.89	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
620	10557	20370	0.89	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
826	10763	20603	1.09	1.3E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
876	10802	20652	1.83	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1010	10928	20771	1.55	1.3E-01	AL1117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1111	11026		2.23	1.3E-01	AL115285.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1197	11107	20952	1.07	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'
1426	11331		1.36	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1916	11811	21689	2.56	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2124	12012		1.29	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidophila pucB5, pucA5, pucB6, pucA7, pucB7, pucA8, pucB8, pucA9 and pucC genes and ORF151
2245	12129		1.17	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2329	12210		2.99	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2542	12416	22306	3.49	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds

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3404	13321	23122	0.95	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3661	13575	23362	1.18	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3661	13575	23363	1.18	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3667	13581	23368	0.78	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrolipoyl dehydrogenase 4 [AKR1C4], exon 2
3714	13575	23362	0.86	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3714	13575	23363	0.86	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3734	13646	23431	0.85	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
3906	13816		1.7	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4046	13948		1.15	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4066	13968		3.44	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081259-036-a03 DT0018 Homo sapiens cDNA
4075	13977	23756	1.89	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4093	13993	23770	16.36	1.3E-01	AW273741.1	EST_HUMAN	xy23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4192	14092	23870	0.85	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPd Homo sapiens cDNA clone NPDAZE02 5'
4192	14092	23871	0.85	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPd Homo sapiens cDNA clone NPDAZE02 5'
4218	14116		1.65	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4433	14328	24116	2.16	1.3E-01	BE272339.1	EST_HUMAN	6011260995F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
4526	14418	24202	0.81	1.3E-01	BF679654.1	EST_HUMAN	602154306F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295544 5'
4771	15075		3.17	1.3E-01	BE884017.1	EST_HUMAN	601510347F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911987 5'
4903	14783		0.86	1.3E-01	AU136619.1	EST_HUMAN	AU136619 PLACE1 Homo sapiens cDNA clone PLACE1004693 5'
5074	14944	24718	1.21	1.3E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5074	14944	24719	1.21	1.3E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5173	15039	24805	0.9	1.3E-01	BF679819.1	EST_HUMAN	602154401F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295305 5'
5173	15039	24806	0.9	1.3E-01	BF679819.1	EST_HUMAN	602154401F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295305 5'
5292	15213	25013	2.51	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA
5428	15348		1.79	1.3E-01	AF058880.1	NT	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds
5904	15810	25936	13.21	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
5956	15861	25983	2.04	1.3E-01	X88891.1	NT	C.jacchus intron 4 of visual pigment gene (red allele)
6305	16169		2	1.3E-01	H46894.1	EST_HUMAN	yc3402.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:207075 5'
6649	16529	26723	1.34	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
6668	16548	26744	1.28	1.3E-01	BF690522.1	EST_HUMAN	6021870151T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
6858	16737		4.54	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
6886	16765		4.14	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
6960	16838	27031	1.27	1.3E-01	BF690522.1	EST_HUMAN	6021870151T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
7452	17261	27457	4.45	1.3E-01	AF023129.1	NT	Oryzodagus cuniculus Ht+K+ATPase alpha 2c subunit mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8029	17921		2.88	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-H08 BT0358 Homo sapiens cDNA
8444	18318	28577	1.83	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
8576	18444		5.13	1.3E-01	9671745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
8873	18685	28076	3.72	1.3E-01	BE270449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
9261	18966	25320	1.97	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3666003 5'
9399	19054		3.18	1.3E-01	AJ242790.1	NT	Gallus gallus sox1 gene for lymphotactin, exons 1-3
9757	19279		1.56	1.3E-01	AB026829.1	NT	Ephydratia fluviatilis mRNA for sALK-6, complete cds
9784	19297		1.32	1.3E-01	AW001114.1	EST_HUMAN	wu24d09.x1 Soares_Dieckgraefe_color_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O60287 O60287 KIAA0539 PROTEIN. ;
9945	19414		1.26	1.3E-01	BF571764.1	EST_HUMAN	602078440F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4253049 5'
378	10362	20185	7.21	1.2E-01	AJ421744.1	EST_HUMAN	#39b02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rna1
418	9985		1.55	1.2E-01	U66912.1	NT	ANNEXIN V (HUMAN);
535	10476		2.63	1.2E-01	AF039442.1	NT	Dictyostellum discoideum ORF DG1016 gene, partial cds
1355	11261	21117	2.78	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1355	11261	21118	2.78	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1361	11267		3.94	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1490	11395		1.13	1.2E-01	AA897474.1	EST_HUMAN	AV735249 cdA Homo sapiens cDNA clone cdAAJB11 5'
1613	11517	21377	1.17	1.2E-01	Q14694	SWISSPROT	al48a09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
1631	11535	21396	2.62	1.2E-01	AJ285402.1	EST_HUMAN	Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1730	11631		29.48	1.2E-01	X89211.1	NT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1877	11773		1.43	1.2E-01	AW449368.1	EST_HUMAN	qt89f09.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
2134	12022	21919	2.1	1.2E-01	AF248490.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
2240	12124	22025	1.01	1.2E-01	AL163213.2	NT	UI-H-B13-aki-e-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2546	12420	22310	2.02	1.2E-01	AW966556.1	EST_HUMAN	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
							Homo sapiens chromosome 21 segment HS21C013
							QV3-BN0046-220300-129-F10 BN0046 Homo sapiens cDNA
2697	12561	22451	0.86	1.2E-01	AJ623388.1	EST_HUMAN	ts18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048
2812	12741	22537	1.5	1.2E-01	U18018.1	NT	COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN, [1] ;contains element PTR5 repetitive element ;
2872	12799	22594	1.96	1.2E-01	AJ720470.1	EST_HUMAN	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2904	12831	22628	2.89	1.2E-01	M16364.1	NT	as80cd09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L06095
							60S RIBOSOMAL PROTEIN L30 (HUMAN);
							Human creatine kinase-B mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2974	12901	22700	0.98	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3192	13117	22923	2	1.2E-01	AW370668.1	EST_HUMAN	QV1-BT0259-261099-021-d05 BT0259 Homo sapiens cDNA
3219	13143		0.97	1.2E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3433	13350		0.79	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3477	13393	23198	1.14	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3477	13393	23199	1.14	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3554	13350		1.2	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3704	13617		0.88	1.2E-01	BF128551.1	EST_HUMAN	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053668.3'
4090	13990	23765	2.2	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
4090	13990	23767	2.2	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
5012	14886		1.04	1.2E-01	P16466	SWISSPROT	HEMOLYSIN PRECURSOR
5174	15040	24807	1.47	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I
5174	15040	24808	1.47	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I
5199	15062		2.47	1.2E-01	AW401836.1	EST_HUMAN	U1-HF-BKO-aah-d-01-q-U1r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053617.5'
5251	15174	24947	2.63	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:321699.5'
5297	15218	25021	1.9	1.2E-01	Z98266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5762	15669	25776	1.69	1.2E-01	BE620945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613.5'
5806	15711	25824	2.19	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
5839	15745	25858	1.56	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6607	16487		1.21	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA
6642	16522	26715	2.46	1.2E-01	AI913753.1	EST_HUMAN	wc99g03.x1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:2326804.3' similar to SW:GST2_HUMAN
6893	16772		9.72	1.2E-01	AW083652.1	EST_HUMAN	Q99735 MICROSMAL GLUTATHIONE S-TRANSFERASE II ; xc49d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597.3' similar to gb:M13452 LAMIN A (HUMAN);
6904	16782		3.86	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
7043	16920		2.27	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
7521	17340	27546	1.5	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
7747	17597	27819	1.51	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CuAAKE08.5'
8260	18140		2.95	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
8417	18291		3.35	1.2E-01	BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283.3'
8487	18360		1.93	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103.5'
8579	18447	28715	2.6	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8798	18612		2.02	1.2E-01	M85109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
9032	18822		2.22	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFIB12 3'
9393	19043		2.78	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
9458	19693	24897	2.58	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
9567	10476		7.69	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
9671	19230		1.41	1.2E-01	X53881.1	NT	R.norvegicus NF68 gene for 68kDa neurofilament
9739	19706	24903	2.36	1.2E-01	BE061418.1	EST_HUMAN	QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
9781	19281	25231	3.68	1.2E-01	AI269903.1	EST_HUMAN	qnt20g05.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
9782	19295		2.07	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
9786	19636		4.72	1.2E-01	O96493	SWISSPROT	CYCLIN T
9960	19424		2.18	1.2E-01	BF314481.1	EST_HUMAN	6019007/63F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
552	10493	20301	0.95	1.1E-01	AI561003.1	EST_HUMAN	tn18d08.x1 NCL CGAP_Co10 Homo sapiens cDNA clone IMAGE:2167983 3'
599	10535	20344	3.38	1.1E-01	AA569006.1	EST_HUMAN	nm03g111.s1 NCL CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb.X06985_rna1
1038	10956	20799	1.53	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN); 602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1069	10985		1.29	1.1E-01	AL161590.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1143	12686	20899	4.06	1.1E-01	AW972158.1	EST_HUMAN	EST384142 IMAGE resequences, MAGL Homo sapiens cDNA
1229	11137	20990	1.72	1.1E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2888767-3002965
1504	11408	21267	2.47	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2266	12150		2.25	1.1E-01	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptrra), mRNA
2492	12663		1.17	1.1E-01	6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2520	12394		1.17	1.1E-01	AW821909.1	EST_HUMAN	RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
2825	12764	22546	1.84	1.1E-01	S82418.1	NT	interleukin-12 p35 subunit [mouse, Genomic, 700 nt, segment 4 of 5]
2997	12925	22717	0.8	1.1E-01	F03265.1	EST_HUMAN	HSC1R1022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3299	13221		1.39	1.1E-01	6763231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Ca α 1g), mRNA
3374	13293	23092	3	1.1E-01	BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3405	13322	23123	1.54	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3534	13450	23246	0.94	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
3648	13562	23348	1.23	1.1E-01	X62708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4021	13925	23698	1.31	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4021	13925	23699	1.31	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4027	13930						Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds;
4159	14089		0.87	1.1E-01	AF030001.1	NT	Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete cds
4189	14089	23867	7.93	1.1E-01	AF157066.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4466	14360	24150	0.8	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4539	14432		0.91	1.1E-01	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4725	14611	24397	2.02	1.1E-01	S44957.1	NT	Tape-1=Integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4819	14702	24487	1.26	1.1E-01	Y07695.1	NT	A. immersus gene for transposase
5479	15399		1.26	1.1E-01	D90908.1	NT	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234
5562	15479	25551	1.43	1.1E-01	AA747216.1	EST_HUMAN	nx76a03.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element ;
5579	15494	25570	1.54	1.1E-01	X68851.1	NT	S. pombe ste8 gene encoding protein kinase
5672	15581	25681	4.73	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
5687	15596	25697	1.46	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
5697	15606	25708	1.79	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
5876	15782	25903	7.01	1.1E-01	AW853699.1	EST_HUMAN	RC3-C.T0254-280999-011-a01 CT0254 Homo sapiens cDNA
5985	15890	26012	1.39	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6027	15931		3.48	1.1E-01	Q69635	SWISSPROT	ACETYL-COENZYMASE A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME)
6068	16062	26198		1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6448	16309	26474	2.9	1.1E-01	11492372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
6448	16309	26475	2.21	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
6513	16372	26550	7.05	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
6531	16390	26570	1.74	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
6777	16656	26845		1.1E-01	AA788784.1	EST_HUMAN	ah31b06.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483 CHROMOGRAMIN A PRECURSOR (HUMAN);
6777	16656	26846	3.07	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
6803	16682	26872	1.57	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
6826	16705		1.22	1.1E-01	X91233.1	NT	H. sapiens IL15 gene
6862	16741	26934	1.24	1.1E-01	AW817918.1	EST_HUMAN	PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA
7118	16995	27186	1.78	1.1E-01	AL134349.1	EST_HUMAN	DKFZp547P194.J1 547 (synonym: hnf1r1) Homo sapiens cDNA clone DKFZp547P194 5'
			2.19	1.1E-01	U02482.1	NT	Pedibococcus acidilactici H plasmid pSMB74 pedlactin AcH production (pap) gene cluster papA, papB, papC and papD genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
7228	17105	27294	2.24	1.1E-01	AA192163.1	EST_HUMAN
7228	17105	27295	2.24	1.1E-01	AA192163.1	EST_HUMAN
7287	17163	27362	2.48	1.1E-01	T72675.1	EST_HUMAN
7467	17327		2.08	1.1E-01	BF085149.1	EST_HUMAN
7861	17711		1.23	1.1E-01	R80590.1	EST_HUMAN
8181	12925	22717	1.84	1.1E-01	F03265.1	EST_HUMAN
8294	18173		3.88	1.1E-01	AF169032.1	NT
8402	18278	28530	2.93	1.1E-01	R23708.1	EST_HUMAN
8519	18391	28655	1.95	1.1E-01	X70058.1	NT
8539	18411	28676	3.21	1.1E-01	Z11910.1	NT
8539	18411	28677	3.21	1.1E-01	Z11910.1	NT
8626	18491	28763	2.79	1.1E-01	P17437	SWISSPROT
9241	18956		3.19	1.1E-01	BE767023.1	EST_HUMAN
9485	19507		2.06	1.1E-01	BE974556.1	EST_HUMAN
9893	19372	25192	2.14	1.1E-01	BF238753.1	EST_HUMAN
1183	11094		4.08	1.0E-01	O62885	SWISSPROT
1251	11188	21007	1.89	1.0E-01	AI985499.1	EST_HUMAN
1370	11276	21132	2.88	1.0E-01	AL161504.2	NT
2439	12316	22213	1	1.0E-01	AW451365.1	EST_HUMAN
3488	13384	23189	0.98	1.0E-01	BF033991.1	EST_HUMAN
3658	13572	23359	1.01	1.0E-01	BF239818.1	EST_HUMAN
3871	13782	23574	2.44	1.0E-01	BF366703.1	EST_HUMAN
4307	14204	23987	1.5	1.0E-01	AE002266.2	NT
4455	14349		1.17	1.0E-01	AF923349.1	EST_HUMAN
4613	14501	24289	1.26	1.0E-01	U50450.1	NT
4838	14719	24502	2.06	1.0E-01	AW952344.1	EST_HUMAN
5158	15025	24792	0.87	1.0E-01	D49683.1	NT
5188	15051	24815	1.44	1.0E-01	BF515935.1	EST_HUMAN
5260	15182		9.16	1.0E-01	W86490.1	EST_HUMAN
5670	15580	25680	11.21	1.0E-01	AF274875.1	NT
						Top Hit Descriptor
					EST_HUMAN	z93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
					EST_HUMAN	z93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
					EST_HUMAN	y019h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to
					EST_HUMAN	gb:M81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
					EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
					EST_HUMAN	y86a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
					EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
					NT	Carassius auratus actvln beta A precursor, mRNA, complete cds
					EST_HUMAN	y035f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131769 5' similar to contains Alu
					NT	repetitive element; contains TAR1 repetitive element ;
					NT	M.musculus cytokine gene
					NT	Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
					NT	Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
					SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
					EST_HUMAN	RG2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
					EST_HUMAN	601680561R2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950604 3'
					EST_HUMAN	601908350F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4134085 5'
					SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
					EST_HUMAN	ws08d01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7 t3
					EST_HUMAN	MER7 repetitive element ;
					NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
					EST_HUMAN	UI-H-B13-alc-d-07-0-UI.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
					EST_HUMAN	601456301F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3855849 5'
					EST_HUMAN	601908489F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4134071 5'
					EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
					NT	Chlamydomonas pneumoniae AR39, section 91 of 94 of the complete genome
					EST_HUMAN	an32c04.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
					NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
					EST_HUMAN	EST364414 MAGC resequences, MAGB Homo sapiens cDNA
					NT	Mouse FTZ-F1 gene
					EST_HUMAN	UI-H-BW1-aca-e-12-0-UI.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084023 3'
					EST_HUMAN	zh62h04.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3'
					NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6187	16072		1.88	1.0E-01	R23821.1	EST_HUMAN	y34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
6549	16407		2.45	1.0E-01	Y12498.1	NT	Mimusculus wlnr gene
7299	17175	27376	1.16	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synamon mRNA, complete cds
7473	17333		1.8	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
7505	17293		2.73	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
7651	17501	27724	1.84	1.0E-01	BE240154.1	EST_HUMAN	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
7713	17563	27788	9.08	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7713	17563	27789	9.08	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7918	17768	28007	1.26	1.0E-01	BE792750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939096 5'
8050	17941		2.02	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
8393	18269	28520	2.9	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
8393	18269	28521	2.9	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
8703	18521	28803	4.43	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
9226	19285		2.5	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
9453	19085		1.34	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
9469	19098		2.03	1.0E-01	X00854.1	NT	Drosophila melanogaster ftz gene
9735	19688		2.57	1.0E-01	U82691.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
9765	19285		2.46	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
9818	19664		8.59	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
9871	19360	25187	1.28	1.0E-01	AJ271049.1	NT	Zea mays mRNA for Toc34-2 protein (toc34B gene)
9877	19363		4.16	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2752	12614	22505	1.09	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R1I) mRNA, complete cds
2757	12619	22511	1.44	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3455365 5'
2757	12619	22512	1.44	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3455365 5'
2950	12877	22675	0.92	9.9E-02	AV730747.1	EST_HUMAN	AV730747 HTF Homo sapiens cDNA clone HTFBND05 5'
3229	13153	22952	1.15	9.9E-02	AF099810.1	NT	Homo sapiens neurxin III-alpha gene, partial cds
4582	14472	24260	22.55	9.9E-02	BE674249.1	EST_HUMAN	7d77c12.x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278998 3'
6161	15118	24962	7.96	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blebicidin S deaminase, complete cds
7332	17236	27440	1.5	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
5511	10492		1.58	9.8E-02	X56338.1	NT	O sativa RAmY3C gene for alpha-amylase
17111	11612	21482	1.53	9.8E-02	4503224	NT	Homo sapiens cytochrome P450, subfamily 11F, polypeptide 1 (CYP2F1) mRNA
3106	13032	22827	3.28	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4131	14031	23805	6.67	9.8E-02	AF257329.1	NT	Leptospaeria maculans beta-tubulin mRNA, complete cds
4131	14031	23806	6.67	9.8E-02	AF257329.1	NT	Leptospaeria maculans beta-tubulin mRNA, complete cds
8755	17904	28148	2.1	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
1328	11235	21092	1.16	9.7E-02	AB005608.1	NT	Alce arborescens mRNA for NADP-malic enzyme, complete cds
1567	11471		0.98	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2214	12100	22004	2.37	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3901	13811		3.56	9.7E-02	Q89795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5661	15572	25669	1.39	9.7E-02	AW954476.1	EST_HUMAN	EST366546 MAGE resequences, MAGC Homo sapiens cDNA
6321	16184	26345	4.27	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 29877771 to 32134410
6655	16535	26731	1.59	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
6655	16535	26732	1.59	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7137	17014	27207	1.32	9.7E-02	A1953984.1	EST_HUMAN	wx78b06.x1 NCL CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2649747 3' similar to gb:X52851_ma1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
8531	18403		1.97	9.7E-02	U98337.1	NT	Mus musculus ligatin (Lgtn) mRNA, partial cds
1969	11862	21753	1.27	9.6E-02	A1080721.1	EST_HUMAN	oz47d11.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
1969	11862	21754	1.27	9.6E-02	A1080721.1	EST_HUMAN	oz47d11.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4248	14147	23921	6.02	9.6E-02	Z32686.2	NT	Proteus mirabilis fimbrial operon, strain HI4320
4932	14810	24579	0.94	9.6E-02	AW966230.1	EST_HUMAN	EST378303 MAGE resequences, MAGI Homo sapiens cDNA
5093	14963	24738	0.8	9.6E-02	BE061729.1	EST_HUMAN	RC6-BT0254-031099-011-a03 BT0254 Homo sapiens cDNA
5713	15621		2.72	9.6E-02	BE910039.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
7502	17371	27580	1.51	9.6E-02	AV687898.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAH02 5'
7677	17527		1.84	9.6E-02	BE894895.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
7772	17622	27855	1.75	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
7772	17622	27856	1.75	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
7839	17689	27933	1.59	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
7839	17689	27934	1.59	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
7886	17736	27980	3.29	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
8125	18013	28260	6.51	9.6E-02	Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162
8957	18764	29056	1.8	9.6E-02	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
9798	19312		1.38	9.6E-02	H14599.1	EST_HUMAN	ym19h03.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:48663 3'
9848	19344	28212	1.26	9.6E-02	BE728219.1	EST_HUMAN	601563355F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832908 5'
4012	13918	23694	2.25	9.5E-02	AW992395.1	EST_HUMAN	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
5082	14932	24704	0.87	9.5E-02	U63374.1	NT	Lycopodium esculentum polygalacturonase isoenzyme 1 beta subunit gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5323	16186	26348	3.72	9.5E-02	AB003473.1	NT	Trimerus flaviviridis DNA for phospholipase A2 inhibitor, complete cds
6467	16327	26494	7.46	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
9599	16479	26666	2.59	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
5599	16479	26667	2.59	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8066	17957	28206	3.29	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8066	17957	28207	3.29	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
1792	11690	21565	3.86	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
1820	11717	21597	0.86	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1820	11717	21598	0.86	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3804	13716	23504	4.34	9.4E-02	Z33059.1	NT	M. capricolum DNA for COX10G MC073
4980	14855	24621	0.89	9.4E-02	6753517	NT	Mus musculus coding region determinant-binding protein (Crdp), mRNA
6999	16876		2.62	9.4E-02	Z46863.1	NT	Acinetobacter sp. cysD, cobQ, cobM, lysS, rubA, rubB, estB, oxyR, ppk, mlgA, ORF2 and ORF3 genes
8304	16338	26505	2.69	9.4E-02	L78633.1	NT	Human BRCA1, Rho7 and vatl genes, complete cds, and ipf35 gene, partial cds
9033	19603		3.36	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
9943	19411	25182	1.42	9.4E-02	U27699.1	NT	Human pepHGT-1 betaine-GABA transporter mRNA, complete cds
2960	12887		1.83	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
2993	12921		5.39	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3218	13142	22945	2.03	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4060	13962	23738	3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4050	13962	23739	3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4628	14516		1.88	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
7599	17460	27665	2.24	9.3E-02	BE962631.2	EST_HUMAN	601655988F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
7855	17705	27949	3.52	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7855	17705	27950	3.52	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7913	17763		3.74	9.3E-02	AW206117.1	EST_HUMAN	U1-H-B1-afx-h-05-0-U1.51 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
9343	19527		1.85	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
9704	19555		8.62	9.3E-02	AW468850.1	EST_HUMAN	hd28h12x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Blnh1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
9806	19602		1.95	9.3E-02	AF100956.1	NT	galactosyl transferase (beta1,3-galactosyl tr>
228	10197	20008	4.32	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	10197	20009	4.32	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	10197	20010	4.32	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2180	12067		2.2	9.2E-02	R54156.1	EST_HUMAN	y99807.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3142	13067	22866	4.53	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3265	13188	22986	1.16	9.2E-02	AA534354.1	EST_HUMAN	nt79e01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:926136 3'
3537	13453		1.12	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra). mRNA
4145	14045		1.34	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4211	14109		1.02	9.2E-02	BE299722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
4538	14431	24213	1.86	9.2E-02	X96402.1	NT	G.gallus Mia-OK gene
6670	18550	26746	1.86	9.2E-02	T49920.1	EST_HUMAN	y99c09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
6756	16635	26823	2.07	9.2E-02	X95256.1	NT	H.vulgaris xylose isomerase gene
417	9984	19776	2.77	9.1E-02	X77665.1	NT	O. cuticulus k12 keratin gene
2365	12245	22139	1.01	9.1E-02	P78985	SWISSPROT	6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)
3618	13532		1.14	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161299-001-f02 BT0349 Homo sapiens cDNA
4383	14279	24058	1.81	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5507	15425	25487	1.73	9.1E-02	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G6b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
6372	18234	26393	11.89	9.1E-02	AW160658.1	EST_HUMAN	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7958	17808		1.65	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3' end
9021	18815		1.29	9.1E-02	9633494	NT	Bacteriophage Mu, complete genome
9256	19692		1.52	9.1E-02	AA179901.1	EST_HUMAN	zc38h12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
9785	19548		5.63	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
727	10659	20490	3.36	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1617	11521	21379	6.45	9.0E-02	BE220482.1	EST_HUMAN	h93g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2772	12634	22528	1.11	9.0E-02	AF139522.1	NT	HIV-1 pbc095-06 from USA envelope glycoprotein (env) gene, partial cds
2772	12634	22529	1.11	9.0E-02	AF139522.1	NT	HIV-1 pbc095-06 from USA envelope glycoprotein (env) gene, partial cds
3294	13216	23018	0.92	9.0E-02	AF279135.1	NT	Dicotyledonous dicotyledon spore coat structural protein SP66 (coIE) gene, complete cds
4202	14101	23883	0.8	9.0E-02	S98757.1	NT	cardiac steroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4202	14101	23884	0.8	9.0E-02	S98757.1	NT	cardiac steroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4321	14218	24001	1.2	9.0E-02	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4568	14460	24248	1.79	9.0E-02	X95740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5142	15009	24780	1.06	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZESTE
5647	15560	25653	8.02	9.0E-02	W56037.1	EST_HUMAN	PIR:S52171 S52171 small G protein - human ;
9967	19428		15.35	9.0E-02	11431759	NT	Homo sapiens chromosome 16 open reading frame 5 (C16orf5), mRNA
1419	11325	21189	2.15	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1419	11325	21190	2.15	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2338	12218	22117	1.41	8.9E-02	BE153572.1	EST_HUMAN	PMO-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4104	14004		1.71	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds
4534	14427	24208	0.92	8.9E-02	AA424887.1	EST_HUMAN	zw03d04.s1 Soares_NHMFu_S1 Homo sapiens cDNA clone IMAGE:768199 3'
5569	15485	25559	3.3	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alo-f08-Q-UI.s1 NCI_OGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5569	15485	25560	3.3	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alo-f08-Q-UI.s1 NCI_OGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5576	15491	25568	3.13	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
6270	16135	26290	1.56	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE]
6460	16320		1.83	8.9E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8
6998	16875	27066	5.28	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9228	18949		4.03	8.9E-02	BF698918.1	EST_HUMAN	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
1351	11257	21113	1.25	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3828	13740	23532	0.96	8.8E-02	AA299128.1	EST_HUMAN	EST11585 Uterus Homo sapiens cDNA 5' end
3948	13856		3.24	8.8E-02	Q00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII135) (TAFII130)
4205	14104		1.13	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
7195	17072	27260	1.83	8.8E-02	AA151872.1	EST_HUMAN	zn99a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
8461	18334	28596	3.19	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
8461	18334	28597	3.19	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
8585	18453	28722	10.63	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1313 5'
9302	19001	25332	1.38	8.8E-02	Z71561.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL285w
3636	13550	23337	3.02	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3636	13550	23338	3.02	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3879	13790	23578	0.82	8.7E-02	W87841.1	EST_HUMAN	zh86a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:417194 5' similar to contains element MER12 repetitive element;
4609	14497	24286	1.22	8.7E-02	AF178638.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5034	14906		1.06	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5255	15177	24951	5.41	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_OGAP_GOB1 Homo sapiens cDNA clone IMAGE:701438 3'
5255	15177	24952	5.41	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_OGAP_GOB1 Homo sapiens cDNA clone IMAGE:701438 3'
8094	17985		2.58	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
8631	18496	28770	1.77	8.7E-02	AJ007783.1	NT	Glucobacter oxydans RNA-1le and RNA-Ala genes
9293	18994		2.58	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
9494	19105		1.81	8.7E-02	6679057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1232	11139	20991	7.05	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2197	12084	21986	2.22	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3151	13076	22876	2.94	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3593	13507		3.07	8.6E-02	AF153362.1	NT	Dicystostelium discoideum adenylyl cyclase (acrA) gene, complete cds
4385	14281	24060	0.87	8.6E-02	U68179.1	NT	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region
5708	15616	25718	4.38	8.6E-02	Y10828.1	NT	Homo sapiens LCN1b gene
5846	15762	26867	1.51	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
5846	15762	26868	1.51	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6628	16508	26995	1.26	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
6628	16508	26996	1.26	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8315	18192	28441	1.98	8.6E-02	AF208551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8315	18192	28442	1.98	8.6E-02	AF208551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8574	18442	28710	3.63	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
8574	18442	28711	3.63	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
8736	17887	28131	4.71	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
8868	18670	28958	1.73	8.6E-02	AF283660.1	NT	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
2347	12227	22124	2.87	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5500	15419		1.8	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
5688	15570	25665	5.34	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
7003	16880	27072	1.93	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7661	17511	27737	3.07	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
7661	17511	27738	3.07	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
8496	18369		11.15	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
8512	18384	28649	4.07	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
9681	19488		1.39	8.5E-02	AJ005596.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
9847	19339		3.28	8.5E-02	AA362934.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2632	12728	22391	4.24	8.4E-02	W69330.1	EST_HUMAN	zd44e11.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5253	15175	24949	7.82	8.4E-02	BE267153.1	EST_HUMAN	601190439F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3534393 5'
6019	15923	26053	1.71	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ000050 protein, partial cds
6680	16560	26755	8.11	8.4E-02	BE068074.1	EST_HUMAN	CM3-BT0790-260400-162-d05 BT0790 Homo sapiens cDNA
7931	17781	28020	1.44	8.4E-02	AI735184.1	EST_HUMAN	as88g10.x1 Barslead colon HP1LRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
1965	11859	21748	0.86	8.3E-02	5835680	NT	Ixodes hexagonus mitochondrion, complete genome
1965	11859	21749	0.86	8.3E-02	5835680	NT	Ixodes hexagonus mitochondrion, complete genome
3544	13460	23254	6.19	8.3E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3567	13481	23271	0.88	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3567	13481	23272	0.88	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
5840	15746	25859	2.82	8.3E-02	AF052683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
6653	16533	26728	3.42	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drp2) mRNA, complete cds
6671	16551		1.47	8.3E-02	AA865285.1	EST_HUMAN	cg88g08.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.t1 L1 L1
6829	16708		1.42	8.3E-02	AA987873.1	EST_HUMAN	repetitive element
7498	17368	27573	1.44	8.3E-02	AW583503.1	EST_HUMAN	cg87f10.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
7506	17294		1.94	8.3E-02	AL161595.2	NT	ia05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ;
9307	19695		1.56	8.3E-02	BE958458.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
1357	11263		7.82	8.2E-02	Y08170.2	NT	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929993 5'
1480	11385	21248	1.21	8.2E-02	AF167077.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
3036	12964		1.78	8.2E-02	AL163206.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3733	13645		1.26	8.2E-02	AL161498.2	NT	Homo sapiens chromosome 21 segment HS21C006
3926	13835	23615	1.11	8.2E-02	AL163206.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4187	14087	23962	5.36	8.2E-02	P48960	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
4187	14087	23963	5.36	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4187	14087	23964	5.36	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5014	14888	24655	2.92	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5271	15193	24968	1.43	8.2E-02	BE897030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
6189	16073	26222	3.14	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7094	16971	27164	3.13	8.2E-02	AW875128.1	EST_HUMAN	RC2-PT0004-031299-011-405 PT0004 Homo sapiens cDNA
7536	17387	27598	5.33	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
7628	17479	27699	2.11	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355595 5'
9314	19006	26336	4.13	8.2E-02	AE002246.2	NT	Chlamydomonas reinhardtii AR39, section 73 of 94 of the complete genome
9706	19480		1.94	8.2E-02	AF275386.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1479	11384	21247	1.72	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcL and mdcM genes), complete cds
7703	17553		1.65	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
8789	18604	28894	3.38	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
5	12657	19784	3.28	8.0E-02	AW954653.1	EST_HUMAN	EST368723 MAGE resequences, MAGC Homo sapiens cDNA
920	10844	20690	1.33	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1671	12701	21440	10.54	8.0E-02	D26535.1	NT	Human gene for dihydrofolamide succinyltransferase, complete cds (exon 1-15)
1671	12701	21441	10.54	8.0E-02	D26535.1	NT	Human gene for dihydrofolamide succinyltransferase, complete cds (exon 1-15)
1861	11757	21632	3.9	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2323	12204	22103	1.01	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2323	12204	22104	1.01	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2421	12298		4.08	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2790	10991	20833	0.91	8.0E-02	M23449.1	NT	Dicystosium discitium cyclic nucleotide phosphodiesterase gene, complete cds
2870	12797	22591	1.01	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3745	13658	23440	0.94	8.0E-02	AW966118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
3980	13887		1.06	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4709	14595		5.62	8.0E-02	X72794.1	NT	M. musculus gene for gelatinase B
4834	14716	24499	0.87	8.0E-02	M28071.1	NT	Herpesvirus saimiri transformation-associated protein (STP), and dihydrofolate reductase (DHFR) genes, complete cds, and small nuclear RNAs (snRNAs)
5591	15506	25581	3.35	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6261	15506	25581	1.63	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6727	16607	26798	3.65	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7401	17268	27471	1.49	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
7401	17268	27472	1.49	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8172	18060	28310	7.42	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
9344	19023	25300	2.94	8.0E-02	AJ005375.1	NT	Drosophila arena hunchback region
9891	13887		1.47	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
9969	19654		3.04	8.0E-02	AJ278435.1	NT	Mus musculus Ranbp7 gene, Slaf gene and Wee1 gene
2127	12015	21913	3.98	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
2948	12875	22673	6.43	7.9E-02	AI582029.1	EST_HUMAN	af98a08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb.Z28876
3776	13688	23471	3.31	7.9E-02	6681044	NT	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3776	13688	23472	3.31	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Gsf1r), mRNA
4595	14483	24269	1.06	7.9E-02	BF348454.1	EST_HUMAN	Mus musculus colony stimulating factor 1 receptor (Gsf1r), mRNA
4706	14592		1.16	7.9E-02	AB008019.1	NT	602019770F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155401 5'
6682	16562	26756	3.25	7.9E-02	U27832.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
7762	17612	27838	5.68	7.9E-02	AI081644.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds
7762	17612	27839	5.68	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
1192	11102	20947	1.43	7.8E-02	AI793275.1	EST_HUMAN	CE08811 ;
1192	11102	20948	1.43	7.8E-02	AI793275.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
4698	14574	24371	0.81	7.8E-02	BE636331.1	EST_HUMAN	CE08811 ;
5019	13603		2.71	7.8E-02	BE250048.1	EST_HUMAN	co59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
5197	15060	24825	1.04	7.8E-02	AI418520.1	EST_HUMAN	co59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
7236	17113	27306	2.06	7.8E-02	AF233437.1	NT	repetitive element ;
7236	17113	27307	2.06	7.8E-02	AF233437.1	NT	repetitive element ;
7389	17307	27513	1.27	7.8E-02	AA469354.1	EST_HUMAN	PM3-FN00588-140700-005-f09 FN0058 Homo sapiens cDNA
1378	12693	21139	1	7.7E-02	AF181897.1	NT	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
3538	13454		2.09	7.7E-02	AJ238093.1	NT	tg48g12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112070 3' similar to contains
6615	16495	26682	4.4	7.7E-02	AA402949.1	EST_HUMAN	MER10.13 MER10 repetitive element ;
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
							nc68b06.f1 NCI_CGAP_P71 Homo sapiens cDNA clone IMAGE:771731
							Homo sapiens WRN (WRN) gene, complete cds
							Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
							zu53d11.f1 Soares ovary tumor NHOt Homo sapiens cDNA clone IMAGE:741717 5' similar to
							TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7660	17510	27736	4.62	7.7E-02	P36080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
8376	18253	28504	5.24	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
9335	19561		2	7.7E-02	11436859	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3341	13261	23067	2.57	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3362	13281	23081	0.94	7.6E-02	AA296447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3512	13428	23229	0.93	7.6E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, OEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
4765	14650		0.96	7.6E-02	AW858844.1	EST_HUMAN	RC3-CT0347-110300-014-a05 CT0347 Homo sapiens cDNA
7393	17311	27518	1.34	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
7955	17545		1.34	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
8927	18735	29028	2.45	7.6E-02	AW996645.1	EST_HUMAN	QV3-BN0046-150400-151-a04 BN0046 Homo sapiens cDNA
767	10698	20535	1.13	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	10698	20536	1.13	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1878	11774	21649	0.87	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4407	14301	24085	0.84	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
					wi52b02.x1 NCI_CGAP_Bm25		Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:U14328 ALPHA
6855	16734	26927	1.19	7.5E-02	AJ864367.1	EST_HUMAN	ENOLASE (HUMAN);
6953	16831	27024	1.21	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
469	10412	20231	1.23	7.4E-02	AW838547.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
1444	11349		1.08	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2536	12410		0.93	7.4E-02	6755069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
3545	13461	23255	0.89	7.4E-02	AJ807885.1	EST_HUMAN	wf43h01.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2358385 3'
4806	14494	24282	3.38	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4867	14573	24370	2.66	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvr1), mRNA
4868	14738	24518	1.7	7.4E-02	6678492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrrp), mRNA
5913	15819		1.75	7.4E-02	R17477.1	EST_HUMAN	yg14g06.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
6612	16492	26678	1.4	7.4E-02	BE880112.1	EST_HUMAN	601483366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
6950	16828	27021	1.37	7.4E-02	U56089.1	NT	Human periodic tyrophenol protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9271	18975		2.08	7.4E-02	11525693	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
9527	19674		2.82	7.4E-02	AW379431.1	EST_HUMAN	CM4-HT0243-081199-037-df11 HT0243 Homo sapiens cDNA
9678	19235	25242	1.81	7.4E-02	BF035099.1	EST_HUMAN	601453813F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857738 5'
461	10405	20222	0.96	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
461	10405	20223	0.96	7.3E-02	BE904961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
669	10603	20420	2.73	7.3E-02	AE001789.1	NT	Thermotoga maritima section 101 of 136 of the complete genome
1465	12695	21237	3.04	7.3E-02	AW900281.1	EST_HUMAN	CMO-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1801	12705		14.61	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4927	14806		1.01	7.3E-02	U12263.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6413	16275	26437	2.44	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6413	16275	26436	2.44	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6749	16628		1.27	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
8548	15788	25910	2.78	7.3E-02	AA779977.1	EST_HUMAN	z24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:102426 26S PROTEASE SUBUNIT 4 (HUMAN);
114	10093	19911	0.94	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
114	10093	19912	0.94	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1460	11365	21228	2.23	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1460	11365	21229	2.23	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2502	12377		2.5	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial . cds
3870	13722	23511	0.82	7.2E-02	AW298322.1	EST_HUMAN	UI-H-BWO-ajl-a-05-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
4249	14148	23922	4.02	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
4594	14482	24268	78.82	7.2E-02	11466563	NT	Rhodomonas salina mitochondrion, complete genome
4997	14872	24636	0.94	7.2E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
5230	15154	24922	3.03	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5231	15155	24923	7.62	7.2E-02	P11120	SWISSPROT	CALMODULIN
6252	16118	26272	9.33	7.2E-02	BF215086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
6281	16145		1.75	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
7545	17396	27608	2.05	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAUUG01 5'
7625	17476	27697	4.23	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
7746	17596	27818	2.64	7.2E-02	AW873187.1	EST_HUMAN	hq24f11.x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
7926	17776	28016	2.05	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7983	17833	28073	5.47	7.2E-02	BE665003.1	EST_HUMAN	601343928F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
7994	17844		3.2	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
8285	18164	28407	4.8	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
9178	18919	28346	1.44	7.2E-02	AA773696.1	EST_HUMAN	af81a04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
9214	18942		3.13	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
9273	18977		1.44	7.2E-02	AA584465.1	EST_HUMAN	no05h03.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1069839 3'
9332	19013		1.62	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
9346	19531		3.89	7.2E-02	AW900962.1	EST_HUMAN	GM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
1862	11758	21633	1.65	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2243	12127		0.9	7.1E-02	AE004890.1	NT	Pseudomonas aeruginosa PA01, section 451 of 529 of the complete genome
2247	12131	22028	5.08	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
9063	18844		4.98	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
517	10459	20270	1.23	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1484	11389		1.46	7.0E-02	X96677.1	NT	Martellia Mitcut-1 gene
1725	11626	21495	1.36	7.0E-02	AA056343.1	EST_HUMAN	2166104.s1 Striatagene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3'
2994	12622	22715	1.72	7.0E-02	AW138152.1	EST_HUMAN	U1H-B1f-acy-c-07-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3822	13734	23523	1	7.0E-02	AA816438.1	EST_HUMAN	ai65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S
3958	13866	23642	1.24	7.0E-02	BE070264.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4047	13949		1.08	7.0E-02	AW782962.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
4121	14021	23799	1.27	7.0E-02	AF077821.1	NT	CMO-JUM001-060300-270-e12 UM0001 Homo sapiens cDNA
4846	14727	24510	7.1	7.0E-02	BF381987.1	EST_HUMAN	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
7259	17136	27329	1.25	7.0E-02	9628113	NT	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7534	17385	27597	1.19	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
8679	18567	28850	2.39	7.0E-02	AA724295.1	EST_HUMAN	Rat lg germ-line epsilon H-chain gene C-region, 3' end
503	10445	20256	5.34	6.9E-02	AL163210.2	NT	ah99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837
503	10445	20257	5.34	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
							Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens chromosome 21 segment HS21C010
1311	11217		1.31	6.9E-02	4507968	NT	
3724	13636	23421	1.42	6.9E-02	Q06364	SWISSPROT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3724	13636	23422	1.42	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5100	14968		1.05	6.9E-02	AF079906.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
							Rabies virus isolate 6615 glycoprotein gene, partial cds

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6978	18655	27048	1.37	6.9E-02	BE567435.1	EST_HUMAN	601340861F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
6978	18655	27049	1.37	6.9E-02	BE567435.1	EST_HUMAN	601340861F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9208	18939		3.95	6.9E-02	X74315.1	NT	Xlae1s XFD2 mRNA for fork head protein
9385	19045		1.5	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFCHOMOLOG
9598	19180		2.19	6.9E-02	AF198953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1839	11736	21610	1.11	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1839	11736		1.11	6.8E-02	AA496759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1865	11761	21611	1.11	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1865	11761	21635	3.91	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3062	12989	22780	1.23	6.8E-02	AA781996.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
3062	12989	22781	1.23	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
3062	12989	22782	1.23	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
4453	14347		0.92	6.8E-02	BE141076.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
6315	16178	26337	7.71	6.8E-02	AL163268.2	NT	MRO-H10069-071099-001-c05 HT0069 Homo sapiens cDNA
6822	16701	26894	6.12	6.8E-02	AJ248287.1	NT	Homo sapiens chromosome 21 segment HS21C088
6822	16701	26895	6.12	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9011	19719		1.37	6.8E-02	T03214.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 5/6
9140	18895		2.98	6.8E-02	AA758014.1	EST_HUMAN	FB4A8 Fetal brain, Stratiogene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
9764	19284		2.97	6.8E-02	9910585	NT	ah67f05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
1511	11416		2.17	6.7E-02	AF15536.1	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1851	11747	21622	2.5	6.7E-02	AJ220285.1	EST_HUMAN	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
3656	13570	23356	3.52	6.7E-02	P17278	SWISSPROT	gg79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
1326	11233	21089	1.05	6.6E-02	AI735509.1	EST_HUMAN	HOMEOBOX PROTEIN HOX-D4 (CHOX-A)
1347	11253	21109	1.5	6.6E-02	AF245116.1	NT	at12e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW:LIN1 NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
2133	12021	21918	3.07	6.6E-02	AJ289241.1	NT	Drosophila melanogaster oactin mRNA, complete cds
3133	13058		1.32	6.6E-02	Q13585	SWISSPROT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3418	13335	23139	8.61	6.6E-02	R64306.1	EST_HUMAN	MELATONIN-RELATED RECEPTOR (H9)
3432	13349	23154	2.19	6.6E-02	7108357	NT	y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3432	13349	23155	2.19	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3989	13896	23673	1.59	6.6E-02	AF280225.1	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4904	14784	24558	8.4	6.6E-02	Q61703	SWISSPROT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4904	14784	24559	8.4	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4904	14784	24559	8.4	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8946	18754	29050	1.86	6.4E-02	U91323.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9289	19635		3.65	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
9337	19017	25295	2.27	6.4E-02	AJ27174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1720	11621						Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLOP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3552	13467	21490	2.43	6.3E-02	AF109905.1	NT	HEAT SHOCK PROTEIN 70 HOMOLOG
7752	17602	27825	2.09	6.3E-02	P37092	SWISSPROT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: GMR-152
8098	15637	25741	3.14	6.3E-02	AB010162.1	NT	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
9373	19039		3.29	6.3E-02	BF210736.1	EST_HUMAN	TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3)
4157	14057	23831	1.49	6.3E-02	P16276	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4243	14142		3.37	6.2E-02	AL161572.2	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4479	14373		1.11	6.2E-02	AF271235.1	NT	52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
4803	14687		5.41	6.2E-02	Q62191	SWISSPROT	AV705701 ADB Homo sapiens cDNA clone ADBBAB03 5'
7459	17319	27525	1.22	6.2E-02	AV705701.1	EST_HUMAN	Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA
8655	18544	28827	1.21	6.2E-02	6677898	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chy1 gene)
9129	19752		1.84	6.2E-02	AJ242735.1	NT	Aquifex acidicus section 82 of 109 of the complete genome
9541	19142	25265	3.53	6.2E-02	AE000750.1	NT	7137m08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to
256	10222	20038	1.98	6.2E-02	BF112039.1	EST_HUMAN	Human mRNA, Xq terminal portion
3909	13819		4.53	6.1E-02	D16471.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AtKIC1) gene, complete cds
5150	15017	24785	2.65	6.1E-02	U73325.1	NT	Homo sapiens mRNA for KIAA1464 protein, partial cds
6809	16688	26877	1.01	6.1E-02	AB040897.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8112	18002	28248	3.46	6.1E-02	X99268.1	NT	IL3-HIT0618-110500-136-C06 HT0618 Homo sapiens cDNA
9088	19670		5.44	6.1E-02	BE179543.1	EST_HUMAN	S. japonicum mRNA for serine-enzyme
9783	19296		7.17	6.1E-02	X70969.1	NT	Homo sapiens chromosome 21 segment HS21C007
1241	11148	20997	3.6	6.1E-02	AL163207.2	NT	Thermoga maritima section 89 of 136 of the complete genome
2641	12508	22399	1.41	6.0E-02	AE001777.1	NT	EST380924 IMAGE resequences, MAGJ Homo sapiens cDNA
2745	12607		1.57	6.0E-02	AW968848.1	EST_HUMAN	Mesocostoides corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2906	10075	19892	1.61	6.0E-02	AB031289.1	NT	zp78c04.1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
			1.22	6.0E-02	AA188730.1	EST_HUMAN	

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2906	10076	19893	1.22	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Strategene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3191	13116	22921	1.2	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3191	13116	22922	1.2	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3583	13497		0.9	6.0E-02	BE964443.2	EST_HUMAN	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
4893	14773	24551	1.17	6.0E-02	Z67739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5314	15235		3.46	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA
6172	15129	24848	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6172	15129	24849	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6265	16130	26284	1.97	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
6524	16383	26562	2.05	6.0E-02	AI204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
7340	17208	27406	1.19	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
7340	17208	27407	1.19	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
7411	17278	27486	1.79	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
7411	17278	27487	1.79	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9336	19016	25294	1.95	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
9715	19256		1.84	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298
229	10198	20011	3.42	5.9E-02	AW934719.1	EST_HUMAN	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA
2955	12882	22681	2.59	5.9E-02	AF190289.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4770	14655	24443	0.88	5.9E-02	AF006304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
7008	16885	27077	1.87	5.9E-02	9055249	NT	Mus musculus iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
8165	18053		2.72	5.9E-02	6679870	NT	Mus musculus follistatin-like (Fst), mRNA
8383	18280	28509	3.15	5.9E-02	11433356	NT	Homo sapiens rhelin (LOC51199), mRNA
8842	18655		1.99	5.9E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere junction
917	10841		4.35	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2830	12759		1.1	5.8E-02	AJ223621.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
3613	13527	23314	1.44	5.8E-02	AE001775.1	NT	Thermotoga maritima section 87 of 136 of the complete genome
4257	14156	23931	4.36	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4257	14156	23932	4.36	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4447	14341	24132	4.21	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4447	14341	24133	4.21	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4471	14365		2.04	5.8E-02	AF096294.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8523	16382	26560	2.79	5.8E-02	M69150.1	NT	Human polymorphic microsatellite DNA
8523	16382	26561	2.79	5.8E-02	M69150.1	NT	Human polymorphic microsatellite DNA
9227	18948		2.34	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
9518	19739		4.56	5.8E-02	AA604269.1	EST_HUMAN	no75e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3018	12946	22738		5.7E-02	AI081644.1	EST_HUMAN	cu63b05.s1 NCI_CGAP_BR2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 (CE08611)
3033	12961	22754	1.34	5.7E-02	AF119177.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3731	13643	23428	1.8	5.7E-02	AW966791.1	EST_HUMAN	EST378865 MAGE resequences, MAGI Homo sapiens cDNA
6740	16619	26808	1.42	5.7E-02	AJ296090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
8524	18396	28661	3.86	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
8524	18396	28662	3.86	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
9437	19558		5.55	5.7E-02	D50320.1	NT	Pig DNA for SPAL-2, complete cds
9682	19630		2.47	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
9796	19727		3.82	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1510	11415	21274	0.86	5.6E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (p16) gene, intron; chloroplast gene for chloroplast product
4540	14433	24215	1.26	5.6E-02	AB013100.1	NT	Lycopersicon esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4598	14486	24272	1.14	5.6E-02	AA290599.1	EST_HUMAN	zs45c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6008	15913	26040	4.74	5.6E-02	AW172708.1	EST_HUMAN	xj02c10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O94979 O94979 KIA00905 PROTEIN ;
6241	16107	26258	2.88	5.6E-02	BE008001.1	EST_HUMAN	QV0-BN0147-280400-214-g07 BN0147 Homo sapiens cDNA
7110	16987	27178	2.29	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
7110	16987	27179	2.29	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
7647	17497	27719	1.15	5.6E-02	AA482864.1	EST_HUMAN	m49cd07.s1 NCI_CGAP_AW1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C ;
8850	18662		2.18	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2618	12486	22375	8.16	5.5E-02	X97899.1	NT	H. sapiens gene encoding La autoantigen
3179	13104	22909	3.6	5.5E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4777	14661	24448	0.81	5.5E-02	AF161266.1	NT	Murray Valley encephalitis virus strain MVE-1-51, complete genome
5472	15392	25456	3.47	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5671	15392	25456	4.31	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6365	16228	26388	1.58	5.5E-02	6755902	NT	Mus musculus tufelin 1 (Tuf1), mRNA
7566	17417	27632	1.3	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
7566	17417	27633	1.3	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
7619	17470	27689	1.48	5.5E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
8382	18259	28508	11.56	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaT), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
2986	12914		0.95	5.4E-02	AJ277468.1	NT	Oryza sativa tbb3-1 gene for putative Bowman Birk trypsin inhibitor
3375	15078		6.34	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
4908	14787	24563	0.92	5.4E-02	U53528.1	NT	Xenopus laevis homeobox protein (Vox-1) mRNA, complete cds
5108	14976	24751	1	5.4E-02	M96761.1	NT	Mus musculus p-glycoprotein (mdrla) gene, exons 1 and 2
8083	17974	26223	1.79	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VII (QCR8) mRNA, complete cds
9323	19562		1.55	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1037	10955	20797	1.62	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1037	10955	20798	1.62	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1489	11394	21255	18.21	5.3E-02	T94759.1	EST_HUMAN	ye37f12.r1 Stratagene lung (#937270) Homo sapiens cDNA clone IMAGE:119951 5' similar to gp:K01506
2447	12324	22222	3.14	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2912	12839	22638	3.91	5.3E-02	M58417.1	NT	Pseudomonas putida tgs gene
2912	12839	22639	3.91	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3113	13038	22834	4.59	5.3E-02	AJ276408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
4506	14399	24185	1.22	5.3E-02	AJ011048.1	NT	Pseudomonas putida tgs gene
5021	14894	24662	7.26	5.3E-02	M80463.1	NT	Arabidopsis thaliana eli5 gene, exons 1-11
5258	15180	24955	1.76	5.3E-02	AE000527.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5258	15180	24956	1.76	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
6115	16009	26145	3.87	5.3E-02	9695413	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
6353	16216		1.94	5.3E-02	S78221.1	NT	Lymphocystis disease virus 1, complete genome
7276	17183	27349	1.78	5.3E-02	X03127.1	NT	nuclear protein TIF1 isoform [rice, mRNA, 4053 nt]
2239	12123		430.66	5.2E-02	5031908	NT	Podospira anserina mitochondrial epsilon-sen DNA
3076	13003	22793	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3076	13003	22794	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4181	14081	23854	3.35	5.2E-02	U07132.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4633	14521	24311	1.04	5.2E-02	U3246.1	NT	Human steroid hormone receptor Nrf-1 mRNA, complete cds
							Drosophila melanogaster filament protein homolog (sep1) gene, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5714	18622		1.73	5.2E-02	AB030665.1	EST_HUMAN	w80e04.x1 NC1 CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains MER15.b1
6768	16647		2.23	5.2E-02	AL163204.2	NT	MER15 repetitive element;
7610	17461	27677	2.03	5.2E-02	D10927.1	NT	Homo sapiens chromosome 21 segment HS21C004
7610	17461	27678	2.03	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9561	19157		1.63	5.2E-02	Q03030	SWISSPROT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
2313	12194		1.02	5.1E-02	AL134071.1	EST_HUMAN	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
4979	14854	24820	1.12	5.1E-02	BE957423.2	EST_HUMAN	DKFZp547D073_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D073 5'
6098	15108	24871	1.65	5.1E-02	BF378626.1	EST_HUMAN	601653565R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3'
8859	16738	26930	1.43	5.1E-02	A131986.1	NT	Q1V0-JM0051-250800-350-b08 UM0051 Homo sapiens cDNA
7645	17495	27716	6.22	5.1E-02	AF012898.1	NT	Spodoptera littoralis mRNA for 3-dehydrodysone 3beta-reductase
7849	17699	27944	2.36	5.1E-02	P40603	SWISSPROT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
8204	18088	28339	2.42	5.1E-02	AF083930.1	NT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
8204	18088	28340	2.42	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
9569	19159		1.81	5.1E-02	AF062467.1	NT	Homo sapiens ES18 mRNA, partial cds
474	10418	20234	1.98	5.0E-02	AF098004.1	NT	Homo sapiens ES18 mRNA, partial cds
1186	11096	20942	7.11	5.0E-02	Z99104.1	NT	Homo sapiens ES18 mRNA, partial cds
1947	11842	21726	4.27	5.0E-02	P02810	SWISSPROT	Cucumis melo polygalacturonase precursor (MPC3) mRNA, complete cds
2788	10894	20742	1.64	5.0E-02	U72742.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
3295	13217	23330	1.17	5.0E-02	7305610	NT	Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080
3629	13543	23330	5.53	5.0E-02	U12789.2	NT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
4890	14770	24548	0.88	5.0E-02	AF188530.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
6450	16311	26477	10.61	5.0E-02	P35616	SWISSPROT	Mus musculus Ure-51 like kinase 2 (C. elegans) (Ulk2), mRNA
7858	17708	27954	1.32	5.0E-02	AF305238.1	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
8782	18987	28886	2.47	5.0E-02	U67600.1	NT	Homo sapiens ubiquitous tetrahydrocortisol containing protein RoXa mRNA, partial cds
9066	19593		2.81	5.0E-02	Q04047	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
218	10188		28.95	4.9E-02	M14230.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
365	10321	20143	2.57	4.9E-02	AF275948.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
365	10321	20144	2.57	4.9E-02	AF275948.1	NT	NO-ON-TRANSIENT A PROTEIN
3251	13174	22972	1.87	4.9E-02	P54258	SWISSPROT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
3522	13438		0.87	4.9E-02	AA189640.1	EST_HUMAN	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3543	13459	23252	1.19	4.9E-02	AA400914.1	EST_HUMAN	Homo sapiens ABCA1 (ABCA1) gene, complete cds
							ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
							zq43a12.s1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632926 3' similar to
							contains Alu repetitive element; contains element MSR1 repetitive element;
							z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'

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PCT/US01/00666

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3543	13459	23253	1.19	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4733	14618	24404	1.89	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_OGAP_U44 Homo sapiens cDNA clone IMAGE:2632386 3'
4733	14618	24405	1.89	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_OGAP_U44 Homo sapiens cDNA clone IMAGE:2632386 3'
5299	15220	25023	1.94	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5299	15220	25024	1.94	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
8705	18523	28805	3.78	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
9490	19107		2.26	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
9751	19276		3.67	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
327	10287	20104	1.45	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
328	10287	20104	1.97	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
480	10424	20239	7.54	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2227	12112	22014	1.92	4.8E-02	W51983.1	EST_HUMAN	zc49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3172	13097	22903	2.12	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3l and histone H4ll intergenic DNA
4572	14464		1.67	4.8E-02	Z54280.1	NT	S scrofa gene for skeletal muscle ryanodine receptor
5076	14946	24722	1.28	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
6731	16611	26801	1.31	4.8E-02	AW388497.1	EST_HUMAN	MR2-ST0129-221099-012-802 ST0129 Homo sapiens cDNA
4940	14818	24586	0.78	4.7E-02	6981261	NT	Rattus norvegicus Nestin (Nes), mRNA
6085	16030	26170	3.41	4.7E-02	W01153.1	EST_HUMAN	yz37f09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element.
6134	15881	26117	1.65	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
6800	16679	26868	9.71	4.7E-02	X15543.1	NT	B.taurus mRNA for RF-36-DNA-binding protein
7179	17056	27245	1.18	4.7E-02	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
7189	17066		2.63	4.7E-02	AB026678.1	NT	Gallus gallus Wpici-8 gene, complete cds
7321	17197	27397	7.44	4.7E-02	X15543.1	NT	B.taurus mRNA for RF-36-DNA-binding protein
8136	18024	28270	1.76	4.7E-02	6754565	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
9305	19740		2.35	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLCBKD02 3'
9652	19743		2.35	4.7E-02	P52951	SWISSPROT	HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2)
9881	19865		1.39	4.7E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
722	10854	20484	2.74	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1270	11177		1.06	4.6E-02	A1014255.1	EST_HUMAN	am50402.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533 P90533 LIMA ;contains element LTR1 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1336	11242	21100	2.74	4.6E-02	AV727059.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCWC01 5'
2438	12315	22212	2.51	4.6E-02	AW236023.1	EST_HUMAN	xn24f03.x1 NCL_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN
2777	10235	20052	1.51	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1
2977	12904	22703	0.98	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3451	12904	22703	0.95	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4033	13936		1.22	4.6E-02	AF220366.1	NT	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
5777	15884	25792	3.64	4.6E-02	X61624.1	NT	Mus musculus nucleolar RNA helicase II/Gu (dck21) gene, complete cds
5777	15884	25793	3.64	4.6E-02	X61624.1	NT	C.reinhardtii alp2 (alpB) mRNA
						NT	C.reinhardtii alp2 (alpB) mRNA
6070	15053	26200	1.31	4.6E-02	A1149574.1	EST_HUMAN	qc0b005.x1 Soares_placenta_8tc0weeks_2NbfIP8tc9W Homo sapiens cDNA clone IMAGE:1713971 3'
7029	16906	27097	3.65	4.6E-02	BE154006.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element;
8707	18524	28806	3.58	4.6E-02	AA913328.1	EST_HUMAN	PMO-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
9633	19738		1.34	4.6E-02	L11692.1	NT	cl27h09.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
9845	19343		2.68	4.6E-02	X57808.1	NT	Oryctolagus cuniculus macrophage scavenger receptor type II mRNA, complete cds
439	10383	20207	1.84	4.5E-02	P22448	SWISSPROT	Human gamma immunoglobulin lambda light chain gene
1200	11110	20955	0.85	4.5E-02	AF005730.1	NT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1200	11110	20956	0.85	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1763	11662	21635	3.55	4.5E-02	P32182	SWISSPROT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
2063	11953	21850	2.04	4.5E-02	AE003964.1	NT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
3662	13576	23364	3.83	4.5E-02	AL163278.2	NT	Xiella fastidiosa, section 110 of 229 of the complete genome
						NT	Homo sapiens chromosome 21 segment HS21C078
5778	15885	25794	1.54	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6891	16770	26965	2.3	4.5E-02	AF036684.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
7718	17568	27793	4.43	4.5E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
9301	19000	25331	1.74	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RFP.L3), mRNA
9691	19637	25009	3.41	4.5E-02	AA191097.1	EST_HUMAN	z043f11.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
213	10184		4.79	4.4E-02	BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
1008	10926	20770	1.29	4.4E-02	L19295.1	NT	Drosophila melanogaster extracellular (EXD) mRNA, complete cds
2049	11940		6.15	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2440	12317	22214	1.29	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-070300-070-g02 PT0012 Homo sapiens cDNA
3588	13502	23291	1.88	4.4E-02	AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4827	14420	24203	1.08	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; P-S1 and hypothetical protein genes, complete cds; and S171 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4527	14420	24204	1.08	4.4E-02	AF109907.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4637	14525		3.12	4.4E-02	AJ222689.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene
7084	15961	27154	1.96	4.4E-02	AA736969.1	EST_HUMAN	hw13h03.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
8423	18297	28552	4.11	4.4E-02	AF060669.1	NT	Hepatitis E virus strain HEV-US2 polypeptide (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
8533	18405	28670	2.39	4.4E-02	AA496739.1	EST_HUMAN	ae33f04.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
9029	18820		1.88	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
9210	19763		1.44	4.4E-02	BF241245.1	EST_HUMAN	601878746f-1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
764	10695	20532	5.74	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2521	12395	22286	1.23	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBACH08 5'
3383	13301	23101	7.04	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C0710
3609	13523		1.07	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5141	15008	24779	0.92	4.3E-02	X51594.1	NT	Pea P4 organ specific gene
5914	15820	25944	4.93	4.3E-02	P30427	SWISSPROT	PLECTIN
5914	15820	25945	4.93	4.3E-02	P30427	SWISSPROT	PLECTIN
8242	18122	28372	2.48	4.3E-02	X17012.1	NT	Rat GFII gene for insulin-like growth factor II
805	10734	20577	2.05	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
848	10775		1.93	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
878	10804	20854	0.83	4.2E-02	AW003645.1	EST_HUMAN	wx34g01.x1 NCI_CGAP_Pit1 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
1650	11592		1.21	4.2E-02	AL445066.1	NT	L1 RETROPOSON, ORF2 mRNA; contains L1.13 L1 L1 repetitive element; Thermoplasma acidophilum complete genome; segment 4/5
3117	13042	22838	0.9	4.2E-02	AI493472.1	EST_HUMAN	qy95f10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gb:M35718
5172	15038		1.07	4.2E-02	D63494.1	NT	FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN); Human mRNA for KIAA0160 gene, partial cds
6444	16305	26470	4.45	4.2E-02	AF276762.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7114	16991	27183	3.88	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
7845	17895	27941	1.28	4.2E-02	Q16680	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
8627	18492	28764	2.33	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
8627	18492	28765	2.33	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
8795	18609	28900	1.73	4.2E-02	AF176468.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
9563	19681		2.69	4.2E-02	AI983494.1	EST_HUMAN	wf49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
2843	12510	22401	0.97	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
3824	13736	23526	0.86	4.1E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533363 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3824	13736	23527	0.86	4.1E-02	BE207236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4372	14268		7.37	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-164-f06 NN0012 Homo sapiens cDNA
6436	19297	28459	1.84	4.1E-02	7662347	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
6565	18423	26604	2.44	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
9873	19682	24994	12.83	4.1E-02	AJ271909.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
3206	13130	22632	2.68	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
5304	15225	25029	4.92	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6528	16387	26567	5.69	4.0E-02	L23638.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7059	16936	27126	2.8	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE 31/52 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
7572	17423	27638	2.42	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A
8983	18788		1.94	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Ca++ ATPase
9196	19506	25135	4.96	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1104	11020	20863	2.77	3.9E-02	BF515149.1	EST_HUMAN	UI-H-BW1-anx-h08-0-UI.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1322	11229	21084	3.46	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1918	11813	21691	3.04	3.9E-02	AJ403356.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2671	12536		2.29	3.9E-02	4508862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5105	14973	24748	0.98	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5105	14973	24749	0.98	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
6581	16461	26654	1.22	3.9E-02	BF239613.1	EST_HUMAN	601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
9056	19644		5.45	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
9697	19248		1.57	3.9E-02	U66061.1	NT	Human germ-line T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
9811	19568		7.38	3.9E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
1909	11804	21683	0.94	3.8E-02	BE885137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6331	16194	28355	1.74	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
7033	16910		1.39	3.8E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
8045	17936	28185	2.45	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
976	10899	20746	4.59	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1366	11272	21128	0.9	3.7E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2190	12077	21982	6.3	3.7E-02	A084806.1	EST_HUMAN	wr85e08.x1 NCL_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2533	12407	22299	0.91	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3012	12940	22733	0.8	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3013	12941	22734	3.45	3.7E-02	BF312963.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126584 5'
3408	13325		1.1	3.7E-02	6680541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
9095	18867	29119	3.4	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
9755	19539	25063	1.62	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3604	13518	23306	0.85	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3612	13526	23313	0.8	3.6E-02	AL098060.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5135	15002	24773	0.84	3.6E-02	AL098810.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
6028	15932	26062	5	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6028	15932	26063	5	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6214	16080	26229	1.82	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cyt precursor (sgp2) gene, complete cds
6324	16187	26349	2.63	3.6E-02	AA714521.1	EST_HUMAN	rw20e05.s1 NCL_OGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN);
7402	17269	27473	2.08	3.6E-02	U20608.1	NT	Dictyostellium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
7402	17269	27474	2.08	3.6E-02	U20608.1	NT	Dictyostellium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
877	10803	20653	1.15	3.5E-02	U09506.1	NT	Drosophila melanogaster tigrin mRNA, complete cds
992	10913	20758	1.53	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1544	11449	21309	1.49	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1544	11449	21310	1.49	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4120	14020	23798	2.01	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4220	14118	23895	1.43	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
4536	14429		0.96	3.5E-02	AW988469.1	EST_HUMAN	EST370539 IMAGE resequences, IMAGE Homo sapiens cDNA
5154	15021		0.84	3.5E-02	P47144	SWISSPROT	HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-CPA2 INTERGENIC REGION
5773	15680	25787	1.88	3.5E-02	J01238.1	NT	Maize actin 1 gene (MAc1), complete cds
7012	18889	27082	2.35	3.5E-02	BE959970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737 3'
7755	17605	27829	1.72	3.5E-02	X76642.1	NT	L lactis MG1363 grpE and dnaK genes
8785	18600	28889	1.76	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
8785	18600	28890	1.76	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
9749	19582		3.51	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:35443833 5'
564	10504	20310	1.78	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
564	10504	20311	1.78	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	10504	20310	3.31	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	10504	20311	3.31	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1035	10953	20795	3.77	3.4E-02	AW274020.1	EST_HUMAN	xv26d07.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:G211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR;
1188	11098		10.22	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2343	12223	22120	2.06	3.4E-02	T57180.1	EST_HUMAN	yc20e06.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3384	13302	23102	1.25	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3709	13622	23405	1.07	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
3845	13756	23550	3.18	3.4E-02	AW794952.1	EST_HUMAN	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4494	14388	24174	2.41	3.4E-02	X59799.1	NT	Musculus S-antigen gene promoter region
4992	14867		3.43	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5010	14884	24850	1.28	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6095	15105	24868	4.19	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
6808	16687		4.78	3.4E-02	AI809629.1	EST_HUMAN	wI99d04.x1 NCI_OGAP_Brm25 Homo sapiens cDNA clone IMAGE:2433031 3'
							zq04f11.s1 Stratagene muscle 937208 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
7169	17046		6.07	3.4E-02	AA194306.1	EST_HUMAN	IPISGKPLPKVTLSRDGVPLKATMRNFTEITAEHLTNLKESVTADAGRYEITAANSSGTTKAFINIVLDRPG
368	10324		13.18	3.3E-02	AA398735.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKYDGGSCVTNYLLKRETSATVWTEVSATVARTMMKVMKL ...;
1151	11064	20907	13.17	3.3E-02	AB035867.1	NT	zI75e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1621	11525	21383	1.08	3.3E-02	AF110763.1	NT	Cricetus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1705	11606		1.28	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2038	11929		2.77	3.3E-02	R09112.1	EST_HUMAN	yf25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
4086	11525	21383	2.24	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds
4366	14262	24047	1.88	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tra1) mRNA
5875	15781	25901	18.26	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
5875	15781	25902	18.26	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8464	18337	28801	3.39	3.3E-02	BF691107.1	EST_HUMAN	60224717F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
9290	18991		1.78	3.3E-02	T96545.1	EST_HUMAN	yef49f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
9441	19078		1.59	3.3E-02	M81890.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
127	10101	19923	1.13	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1110	11025	20867	12.7	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1110	11025	20868	12.7	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1734	11635	21503	1.14	3.2E-02	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
2072	11962		0.91	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
2809	10101	19923	1.15	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
3095	13022	22817	10.71	3.2E-02	BE867353.1	EST_HUMAN	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3653	13557	23354	1.05	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4124	14024		12.36	3.2E-02	X94788.1	NT	H. sapiens RP3 gene (XLRP gene 3)
4658	14544	24333	2.88	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5399	15318	25365	1.46	3.2E-02	X68709.1	NT	S. griseocarneum whiG-Stv gene
5399	15318	25366	1.46	3.2E-02	X68709.1	NT	S. griseocarneum whiG-Stv gene
5931	15836	25959	2.26	3.2E-02	M82437.1	NT	Rat/polyomavirus left junction in cell line W98.14
5932	15837						ycd3h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
5986	15891	26013	26.54	3.2E-02	T89387.1	EST_HUMAN	Alu repetitive element/contains LTR1 repetitive element ;
6830	16709	26902	3.72	3.2E-02	AF173845.1	NT	Saguinus oedipus tissue kallikrein gene, complete cds
			3.48	3.2E-02	6680565	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
7786	17636		3.82	3.2E-02	AA719795.1	EST_HUMAN	zg54b12.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to
9652	19487		1.38	3.2E-02	AB021684.1	NT	gb:U08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
1293	11146		2.05	3.1E-02	4503416	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
1283	11191	21043	1.26	3.1E-02	P18845	SWISSPROT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1850	11746	21621	1.35	3.1E-02	6671564	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1931	11826		1.09	3.1E-02	Z50097.1	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
							Drosophila melanogaster mRNA for headcase protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4152	14952		0.82	3.1E-02	AU119006.1	EST_HUMAN	AU119006 HEMBA1 Homo sapiens cDNA clone HEMBA1004942 5'
4767	14652	24440	0.99	3.1E-02	AW835313.1	EST_HUMAN	QV0-LT0014-250200-129-h09 LT0014 Homo sapiens cDNA
5290	15211		2.33	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703856 5'
7765	17615	27843	2.62	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1606	11511		2.82	3.0E-02	AF187125.1	NT	Pityokines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2541	12415	22305	1.07	3.0E-02	AA402242.1	EST_HUMAN	z68h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3518	13434	23234	1.07	3.0E-02	M94176.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3903	13517	23305	2.61	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3985	13598		0.96	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0266-150200-040-e09 ST0266 Homo sapiens cDNA
3966	13777		1.18	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end
4773	14657	24444	0.89	3.0E-02	BE782830.1	EST_HUMAN	601472331F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3875503 5'
4983	14858	24624	6.02	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4983	14858	24625	6.02	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5312	15233		2.88	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6066	16050	26196	2.71	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene
6127	15974	26109	3.58	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6127	15974	26110	3.58	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6207	15967	26101	1.79	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6207	15967	26102	1.79	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6292	16156	26311	1.54	3.0E-02	M86524.1	NT	Human dystrophin gene
7106	16983		2.11	3.0E-02	AF275654.1	NT	Omlithorhynchus anathinus coagulation factor X mRNA, complete cds
7978	17828	28068	1.71	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 135 of the complete genome
8562	18432	28701	3.09	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
8937	18745	29039	7.7	3.0E-02	AA483216.1	EST_HUMAN	ne87f04.s1 NCL_CGAP_Kd1 Homo sapiens cDNA clone IMAGE:911263
9396	19730	24909	1.66	3.0E-02	R32019.1	EST_HUMAN	yh63d04.s1 Soares placent. Nb2-IP Homo sapiens cDNA clone IMAGE:134407 3'
9740	19273		4.67	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
9780	19723		2.09	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Galactose 4-epimerase beta-1,4-galactosyltransferase mRNA, complete cds
2385	12720	22157	1.1	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
2362	12889	22687	1.07	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2952	12889	22688	1.07	2.9E-02	BE565944.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3880695 5'
3951	13762	23555	0.92	2.9E-02	H72805.1	EST_HUMAN	yuo7e10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
4950	14827	24693	1.32	2.9E-02	X65137.1	NT	S.vulgaris pepC gene for PEP carboxylase
4950	14827	24594	1.32	2.9E-02	X65137.1	NT	S.vulgaris pepC gene for PEP carboxylase
5799	15705	25817	6.47	2.9E-02	BF032233.1	EST_HUMAN	601462061F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5'
6298	16162	26319	10.33	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7568	17419	27635	1.94	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
7568	17419	27636	1.94	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
553	10494		0.87	2.9E-02	AF970153.1	EST_HUMAN	EST382234 IMAGE resequences, MAGK Homo sapiens cDNA
3321	13241	23046	1.27	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3321	13241	23047	1.27	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4214	14112		0.98	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5373	15293	25140	11.41	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
6847	16726	26920	1.33	2.8E-02	AJ005920.1	NT	Craterosigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
9674	19874		1.51	2.8E-02	R09966.1	EST_HUMAN	yf12h02.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126675 5'
9680	19237		1.33	2.8E-02	X06322.1	NT	Yeast GN31C chromosome III RAHS DNA (right arm transcription hot-spot)
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S>
1473	11378	21242	1.26	2.7E-02	U66059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
3385	13303	23103	2	2.7E-02	AL161494.2	NT	y86h12.1 Soares multiple sclerosis 2Nbl-IMSP Homo sapiens cDNA clone IMAGE:280487 5'
4107	14007	23783	2.07	2.7E-02	N47258.1	EST_HUMAN	y86h12.1 Soares multiple sclerosis 2Nbl-IMSP Homo sapiens cDNA clone IMAGE:280487 5'
4107	14007	23784	2.07	2.7E-02	N47258.1	EST_HUMAN	y86h12.1 Soares multiple sclerosis 2Nbl-IMSP Homo sapiens cDNA clone IMAGE:280487 5'
6205	15965	26099	1.9	2.7E-02	AA993571.1	EST_HUMAN	ole6h03.s1 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'
9648	19500	25134	1.52	2.7E-02	BF514859.1	EST_HUMAN	UI-H BW1-antj-f-05-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082520 3'
559	10499	20305	1.14	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1345	11251		1.04	2.6E-02	AW850515.1	EST_HUMAN	IL3-CT0219-280100-062-C09 CT0219 Homo sapiens cDNA
2315	12196	22093	2.9	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2317	12198	22095	2.86	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2317	12198	22096	2.86	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2885	12812		1.55	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC701, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
3983	13794		1.13	2.6E-02	AW181945.1	EST_HUMAN	xf68f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2662409 3'
4517	14410		1.13	2.6E-02	BE968922.1	EST_HUMAN	601649877R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933786 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4811	14895	24481	3.69	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
4998	14873	24637	1.67	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5025	14898	24667	2.06	2.6E-02	AW241154.1	EST_HUMAN	xa52b04.x1 NCL_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
5771	15678		6.95	2.6E-02	AI206030.1	EST_HUMAN	Q15041 HYPOTHETICAL PROTEIN KIAA0069;
5870	15776	25895	2.08	2.6E-02	BE621748.1	EST_HUMAN	gg27f11.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6130	15977	26113	6.09	2.6E-02	6981271	NT	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
7388	17306	27512	1.19	2.6E-02	11432020	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7948	17798	28038	4.87	2.6E-02	AL163303.2	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
8692	18579		2.1	2.6E-02	AA276351.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
8848	18660	28949	1.89	2.6E-02	AW500547.1	EST_HUMAN	zs84c02.t1 NCL_CGAP_GOB1 Homo sapiens cDNA clone IMAGE:704182 5'
9320	19715	24906	1.55	2.6E-02	BF343827.1	EST_HUMAN	UI-HF-BN0-afj-e-10-0-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
521	10463	20274	1.45	2.5E-02	AI793130.1	EST_HUMAN	602015501F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150944 5'
521	10463	20275	1.45	2.5E-02	AI793130.1	EST_HUMAN	on26f06.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
792	10721	20562	12.83	2.5E-02	BE974314.1	EST_HUMAN	on26f06.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
851	10778	20628	4.77	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2735	12697		2.59	2.5E-02	U12571.1	NT	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2926	12853	22652	4.4	2.5E-02	X99697.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2926	12853	22653	4.4	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
3959	15070	23643	1.09	2.5E-02	BE701165.1	EST_HUMAN	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
3959	15070	23644	1.09	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4111	14011	23788	5.07	2.5E-02	AW592114.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
5759	15667		4.48	2.5E-02	BE670128.1	EST_HUMAN	h136h08.x1 Scarses NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5767	15674		3.86	2.5E-02	BE746888.1	EST_HUMAN	7e30e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.11 L1 repetitive element
6519	16378	26555	1.57	2.5E-02	BF526722.1	EST_HUMAN	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6519	16378	26556	1.57	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213406 5'
8185	18071	28320	2.45	2.5E-02	Q10335	SWISSPROT	602070562F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213406 5'
8185	18071	28321	2.45	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
8238	18118	28370	3.38	2.5E-02	AJ237936.1	NT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
							Bos taurus partial stat5B gene, exons 17-19
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Iaalpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-lp
8255	18135		3.33	2.5E-02	AF050157.1	NT	Homo sapiens gene for LECT2, complete cds
8978	18783		1.74	2.5E-02	AB007546.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9280	19657		2.19	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
9463	19528		1.63	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9581	19167	25271	2.39	2.5E-02	BE973327.1	EST_HUMAN	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
167	10139	19556	1.01	2.4E-02	AI378582.1	EST_HUMAN	tc72c07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
1580	11484	21344	1.89	2.4E-02	H65884.1	EST_HUMAN	yr75f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5'
1998	12710	21784	2.22	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
1998	12710	21785	2.22	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4272	14171	23948	1.4	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TOBP 25) protein mRNA, complete cds
4420	14314	24099	1.43	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4420	14314	24100	1.43	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5119	14987		11.51	2.4E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
6962	18640	27032	10.36	2.4E-02	N69442.1	EST_HUMAN	za35g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294596 3' similar to gb K02909 RATSR7K Rat (rRNA), contains A3R.b1 A3R repetitive element ;
7643	17493	27714	2.17	2.4E-02	AV692954.1	EST_HUMAN	AY769295.4 GK Homo sapiens cDNA clone GKCDSC03 5'
7734	17584	27808	2.98	2.4E-02	AA493894.1	EST_HUMAN	h07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:9433583 similar to contains Alu repetitive element; contains element PTR6 repetitive element ;
8857	18669	28956	1.96	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
8857	18669	28957	1.96	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
9080	18856		1.95	2.4E-02	9627909	NT	Bacteriophage b167, complete genome
9224	18947	25357	2.72	2.4E-02	6753635	NT	Mus musculus DnB homolog 1 (E. coli) (DnB1), mRNA
9282	18984	25326	2.03	2.4E-02	BE928869.1	EST_HUMAN	MRO-F70175-310800-202-a06 F70175 Homo sapiens cDNA
9368	19036		1.27	2.4E-02	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9505	19120		3.87	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
9832	19138		1.6	2.4E-02	N42980.1	EST_HUMAN	y008a06.r1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:270610 5'
9538	19141		1.38	2.4E-02	BF679477.1	EST_HUMAN	6021533281F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294173 5'
9977	19667		1.59	2.4E-02	P54643	SWISSPROT	SPORE COAT PROTEIN SP87 PRECURSOR (PL3 PROTEIN)
1829	11726		5.79	2.3E-02	W05340.1	EST_HUMAN	za84g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:269294 5'
1844	11740		7.89	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2302	12183	22081	2.52	2.3E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3628	13542	23329	4.79	2.3E-02	Z20377.1	EST_HUMAN	HSAAAACADH P1 Human foetal Brain Whole tissue Homo sapiens cDNA
4057	13959	23735	1.19	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4057	13959	23736	1.19	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4323	14220	24002	1.26	2.3E-02	AW899107.1	EST_HUMAN	CM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA
4347	14244	24027	0.81	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4347	14244	24028	0.81	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4348	15072	24029	0.94	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4348	15072	24030	0.94	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4472	14366	24155	1.75	2.3E-02	BE143150.1	EST_HUMAN	MRO-HT0159-151099-001-e03 HT0159 Homo sapiens cDNA
4490	14384	24171	2.39	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4490	14384	24172	2.39	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4948	14825	24591	1	2.3E-02	AI793177.1	EST_HUMAN	q235c03.x5 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028668 3'
4948	14825	24592	1	2.3E-02	AI793177.1	EST_HUMAN	q235c03.x5 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028668 3'
5302	15223	25027	3.57	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pcdB) homolog gene, partial cds
5990	15895	26018	4	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
6598	16478	26665	5.67	2.3E-02	U63610.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
7764	17614	27841	1.51	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 88 of 400 of the complete genome
7764	17614	27842	1.51	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
8162	18050	28302	2.15	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9201	19512		4.41	2.3E-02	BE278331.1	EST_HUMAN	80117958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
9713	19254	25219	1.94	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
9767	19756		2.27	2.3E-02	U11077.1	NT	Dictyostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
9961	19609		1.27	2.3E-02	11426388	NT	Homo sapiens dead ringar (Drosophila)-like 1 (DRIL1), mRNA
720	10652	20482	3.09	2.2E-02	AF018267.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1713	11814		1.53	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1968	11861	21752	1.78	2.2E-02	Z82001.1	NT	S.pneumoniae pcpA gene and open reading frames
2695	12730	22448	1.4	2.2E-02	AF109633.1	NT	Mus musculus ets variant protein ER81 gene, exons 1 through 4
3388	13306		1.93	2.2E-02	AA577785.1	EST_HUMAN	nm24a04.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3595	13509		3.27	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3779	13691	23477	1.05	2.2E-02	AW601317.1	EST_HUMAN	PM0-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3844	13755	23549	0.99	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
6297	16161	26318	3.78	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
6876	16755	26952	2.26	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
6876	16755	26953	2.26	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7585	17436	27651	2.33	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
7585	17436	27652	2.33	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9466	19096		2.24	2.2E-02	AA603553.1	EST_HUMAN	ne47h07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element;
413	10359		5.56	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
441	10385		7.99	2.1E-02	AF029726.1	NT	Dictyostelium discoideum histidine kinase C (dhkC) mRNA, complete cds
1242	11149	20698	7.43	2.1E-02	U72073.1	NT	Bacillus subtilis cotLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1365	11270	21125	1.91	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1365	11270	21126	1.91	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1920	11815	21694	0.95	2.1E-02	AF190899.1	NT	Tegula aurectincta major acrosomal protein precursor (TMAP) mRNA, complete cds
2785	10693	20530	3.98	2.1E-02	N28266.1	EST_HUMAN	y43h07.t1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264541 5'
3110	11883	21776	0.85	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3110	11883	21777	0.85	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3535	13451	23247	1.23	2.1E-02	AA461271.1	EST_HUMAN	z63b09.r1 Soares total_fetus Nb2HF8.9w Homo sapiens cDNA clone IMAGE:796121 5'
4038	13941	23719	0.89	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4342	14239	24022	1.61	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
4351	14247	24033	1.03	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4611	14499	24288	4.65	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4714	14600	24386	0.86	2.1E-02	A1823492.1	EST_HUMAN	wn54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
7553	17404	27618	1.8	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
7553	17404	27619	1.8	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9449	15095		4.99	2.1E-02	Y19213.1	NT	Homo sapiens putative psih1bA pseudogene for hair keratin, exons 2 to 7
9857	19348	25184	3.33	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds
17	10004	19795	1.35	2.0E-02	BF002932.1	EST_HUMAN	Tg51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13 MER1 repetitive element;
18	10005	19796	7.96	2.0E-02	AW895655.1	EST_HUMAN	QV4-NN0038-270400-187-105 NN0038 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
259	10225	20040	2.63	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
292	10256	20077	2.62	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
781	10711	20550	1.75	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1071	10987	20630	0.97	2.0E-02	AL096805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[1p36.33] of Homo sapiens
1181	11092	20938	1.61	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1181	11092	20939	1.61	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1830	11727	21600	2.31	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1830	11727	21601	2.31	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2768	12630		1.75	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3040	10004	19795	1.96	2.0E-02	BF002932.1	EST_HUMAN	Tg51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13 MER1 repetitive element;
3105	13031		1.16	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3189	13114		3.33	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
3925	13834	23614	1.5	2.0E-02	M18095.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5079	14949	24725	0.99	2.0E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5085	14955	24730	0.99	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
7679	17529		1.8	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
7930	17780	28019	1.59	2.0E-02	AI640342.1	EST_HUMAN	wa17b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288315 3'
8037	17929	28175	2.01	2.0E-02	Z73966.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 93/162
8678	18566	28849	2.55	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
8931	18739	29031	3.09	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
8931	18739	29032	3.09	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
9019	14955	24730	1.41	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
9481	12630		1.56	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9928	19336		1.72	2.0E-02	BE786595.1	EST_HUMAN	601478819f1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881477 5'
9935	19404		4.08	2.0E-02	T80037.1	EST_HUMAN	y004c09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24675 5'
578	10611	20432	1.68	1.9E-02	AA572764.1	EST_HUMAN	nf19a07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.t1 L1 repetitive element;
1599	11504	21364	0.84	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
1993	11887	21779	2.52	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
1993	11887	21780	2.52	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2458	12335	22230	0.87	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2875	12802	22596	7.08	1.9E-02	AA713856.1	EST_HUMAN	nm0405.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1238337 3'
2823	12850	22650	1.53	1.9E-02	AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLOBLH07 3'
3222	13146		0.82	1.9E-02	AB033611.1	NT	Utrichius talpoides mitochondrial gene for cytochrome b, complete cds
3560	13474		1.25	1.9E-02	N52250.1	EST_HUMAN	y28b02.s1 Soares_multiple_sclerosis_2NkHMSP Homo sapiens cDNA clone IMAGE:284331 3'
3644	13558		5.75	1.9E-02	BE738088.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
3654	13668	23355	0.98	1.9E-02	AI301183.1	EST_HUMAN	qt04c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1887260 3' similar to contains Alu repetitive element;
3661	13668	23646	1.14	1.9E-02	AF141940.1	NT	Mycoplasma litans VlhA1 precursor (VlhA1) and VlhA2 precursor (VlhA2) genes, partial cds
4099	13999	23777	1.47	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4099	13999	23778	1.47	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4441	14335	24125	2.51	1.9E-02	AI452999.1	EST_HUMAN	ij46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
4944	12335	22230	1.9	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 50
5356	15276	25106	1.29	1.9E-02	L47572.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
6985	16862		1.29	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
7377	17246	27452	1.47	1.9E-02	BF316129.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
7777	17627	27859	1.31	1.9E-02	BF695832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076283 5'
9234	19516	25137	2.55	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gliatin mRNA, complete cds
343	10302	20117	1.44	1.8E-02	AW771104.1	EST_HUMAN	hm52s06.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element;
670	10604	20421	1.14	1.8E-02	BF308122.1	EST_HUMAN	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1144	11057	20900	1.34	1.8E-02	X17664.1	NT	H.francisci mRNA for myelin basic protein (MBP)
1417	11323	21187	1.23	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encode (enc) mRNA, complete cds
2846	12512	22403	1.51	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3174	13099		0.89	1.8E-02	AI805629.1	EST_HUMAN	ie52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3812	13724	23513	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3812	13724	23514	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3936	13903		1.15	1.8E-02	AA861446.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406835 3'
4932	14229	24011	1.44	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301298-071-b11 DT0021 Homo sapiens cDNA
4873	14753	24532	1.05	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
4887	14767	24543	1.06	1.8E-02	AI288701.1	EST_HUMAN	qm06b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881007 3'
6075	16058	26207	3.96	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
							aj62709.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb.L11672 ZINC FINGER PROTEIN 91 (HUMAN);
7560	17411		2.49	1.8E-02	AA897543.1	EST_HUMAN	

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7790	17640	27873	1.51	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868983 5'
7871	17721	27066	1.23	1.8E-02	XG6933.1	NT	L.stegialis mRNA for myomodulin neuropeptide precursor
8735	17884	28126	1.78	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8735	17884	28127	1.78	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8886	18697	28991	1.76	1.8E-02	AF000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (617)
8897	18706	29000	3.12	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
9912	19496		1.29	1.8E-02	AF047475.1	NT	Drosophila melanogaster projectin (projectin) gene, partial cds
888	10814	20662	1.29	1.7E-02	BE394869.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1750	11650	21519	2.24	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element;
1750	11650	21520	2.24	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element;
1828	11725		3.08	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2066	11956		13.03	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for misugumin29, complete cds
2803	12471		1.35	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GTP exchange factor homologue (RABEX5), mRNA
2968	12895	22695	0.92	1.7E-02	AI1147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3467	13383		4.17	1.7E-02	AW827388.1	EST_HUMAN	hm45a04.x1 NCL_OGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
3573	13487		0.88	1.7E-02	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4078	13980		0.98	1.7E-02	AA669618.1	EST_HUMAN	act19f04.s1 Stralagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4105	14005		1.78	1.7E-02	R02506.1	EST_HUMAN	yes5f08.f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4427	14322	24109	1.24	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element;
4615	14503	24291	1.77	1.7E-02	V00841.1	NT	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
4708	14594		5.27	1.7E-02	AI015076.1	EST_HUMAN	ov51602.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
4967	14842	24612	5.47	1.7E-02	AF106037.1	NT	Murid herpesvirus 4 complete genome
5725	15632	25735	1.53	1.7E-02	AI769247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6276	16140	26296	2.31	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
6554	16412		1.81	1.7E-02	AJ010770.1	NT	Homo sapiens hypeton gene, exons 1-50
7502	17443	27659	1.48	1.7E-02	AL040554.1	EST_HUMAN	DKFZp434i0314_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434i0314 5'
9781	19683	24995	2.25	1.7E-02	AW903482.1	EST_HUMAN	CM4-NN1030-040400-130-f06 NN1030 Homo sapiens cDNA
9861	19362		1.96	1.7E-02	Q03211	SWISSPROT	P1STIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
501	10443		1.58	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 13162
1635	11539	21399	1.13	1.6E-02	Y18889.1	NT	Treponema mallophilum flaB2, flaB3 and flilD genes for flagellin subunit proteins and CAP protein homologue
2202	12089	21990	1.13	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2202	12089	21991	1.13	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2518	12392	22284	0.98	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQ11 gene
2806	12474	22368	1.47	1.6E-02	AA434872.1	EST_HUMAN	ne81d06.s1 NCI CGAP EWI Homo sapiens cDNA clone IMAGE:910867
2662	12529		1.14	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3481	13397	23202	3.83	1.6E-02	AW850682.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
4084	13986		2.16	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4203	14102	23885	0.94	1.6E-02	AW 875407.1	EST_HUMAN	QV2-P70012-140100-030-707 P70012 Homo sapiens cDNA
5456	15377	25437	1.31	1.6E-02	6671715	NT	Mus musculus CD8 antigen (Cd8), mRNA
6003	15908	26032	2.11	1.6E-02	AB015281.1	NT	Candida albicans CaGOR3 gene, complete cds
6758	16637		4.01	1.6E-02	X06151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
7773	17623		2.71	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
7954	17804	28044	1.47	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI CGAP Pr1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
7954	17804	28044	1.47	1.6E-02	AA572818.1	EST_HUMAN	P29294 TELOKIN. [1];
8260	19473	28401	2.17	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI CGAP Pr1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
8544	18416	28683	2.52	1.6E-02	AL161508.2	NT	G.gallus microsatellite DNA (LEI0260) (=T1611E11)
8544	18416	28684	2.52	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8801	18615	28905	1.91	1.6E-02	AI373558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
9211	12089	21990	1.35	1.6E-02	Q64176	SWISSPROT	q296e10.x1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:2042442 3'
9211	12089	21991	1.35	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
9577	19165		2.3	1.6E-02	X92751.1	NT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
9973	19433		1.42	1.6E-02	11417966	NT	R.norvegicus gene for choline acetyltransferase, exon 1 (non coding)
734	10666		24.9	1.5E-02	8923734	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
2095	11984	21879	3.81	1.5E-02	N39521.1	EST_HUMAN	Homo sapiens transcription factor (HSA130894), mRNA
2128	12016	21914	2.38	1.5E-02	AL161594.2	NT	YW27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
3023	12951	22743	1.44	1.5E-02	AJ006216.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3023	12951	22744	1.44	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
						NT	Homo sapiens CACNA1F gene, exons 1 to 48

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3663	13577	23365	0.9	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
4049	13951	23727	1.23	1.5E-02	AA160967.1	EST_HUMAN	zq40g10.r1 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:6322226 5'
4367	14263	24048	0.91	1.5E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5801	15707	25819	1.91	1.5E-02	Q08711	SWISSPROT	HYPOTHEICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I
6332	16195		1.66	1.5E-02	11467282	NT	Cyanophora paradoxa cyenelle, complete genome
6377	16239	26399	1.36	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
6596	16476	26684	1.53	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6600	16480	26688	3.44	1.5E-02	11417739	NT	Homo sapiens valy-IRNA synthetase 2 (VAR52), mRNA
7126	17003	27195	1.23	1.5E-02	BF345554.1	EST_HUMAN	802019135F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4154504 5'
7520	17339	27545	2.07	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
7646	17496	27717	1.25	1.5E-02	R32687.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
7646	17496	27718	1.25	1.5E-02	R32687.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
8508	18380	28647	2.5	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds
9429	19559		1.32	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
9980	19437		1.47	1.5E-02	AU134730.1	EST_HUMAN	AU134730 PLACET Homo sapiens cDNA clone PLACE1000374 5'
411	10357		1.45	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1102	11018	20860	3.58	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1236	11143		1.35	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1276	11184		2.82	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1374	11280		0.94	1.4E-02	AF216854.1	NT	Homo sapiens headpin gene, complete cds
1501	11405		0.96	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
3176	13101	22905	1.9	1.4E-02	AF160969.2	NT	Bifidobacterium longum Nav/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (negC/xyR) gene, partial cds
3352	13272	23074	0.99	1.4E-02	AW074212.1	EST_HUMAN	xb09d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3439	13356	23161	5.21	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3439	13356	23162	5.21	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3476	13392	23197	0.98	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3606	13520	23308	6.16	1.4E-02	6996918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4387	14283	24062	7.29	1.4E-02	AW962688.1	EST_HUMAN	EST1374761 IMAGE resequences, MAGG Homo sapiens cDNA
4387	14283	24063	7.29	1.4E-02	AW962688.1	EST_HUMAN	EST1374761 IMAGE resequences, MAGG Homo sapiens cDNA
4775	14659	24445	6.7	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4775	14659	24446	6.7	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5862	15768	25887	4.62	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
5862	15768	25888	4.62	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
6732	16612		1.82	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
7403	17275	27481	2.07	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
9128	18885	28790	4.79	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
9476	19102		1.55	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
9753	19277		1.89	1.4E-02	11426968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1821	11718		0.86	1.3E-02	BE739253.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'
1912	11807	21684	2.41	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3177	13102	22906	1.99	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3177	13102	22907	1.99	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3883	13789		1.41	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5176	11807	21684	1	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5212	15135	24854	1.36	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
5212	15135	24855	1.36	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
6156	15114	24856	1.35	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6156	15114	24857	1.35	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6473	16332	26499	4.77	1.3E-02	AI031593.1	EST_HUMAN	ow06q05.x1 Soares_parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
6939	16817	27010	1.74	1.3E-02	AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
7862	17712	27956	1.87	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
8360	18237	28484	4.39	1.3E-02	AW268593.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
8360	18237	28485	4.39	1.3E-02	AW268593.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
9102	19705		2.92	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
9482	19694		1.6	1.3E-02	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
9586	19170		1.8	1.3E-02	9633069	NT	Human herpesvirus 6B, complete genome
9758	19486		28.64	1.3E-02	AF152239.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
9949	19744	24912	1.32	1.3E-02	AF009179.1	NT	Oryza sativa replication protein A1 (Os-RPA1) mRNA, complete cds
206	10177		0.94	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
352	10310	20128	1.74	1.2E-02	AA059299.1	EST_HUMAN	zfb5g01.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
445	10389	20210	1.48	1.2E-02	P39898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
721	10653	20483	2.98	1.2E-02	A1183522.1	EST_HUMAN	qd89e12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.1 L1 repetitive element;
2130	12018	21916	1.99	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2393	12271	22167	1.23	1.2E-02	AW172350.1	EST_HUMAN	xj37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2448	12325	22223	1.1	1.2E-02	BE538310.1	EST_HUMAN	601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2448	12325	22224	1.1	1.2E-02	BE538310.1	EST_HUMAN	601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2596	12271	22167	1.27	1.2E-02	AW172350.1	EST_HUMAN	xj37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3063	12990		6.18	1.2E-02	AA075418.1	EST_HUMAN	zn88e03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3250	13173	22971	1.89	1.2E-02	R62805.1	EST_HUMAN	yt11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
4830	14712	24495	2.04	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4974	14849		1.73	1.2E-02	AB019786.1	NT	Cynops pyrogastrer CpUbiqT mRNA, partial cds
5017	14891	24659	2.12	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5516	15434	25497	1.96	1.2E-02	D78589.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6180	16066	26216	5.33	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
6327	16190	26352	6.37	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
6865	16545	26742	2.11	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
6765	16644	26832	1.22	1.2E-02	AF193812.1	NT	Homo sapiens fringe protein mRNA, partial cds
6765	16644	26833	1.22	1.2E-02	AF193812.1	NT	Homo sapiens fringe protein mRNA, partial cds
7152	17029		1.17	1.2E-02	T78887.1	EST_HUMAN	yt72c08.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:113774 3'
7557	17408	27623	2.45	1.2E-02	AB031013.1	NT	Nonwalk-like virus genogroup 2 gene for capsid protein, complete cds
7575	17426	27640	1.23	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
9177	18918	25345	1.78	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU) (HPER)
9588	19575		1.5	1.2E-02	P17139	SWISSPROT	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR
9766	19286		3.47	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TF-ujivara) Homo sapiens cDNA clone GEN-557G06 5'
1248	11155	21004	1.32	1.1E-02	AA070364.1	EST_HUMAN	zn69e11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1679	11581	21451	1.99	1.1E-02	X75491.1	NT	H sapiens LIPA gene, exon 4
1679	11581	21452	1.99	1.1E-02	X75491.1	NT	H sapiens LIPA gene, exon 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1992	11886	21778	4.35	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4163808 5'
2848	12776		3.53	1.1E-02	N99523.1	EST_HUMAN	za40e05.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:295040 5'
2933	12860	22660	10.39	1.1E-02	AF055066.1	NT	Homo sapiens MHC class 1 region
3478	13394	23200	2.46	1.1E-02	A1653508.1	EST_HUMAN	tg95b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218539 3' similar to SW:XPFP_HUMAN
3937	13846		0.87	1.1E-02	BE144637.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4016	13921		0.97	1.1E-02	BE144637.1	EST_HUMAN	PM3-HT0175-300999-001-h06 HT0175 Homo sapiens cDNA
4723	14609	24395	1.81	1.1E-02	AW813796.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
4821	14704		0.92	1.1E-02	AL048383.2	EST_HUMAN	DKFZp586E0924.s1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586E0924
6480	16339	26506	2.26	1.1E-02	BE149611.1	EST_HUMAN	QV2-ST0296-150200-028-c11 ST0296 Homo sapiens cDNA
7160	17037	27230	6.87	1.1E-02	Q61982	SWISSPROT	RC1-HT0256-100300-015-h07 HT0256 Homo sapiens cDNA
7710	17560	27785	2.25	1.1E-02	AA082578.1	EST_HUMAN	NEUROGENIC LOCUS NOTCH 3 PROTEIN
7810	17660	27900	4.1	1.1E-02	AA314665.1	EST_HUMAN	zn24a01.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
8347	18224	28476	3.38	1.1E-02	11435505	NT	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
9064	18845		2.23	1.1E-02	AA668239.1	EST_HUMAN	Homo sapiens T-box 5 (TBX5), mRNA
6	9892	19785	3.35	1.0E-02	AW846120.1	EST_HUMAN	ab77f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
1506	11411	21270	0.91	1.0E-02	AW368128.1	EST_HUMAN	Alu repetitive element;
2525	12399		1.2	1.0E-02	AA806389.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA
3051	12978	22771	2.37	1.0E-02	BE835556.1	EST_HUMAN	GM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3226	13150	22950	1.18	1.0E-02	BE968999.1	EST_HUMAN	cc22h08.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3454	13380		0.99	1.0E-02	AW848621.1	EST_HUMAN	RC0-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
3805	13717	23505	0.79	1.0E-02	A1655086.1	EST_HUMAN	601649987R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
4667	14553	24345	4.26	1.0E-02	6753521	NT	MR0-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA
4736	14621	24407	2.38	1.0E-02	R96667.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4895	14870	24633	0.85	1.0E-02	AF218910.1	NT	Mus musculus corticotroph releasing hormone receptor 2 (Chr2), mRNA
5149	15016		0.82	1.0E-02	BE876539.1	EST_HUMAN	yq54h01.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:199633 5'
5751	15659	25786	2.74	1.0E-02	AW577113.1	EST_HUMAN	Homo sapiens attractin precursor (ATRN) gene, exon 25 and complete cds, alternatively spliced
5751	15659	25787	2.74	1.0E-02	AW577113.1	EST_HUMAN	601486286F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888908 5'
6054	16037	26178	2.06	1.0E-02	Z29642.1	NT	MR4-BT0355-070100-201-h01 BT0355 Homo sapiens cDNA
7403	17270	27475	4.65	1.0E-02	BF036331.1	EST_HUMAN	MR4-BT0355-070100-201-h01 BT0355 Homo sapiens cDNA
7403	17270	27476	4.65	1.0E-02	BF036331.1	EST_HUMAN	Z.mays U3snRNA pseudogene
							601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
							601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8586	18454		2.1	1.0E-02	AF157559.1	NT	Crithidia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
8674	18562	28846	2.03	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
9142	19762		1.7	1.0E-02	Q62203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
9202	19835	25061	2.95	1.0E-02	AW935521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
9217	19590		5.22	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
9745	19845		2.44	1.0E-02	X62654.1	NT	H. sapiens gene for Me491/CD63 antigen
875	10901	20651	1.7	9.0E-03	A1799126.1	EST_HUMAN	win42f09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1243	11150		1.97	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element;
2346	12226	22123	3.26	9.0E-03	AL161559.2	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2593	12463	22355	1.08	9.0E-03	AJ243727.1	NT	A. rabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2593	12463	22356	1.08	9.0E-03	AJ243727.1	NT	Oncorhynchus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene)
2876	12803	22597	0.83	9.0E-03	AJ251744.1	EST_HUMAN	Oncorhynchus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene)
2876	12803	22598	0.83	9.0E-03	AJ251744.1	EST_HUMAN	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3617	13531	23317	0.92	9.0E-03	J05184.1	NT	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
4914	14793	24568	1.17	9.0E-03	BE047949.1	EST_HUMAN	S. acidocaldarius thermopsis gene, complete cds
5181	15045		2.56	9.0E-03	AF137240.1	NT	tz44e10.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291466 5'
5997	15902		4.17	9.0E-03	BE745988.1	EST_HUMAN	Sargocentron sp. mixed lineage leukemia-like protein (Mll) gene, partial cds
6597	16477		1.18	9.0E-03	AL039991.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
7673	17523	27749	1.47	9.0E-03	P20908	SWISSPROT	DKFZp434L0412_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0412 5'
8354	18231		1.95	9.0E-03	Y18000.1	NT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
9352	19763		1.34	9.0E-03	BF351141.1	EST_HUMAN	Homo sapiens NF2 gene
9557	19758		11.59	9.0E-03	BE348385.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
9562	15045		1.27	9.0E-03	AF137240.1	NT	hw17b09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
9649	19215	25259	1.52	9.0E-03	AL163267.2	NT	Sargocentron sp. mixed lineage leukemia-like protein (Mll) gene, partial cds
9843	19341		27.64	9.0E-03	BF351141.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C067
493	10436		3.2	8.0E-03	AA723007.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
973	10897	20744	45.2	8.0E-03	AF106556.1	NT	zh30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains
2113	12002	21900	2.38	8.0E-03	AL163283.2	NT	Alu repetitive element;
							Homo sapiens adenylosuccinate lyase gene, complete cds
							Homo sapiens chromosome 21 segment HS21C083

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2930	12857		0.86	8.0E-03	U47048.1	NT	Escherichia coli microcin 24 region, DNA binding protein (mdbA), immunity protein (mtfI), microcin 24 (mtfS), and microcin transport protein (mtfA, mtfB) genes, complete cds
3270	13191	22990	0.97	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA
3314	13235	23039	0.89	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3792	13704		1.07	8.0E-03	AF058764.1	NT	Xenopus laevis bone morphogenetic protein 4 (BMP-4) gene, complete cds
4286	14185	23966	5.12	8.0E-03	BF363327.1	EST_HUMAN	GM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
5391	15310	25164	2.7	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
5761	19453	25775	1.35	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (217)
6048	15951	26081	4.52	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6279	16143	26299	2.19	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
6453	16314		1.86	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7166	17043	27235	3.81	8.0E-03	AW808692.1	EST_HUMAN	MR1-BT0111-111199-011-h06 ST0111 Homo sapiens cDNA
7717	17567		4.72	8.0E-03	BE086509.1	EST_HUMAN	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
8148	18036	28284	1.92	8.0E-03	BE788441.1	EST_HUMAN	601475619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
8353	18230		2.78	8.0E-03	Z49652.1	NT	S. cerevisiae chromosome X reading frame ORF YJR152w
8687	18575	28858	1.75	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.st NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
8687	18575	28859	1.75	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.st NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
8953	18760	29053	4.83	8.0E-03	AF064599.1	NT	Homo sapiens melanoma-associated antigen (IMAGE-C1) gene, complete cds
9075	18852		1.34	8.0E-03	M69035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
9121	18882		3.36	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
679	10612	20433	11.58	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
679	10612	20434	11.58	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
961	10884	20732	2.01	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1100	11016	20858	2.6	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1341	11247		1.19	7.0E-03	Q61060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1373	11279	21135	13.73	7.0E-03	AA668298.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HNF-2)
1486	11391	21251	4.6	7.0E-03	AW303599.1	EST_HUMAN	ab79k09.st Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
2210	12715	22001	2.24	7.0E-03	P04929	SWISSPROT	x21b02.11 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
3702	13616	23400	1.27	7.0E-03	AW444463.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
							UI-H-B13-akt-c-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3741	13653	23436	1.01	7.0E-03	AF196344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4434	14329		1.23	7.0E-03	AW117711.1	EST_HUMAN	xe34f09.x1 NCL_CGAP_U1r Homo sapiens cDNA clone IMAGE:2609033 3' similar to TR:Q12987 Q12987
4495	14389		1.01	7.0E-03	AW630988.1	EST_HUMAN	ACIDIC 82 KDA PROTEIN ;
4916	14795		1.76	7.0E-03	AL163278.2	NT	hh89a05.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969936 5'
5038	14910	24683	1.1	7.0E-03	BE044191.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
5039	14910	24684	1.1	7.0E-03	BE044191.1	EST_HUMAN	ho39h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:O93434
5717	19452		5.07	7.0E-03	AW861059.1	EST_HUMAN	O93434 RETICULOCALBIN ;
5813	15718	25831	1.49	7.0E-03	W68251.1	EST_HUMAN	ho39h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:O93434
5939	15844	25967	3.46	7.0E-03	AA327129.1	EST_HUMAN	O93434 RETICULOCALBIN ;
5954	15859	25980	1.3	7.0E-03	BE867385.1	EST_HUMAN	ho39h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:O93434
6210	15992	26127	2.39	7.0E-03	BE928133.1	EST_HUMAN	O93434 RETICULOCALBIN ;
6441	16302	26466	4.98	7.0E-03	Z35838.1	NT	RC1-CT0286-060400-018-c08 CT0286 Homo sapiens cDNA
6441	16302	26467	4.98	7.0E-03	Z35838.1	NT	RC1-CT0286-060400-018-c08 CT0286 Homo sapiens cDNA
6723	16603	26792	2.29	7.0E-03	BE176667.1	EST_HUMAN	zdc3f10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'
7605	17456	27670	2.53	7.0E-03	P48982	SWISSPROT	EST30674 Colon 1 Homo sapiens cDNA 5' end
7605	17456	27671	2.53	7.0E-03	P48982	SWISSPROT	7g34b10.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
7906	17755		1.27	7.0E-03	AV687379.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 394D8_2 ; contains TAR1.12 TAR1 TAR1 repetitive element ;
8201	18086	28337	3.36	7.0E-03	AB008852.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
9609	19750		1.55	7.0E-03	H94065.1	EST_HUMAN	S. cerevisiae chromosome II reading frame ORF YBL077w
9615	19194		1.88	7.0E-03	BE263253.1	EST_HUMAN	S. cerevisiae chromosome II reading frame ORF YBL077w
9962	19425		1.83	7.0E-03	AW868110.1	EST_HUMAN	RC6-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
1220	11129	20979	9.29	6.0E-03	AW511148.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
1220	11129	20980	9.29	6.0E-03	AW511148.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
2744	12606	22499	1.09	6.0E-03	AF112374.1	NT	AV687379 GKc Homo sapiens cDNA clone GKCAFC07 5'
2862	12790	22681	3.11	6.0E-03	AA759135.1	EST_HUMAN	Bos taurus mRNA for NDP52, complete cds
2862	12790	22682	3.11	6.0E-03	AA759135.1	EST_HUMAN	yv15h01.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
							Alu repetitive element;
							601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
							RCO-SN0052-110400-021-a04 SN0052 Homo sapiens cDNA
							hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
							SW_PXR_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR ;
							hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
							SW_PXR_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR ;
							Danio rerio odorant receptor gene cluster
							ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
							ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3208	13132		2.06	6.0E-03	H75690.1	EST_HUMAN	y77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3264	13187		0.82	6.0E-03	AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3336	13256	23062	1.24	6.0E-03	U90890.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3336	13256	23063	1.24	6.0E-03	U90890.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3499	13416		1.05	6.0E-03	W37985.1	EST_HUMAN	zot13a11.1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3610	13524	23311	3.62	6.0E-03	BF510986.1	EST_HUMAN	UI-H-BI4-apm-c-08-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3711	13624	23407	1.28	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnp), mRNA
3846	13757	23551	0.93	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240999-021-b10 CT0204 Homo sapiens cDNA
3873	13784		1.18	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5'
4231	14129		0.87	6.0E-03	N58946.1	EST_HUMAN	yg62h10.s1 Soares multiple sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278179 3'
4267	14166		1.37	6.0E-03	A016833.1	EST_HUMAN	ov33c11.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4597	14485	24271	6.82	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5115	14963	24758	1.83	6.0E-03	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5129	14996	24767	0.89	6.0E-03	AA889972.1	EST_HUMAN	ag95g09.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404266 3'
6506	16365	26542	1.97	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
6586	16466	26657	7.04	6.0E-03	A1033980.1	EST_HUMAN	ow13a04.x1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element;
6650	16530	26724	2.44	6.0E-03	AW799337.1	EST_HUMAN	RCO-JM0051-210300-032-g02 UM0051 Homo sapiens cDNA
6659	16569		1.41	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
7509	17297	27506	8.21	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
7776	17626		1.94	6.0E-03	A1432661.1	EST_HUMAN	t122c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
7949	17799	28039	1.5	6.0E-03	X68366.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A ;
8127	18015	28263	2.23	6.0E-03	AW962164.1	EST_HUMAN	M.thermoformicum complete plasmid pFV1 DNA
8186	18072		2.21	6.0E-03	11545814	NT	EST374237 MAGG resequences, MAGG Homo sapiens cDNA
8220	18102	28356				EST_HUMAN	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
8220	18102	28357				EST_HUMAN	tes1c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 C00519
8350	18227					EST_HUMAN	FATTY ACID AMIDE HYDROLASE ;
8351	18228	28479				EST_HUMAN	te91c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 C00519
						EST_HUMAN	FATTY ACID AMIDE HYDROLASE ;
						EST_HUMAN	FATTY ACID AMIDE HYDROLASE ;
						EST_HUMAN	Mus musculus zinc-finger protein mRNA, complete cds
						EST_HUMAN	601672746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9185	19922		1.59	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
9310	19519		3.6	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450296 (section 39 of 148) of the complete genome
9372	19038		1.34	6.0E-03	AB028356.1	NT	Anguilla japonica mRNA for activin B, complete cds
9392	19583		2.21	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcgr1) gene, complete cds
9722	19262		1.57	6.0E-03	BE789019.1	EST_HUMAN	601482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5'
9741	19274		1.34	6.0E-03	AJ245480.1	NT	Brassica napus slg gene for S-locus glycoprotein, cultivar T2
653	10589	20406	1.9	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
653	10589	20407	1.9	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	10589	20406	2.92	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	10589	20407	2.92	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1096	11012	20854	1.38	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
1552	11457		0.91	5.0E-03	A1138977.1	EST_HUMAN	q079d05.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2648	12515	22405	3.44	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2905	12832	22629	0.95	5.0E-03	BE266057.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3097	13024	22620	4.08	5.0E-03	T87623.1	EST_HUMAN	yc81f09.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3116	13041		1.75	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3129	13054	22853	1.04	5.0E-03	R71794.1	EST_HUMAN	y86g02.s1 Soares breast 2N1bHBst Homo sapiens cDNA clone IMAGE:155666 3'
3240	13163		1.08	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3641	13555	23341	4.16	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3698	13612	23396	0.83	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3800	13801		1.38	5.0E-03	AA299675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4207	14106	23886	0.93	5.0E-03	H78355.1	EST_HUMAN	yc79g10.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:240066 5'
4209	13612	23396	0.91	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4503	14396	24181	0.94	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4619	14507	24296	2.49	5.0E-03	A1752357.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5541	15458	25528	5.34	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5685	15594	25695	2.43	5.0E-03	Q00507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
5977	15881		6.17	5.0E-03	BE300091.1	EST_HUMAN	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2660871 3'
6091	15101	24877	6.02	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6566	16424	26605	6.26	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
6794	16673	26865	1.97	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
7008	16983		6.92	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
8103	17993		7.44	5.0E-03	T19586.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
8310	18187	28435	3.17	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.L2 L1 repetitive element;
8310	18187	28436	3.17	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.L2 L1 repetitive element;
8399	18275	28527	1.95	5.0E-03	T49153.1	EST_HUMAN	60904.1 Stratagene placenta (#637225) Homo sapiens cDNA clone IMAGE:70686 5'
8433	18307	28563	1.77	5.0E-03	10946753	NT	Mus musculus hypothetical protein, MNCb-4760 (LOC58212), mRNA
8644	18508		3.73	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291622 5'
9327	19709		5.04	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
9460	19091		8.65	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
9555	19153		1.55	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
9592	19174		1.28	5.0E-03	AA456597.1	EST_HUMAN	zx75a03.s1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:806548 3' similar to SW:DXA2 MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT;
9616	19529		4.16	5.0E-03	BF672332.1	EST_HUMAN	602077774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
9791	19301	25197	1.94	5.0E-03	AW449109.1	EST_HUMAN	U1-H-B13-akf-f-08-0-U1.s1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2794215 3'
9808	19601		1.4	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
9929	19400		1.41	5.0E-03	A1668709.1	EST_HUMAN	zb74g05.x5 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:309368 3'
232	10201	20015	2.97	4.0E-03	AW500196.1	EST_HUMAN	U1HF-BN0-akc-h-04-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
318	10280	20097	2.18	4.0E-03	R46482.1	EST_HUMAN	y951e04.s1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:35988 3'
436	10380	20203	0.94	4.0E-03	P54575	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
588	10526	20333	3	4.0E-03	AA939339.1	EST_HUMAN	on75g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562566 3'
859	10785	20637	1.81	4.0E-03	R46482.1	EST_HUMAN	y951e04.s1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:35988 3'
893	10819		3.43	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-f01 BT0333 Homo sapiens cDNA
1133	11047	20869	32.55	4.0E-03	AA099777.1	EST_HUMAN	z181a08.r1 Stratagene colon (#637204) Homo sapiens cDNA clone IMAGE:510988 5'
1153	11066	20910	1.58	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1281	11189	21040	1.33	4.0E-03	AA284374.1	EST_HUMAN	zs59a01.r1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:701736 5'
1568	11472		1.31	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
1709	11610	21480	2.2	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds
1971	11864	21757	20.87	4.0E-03	AA099777.1	EST_HUMAN	z181a08.r1 Stragene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2200	12087		1.66	4.0E-03	BE410556.1	EST_HUMAN	601304161FT NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3638510 5'
2232	12117	22019	1.46	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2526	12400	22290	1.89	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2526	12400	22291	1.89	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2659	12526	22414	2.86	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2659	12526	22415	2.86	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2664	12530	22418	1.02	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3487	13403	23207	0.94	4.0E-03	AW188426.1	EST_HUMAN	X88104.x1 NCI_CGAP_Cot8 Homo sapiens cDNA clone IMAGE:2685279 3'
3487	13403	23208	0.94	4.0E-03	AW188426.1	EST_HUMAN	X88104.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2685279 3'
3572	13486	23278	0.8	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3836	13486	23278	0.83	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3852	13763	23556	0.85	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
3914	13823		1.79	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4509	14402	24190	1.13	4.0E-03	AJ732754.1	EST_HUMAN	ab18a08.x5 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
5194	15030	24796	13.17	4.0E-03	J02187.1	NT	Foot and mouth disease virus serotype A-12 119ab capsid protein VP3
5225	15149	24916	1.66	4.0E-03	AF005859.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5315	15236	25039	19.53	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5540	15457	25527	4.23	4.0E-03	P04196	SWISSPROT	(HPRG)
5542	15469	25529	1.5	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR
5704	15612		3.23	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
5809	15714	25627	1.76	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC 12 Homo sapiens cDNA clone IMAGE:3461954 5'
6082	16045	26190	1.62	4.0E-03	U79408.1	NT	Lycopodium obscurum knotted 3 protein (TKn3) mRNA, complete cds
6271	16136	26291	4.14	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
6690	16570	26762	3.61	4.0E-03	AF111944.1	NT	Dictyostelium discoideum AX4 development protein DG1122 (DG1122) gene, partial cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6774	16653	26841	2.02	4.0E-03	7682067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
7056	16933	27123	7.4	4.0E-03	AI553983.1	EST_HUMAN	te49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element;
7151	17028		4.41	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7159	17036	27229	3.38	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
8472	18345	28609	5.64	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
9295	19725		3.95	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
9317	19009		2.25	4.0E-03	BE298290.1	EST_HUMAN	601118194F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
9628	19202		3	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
9666	19640		1.57	4.0E-03	AW614596.1	EST_HUMAN	hn02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2963932 3' similar to contains element
9679	19236		1.57	4.0E-03	AW819141.1	EST_HUMAN	LTR5 repetitive element;
9950	19416	25168	1.52	4.0E-03	11436955	NT	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA
367	10323	20146	1.62	3.0E-03	AF011920.1	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
861	10787	20638	7.66	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1638	11542	21401	1.84	3.0E-03	AA468110.1	EST_HUMAN	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
2211	12097		0.87	3.0E-03	AF055066.1	NT	nc73c05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2248	12132		3.9	3.0E-03	Z32521.1	NT	Homo sapiens MHC class 1 region
2249	12133	22029	1.12	3.0E-03	U46558.1	NT	S.cereale (cv. Halo) mRNA for triphosphate isomerase
2249	12133	22030	1.12	3.0E-03	U46558.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2963	12890		0.84	3.0E-03	Y09006.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3044	12971	22765	4.53	3.0E-03	BE379296.1	EST_HUMAN	Arabidopsis thaliana pcdMt gene
3112	13037	22833	2.62	3.0E-03	AW802687.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3371	13290	23098	1.95	3.0E-03	U34606.1	NT	IL2-UM0076-240300-086-D03 UM0076 Homo sapiens cDNA
3379	13297		6.75	3.0E-03	Y12500.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3895	13805	23591	7.43	3.0E-03	AV762392.1	EST_HUMAN	C.elegans samdc gene
3895	13805	23592	7.43	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
3950	13858	23632	1.58	3.0E-03	AI792278.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4058	13960		1.34	3.0E-03	Z32521.1	NT	ar04f09.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4296	14194	23978	11.91	3.0E-03	AJ011432.1	NT	S.cereale (cv. Halo) mRNA for triphosphate isomerase
4417	14311	24096	4.37	3.0E-03	AI538141.1	EST_HUMAN	Rattus norvegicus gdnf gene
4630	14518	24309	0.88	3.0E-03	AL119067.1	EST_HUMAN	ratP10.H3 conorm Homo sapiens cDNA 3'
							DKFZp761B0712.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4727	14613	24399	1.54	3.0E-03	A1732754.1	EST_HUMAN	ab18a08.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4745	14630	24416	7.09	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5089	14959	24733	1.11	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5089	14959	24734	1.11	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5220	15143	24837	3.17	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5410	15330	25380	1.41	3.0E-03	AJ249981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5946	15851	25974	9.97	3.0E-03	AA466701.1	EST_HUMAN	aat13f10.t1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
6277	16141	26297	1.54	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pep3 gene for purine-cytosine permease
6442	16303	26468	3.71	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
6741	16620	26809	2.01	3.0E-03	N92590.1	EST_HUMAN	2b27b04.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
6928	16806	27001	1.29	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
6940	16818	27011	1.57	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
6991	16868		1.38	3.0E-03	Q9QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
7199	17076					EST_HUMAN	hh80f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969131 3' similar to contains L1.1 L1 repetitive element;
7230	17107	27297	8.52	3.0E-03	AW613774.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
7244	17121	27317	8.9	3.0E-03	A016731.1	EST_HUMAN	ov03d12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb.X57138_rna1 HISTONE H2B.2 (HUMAN);
7598	17449		3.48	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZOTE PROTEIN PRECURSOR (CS)
7694	17544	27768	1.29	3.0E-03	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
7742	17592	27813	1.46	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
7836	17686	27931	4.05	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8222	18104		2.69	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
8685	18573	28856	2.11	3.0E-03	A7009222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
8744	17893	28137	2.01	3.0E-03	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
8773	18590	28877	3.06	3.0E-03	A7094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
8773	18590	28878	3.06	3.0E-03	A7094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
8841	18654	28942	1.93	3.0E-03	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9068	19542		2.02	3.0E-03	A1525056.1	EST_HUMAN	promrna-5.E07.r bvtumor Homo sapiens cDNA 5'
9103	18870	28780	1.54	3.0E-03	AA993154.1	EST_HUMAN	af77b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER26 repetitive element;

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9159	19668		1.35	3.0E-03	AB009698.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
9339	19019	25296	2.33	3.0E-03	AJ296282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
504	10446	20268	0.89	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
504	10446	20259	0.89	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
768	12677		7.01	2.0E-03	T70874.1	EST_HUMAN	yf15h03.r1 Soares fetal liver spleen 4N1LS Homo sapiens cDNA clone IMAGE:108341 5'
1340	11246	21104	1.93	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1343	11249	21106	1.59	2.0E-03	AA661605.1	EST_HUMAN	nu86601.s1 NCL CGAP_AMT Homo sapiens cDNA clone IMAGE:1217593
1353	11259	21115	12.6	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1474	11379	21243	1.11	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1500	11404	21263	1.91	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1500	11404	21264	1.91	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1573	11477		4.94	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1733	11634	21502	1.38	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1960	11845	21731	2.17	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2203	12090	21992	1.04	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2535	12409		4.62	2.0E-03	AW137782.1	EST_HUMAN	UIH-B11-adi-g-10-0-UI.st NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3370	13289	23088	4.03	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3376	13294	23093	1.02	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3615	13529	23315	4.87	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IAPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
3859	13780	23572	0.92	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4024	13927	23703	2.15	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4127	14027		9.77	2.0E-03	U88491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4446	14340	24130	1.93	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4446	14340	24131	1.93	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4608	14496	24285	0.94	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4612	14500		1.7	2.0E-03	R87773.1	EST_HUMAN	y045e02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
5077	14947		0.82	2.0E-03	AJ245167.1	NT	Carnelius dromedarius cvfp19 gene for immunoglobulin heavy chain variable region
5194	15057	24820	1.04	2.0E-03	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
5194	15057	24821	1.04	2.0E-03	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5372	15292	25128	1.37	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5457	19445	25438	1.76	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5501	15420	25482	1.87	2.0E-03	U63711.1	NT	Xenopus laevis xefitin mRNA, complete cds
5716	15624	25725	3.25	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
5716	15624	25726	3.25	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
5829	15735	25846	1.82	2.0E-03	Q98203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
5829	15735	25847	1.82	2.0E-03	Q98203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
5831	15737	25849	7.14	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
5850	15756	25874	2.2	2.0E-03	Q9UJPK4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5861	15767	25886	1.95	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-tRNA synthetase (LysRS)
5979	15884		1.36	2.0E-03	A1991089.1	EST_HUMAN	wu36h09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW_RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element MSR1 repetitive element ;
6212	15994	26129	2.88	2.0E-03	BE067986.1	EST_HUMAN	CM4-BT0366-061299-054-401 BT0366 Homo sapiens cDNA
6691	16571	26763	2.11	2.0E-03	AW592004.1	EST_HUMAN	hf37b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60976 Q60976 JERKY. ;
6784	16663	26853	5.19	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
6784	16663	26854	5.19	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
7513	17301	27508	3.12	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
7775	17625		5.41	2.0E-03	AA251376.1	EST_HUMAN	zs10a05.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
8379	18256		2.78	2.0E-03	M86524.1	NT	Human dystrophin gene
8779	18350	26520	1.78	2.0E-03	P07364	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8829	18642		1.77	2.0E-03	BF330909.1	EST_HUMAN	RC9-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
8836	18649	28336	12.17	2.0E-03	Z11740.1	NT	H.sapiens variable number tandem repeat (VNTR) locus DNA
9052	18835		2.07	2.0E-03	A1625745.1	EST_HUMAN	ty55h03.x1 NCI CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
9066	18847	29115	2.88	2.0E-03	AF157516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ;
9113	14947		4.48	2.0E-03	AJ245167.1	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds
9322	19703		2.76	2.0E-03	AV697966.1	EST_HUMAN	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9414	19066	25278	1.59	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
9455	19087		9.62	2.0E-03	D84278.1	NT	Human DNA for CD38, exon 1
9525	19134		2.92	2.0E-03	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9592	19569		1.57	2.0E-03	AI375037.1	EST_HUMAN	ta66f02.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element;
9696	19247		1.27	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
9856	19621		1.66	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCXD08 5'
432	10377	20198	1.38	1.0E-03	H96471.1	EST_HUMAN	y98c08.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
812	10740	20687	2.38	1.0E-03	AI720263.1	EST_HUMAN	as70f008.x1 Barstead_colon_HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;
812	10740	20588	2.38	1.0E-03	AI720263.1	EST_HUMAN	as70f008.x1 Barstead_colon_HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;
1079	10995	20836	2.14	1.0E-03	AI865788.1	EST_HUMAN	wk86a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422288 3'
1099	11015	20857	1.44	1.0E-03	AI954572.1	EST_HUMAN	w93ef10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
1150	11063	20906	1.45	1.0E-03	AI892816.1	EST_HUMAN	wd86a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
1982	11875	21768	3.61	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMI)
2108	11997	21896	8.02	1.0E-03	AJ131016.1	NT	Homo sapiens SOL gene locus
2951	12878	22876	1.15	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3154	13079	22879	2.26	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3154	13079	22880	2.26	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3282	13185	22984	1.16	1.0E-03	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3496	13413	23218	0.79	1.0E-03	U68081.1	NT	Human MUC2 gene, promoter region
3496	13413	23219	0.79	1.0E-03	U68081.1	NT	Human MUC2 gene, promoter region
3614	13528		1.24	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
3855	13766	23559	1.02	1.0E-03	Z49649.1	NT	S.cerevisiae chromosome X reading frame ORF YJR149w
4334	14231	24013	3.54	1.0E-03	BE639162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4377	14273	24054	3.77	1.0E-03	BE246536.1	EST_HUMAN	TCBAP-ID4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4564	14456	24244	0.87	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4717	14603	24388	1.78	1.0E-03	A073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4717	14603	24389	1.78	1.0E-03	A073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4718	14604		8.23	1.0E-03	BE154067.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5009	14883	24649	16.98	1.0E-03	O46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5103	14971	24747	0.93	1.0E-03	AV689870.1	EST_HUMAN	AV689870 GKCC Homo sapiens cDNA clone GKCDME11 5'
5280	15173	24946	2.03	1.0E-03	AA290951.1	EST_HUMAN	zs44f01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5317	15238	25042	3.06	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQ11 gene
5349	15269	25096	2.01	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5349	15269	25097	2.01	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5423	15344	25397	1.69	1.0E-03	Q02398	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5696	15577		4.08	1.0E-03	X07699.1	NT	Mouse nucleolin gene
5758	15666		8.56	1.0E-03	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
5824	15730	25842	1.32	1.0E-03	T87761.1	EST_HUMAN	yd93a11.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:115772 5'
5857	15763		1.4	1.0E-03	AW902585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
6242	16108	26259	2.4	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
6419	16281		1.37	1.0E-03	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
6503	16362	26537	1.63	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cez2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
6536	16394	26573	3.13	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1, 2 and 3
6636	16516	26707	5.35	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
6798	16577	26867	2.39	1.0E-03	AF153980.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
7175	17032		1.4	1.0E-03	Y11204.1	NT	V.carteri gene encoding volvoxpsin
7273	17150	27345	4.27	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
7273	17150	27346	4.27	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
7541	17392	27602	1.85	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (ega1A) gene, complete cds
7541	17392	27603	1.85	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (ega1A) gene, complete cds
8056	17947	28196	22.37	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
8056	17947	28197	22.37	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
8133	18021	28268	2.44	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
8198	18083		2.69	1.0E-03	A1583847.1	EST_HUMAN	h73e12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195 PVA1 GENE.:
8497	18370		3.4	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
9046	18831	29113	2.82	1.0E-03	BE594488.1	EST_HUMAN	501433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9491	19108	25287	1.95	1.0E-03	9507208	NT	Rattus norvegicus transformation related protein 63 (Trp63), mRNA
9517	19687		2.15	1.0E-03	AI347355.1	EST_HUMAN	tc05h11.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
9626	19707	24904	4.2	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
5131	14988	24769	0.81	9.0E-04	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5485	15404		1.56	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
7561	17412		1.42	9.0E-04	AB037203.1	NT	Glycyrrhiza glabra GgbAS1 mRNA for beta-amylin synthase, complete cds
1472	11377		1.39	8.0E-04	X98469.1	NT	X laevis mRNA for C4SR protein
3843	13754	23548	1.27	8.0E-04	R07008.1	EST_HUMAN	yf12h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126691 5'
4089	13989		4.2	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4656	14542	24332	2.39	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
8455	18358		2.08	8.0E-04	AA777084.1	EST_HUMAN	z24-10.s1 Soares_fetal_heart_Nb1H19W Homo sapiens cDNA clone IMAGE:377874 3'
8616	18483		2.16	8.0E-04	AI571099.1	EST_HUMAN	tn85a08.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
1786	11694	21562	1.61	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2950	12230	22127	1.13	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2692	12547	22437	3.26	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3243	13166	22965	1.03	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
5923	15823		2.24	7.0E-04	AI769331.1	EST_HUMAN	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
8851	18663		3.2	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8871	18683	28973	2.61	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
9558	19155		3.29	7.0E-04	BE077941.1	EST_HUMAN	CM1_BT0614-110300-142-b12 BT0614 Homo sapiens cDNA
9790	19300		2.72	7.0E-04	R17336.1	EST_HUMAN	y913c06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:332298 5'
9813	19321		3.28	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
3877	13788	23576	1.34	6.0E-04	AI862525.1	EST_HUMAN	wf15a11.x1 NCL CGAP_K1212 Homo sapiens cDNA clone IMAGE:2402876 3'
3999	13905	23680	0.85	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHF1) gene, 5' flanking region
3999	13905	23681	0.85	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHF1) gene, 5' flanking region
4092	13992	23769	3.28	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6590	16470		4.35	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESINE (FRUCTOSE TRANSPORTER)
7733	17583		3.13	6.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_T1 586 (synonym: huler1) Homo sapiens cDNA clone DKFZp586M2024
7800	17650	27887	2.24	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
8765	18593	28881	2.07	6.0E-04	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
8852	18694	28950	6.32	6.0E-04	AW013847.1	EST_HUMAN	UH-H-B10-eab-e-09-C-UJ_s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
8906	18714		2.45	6.0E-04	Q01788	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9225	19598		2.26	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0269-261199-012-d08 HT0269 Homo sapiens cDNA
9958	19421	25170	1.49	6.0E-04	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1l subunit (CACNA1L), mRNA
635	10572	20385	5.82	5.0E-04	O10341	SWISSPROT	HYPOPHOSPHATASE 2, alpha 1 subunit (HYPH2A1), mRNA
1485	11390		1.83	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3367	13286	23085	1.42	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCL CGAP Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;
5361	15281	25113	2.19	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5996	15901	26026	5.72	5.0E-04	AA156080.1	EST_HUMAN	z033b08.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:588663 5'
6364	16227	26387	13.6	5.0E-04	M23604.1	NT	Gonilla gorilla involucrin gene medium allele, complete cds
6639	16519	26710	5.57	5.0E-04	AI188382.1	EST_HUMAN	gc13f06.x1 Soares placenta_806weeks_2Nb-HP809W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602 cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element;
7345	17213	27412	1.45	5.0E-04	AA846545.1	EST_HUMAN	g16b03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
7543	17394	27606	4.69	5.0E-04	AW270938.1	EST_HUMAN	xs06e02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
8343	18220		4.17	5.0E-04	AL048507.2	EST_HUMAN	DKFZp686M2024_r1 568 (synonym: hute1) Homo sapiens cDNA clone DKFZp686M2024
8950	15281	25113	17.6	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
9164	19530		2.27	5.0E-04	AA568513.1	EST_HUMAN	trf15h02.s1 NCL CGAP_Pr1 Homo sapiens cDNA clone IMAGE:913875
9944	19413		1.46	5.0E-04	AW241666.1	EST_HUMAN	xm77h09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2690273 3'
386	10333		1.13	4.0E-04	BF241482.1	EST_HUMAN	607876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
657	10592	20410	1.42	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
829	10756	20606	1.57	4.0E-04	AI70263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
829	10756	20607	1.57	4.0E-04	AI720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;
1449	11354	21218	3.92	4.0E-04	AW753356.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2037	11928	21823	1.68	4.0E-04	AL163278.2	NT	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;
2086	11976		1.19	4.0E-04	AL046704.1	EST_HUMAN	RC3-CT0254-130100-023-01 CT0254 Homo sapiens cDNA
2586	12457	22348	2.73	4.0E-04	O96615	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
3127	13052	22850	1.89	4.0E-04	AF281074.1	NT	DKFZp434D059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'
3316	13237	23041	0.84	4.0E-04	AV096624.1	EST_HUMAN	SERPIN-2 (SILK GUM PROTEIN 2)
4228	14126	23900	2.75	4.0E-04	AA576331.1	EST_HUMAN	Homo sapiens neuropilin 2 (NRP-2) gene, complete cds, alternatively spliced
							AV696624 GKGC Homo sapiens cDNA clone GKCFH07 5'
							rh10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4228	14126	23901	2.75	4.0E-04	AA576331.1	EST_HUMAN	h10a10.s1 NCL_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL
4437	14332	24121	1.28	4.0E-04	AA096324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5020	14393	24661	3.72	4.0E-04	BE560660.1	EST_HUMAN	zn61c08.s1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
							601345895.F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
5132	14999	24770	0.9	4.0E-04	N48313.1	EST_HUMAN	w78b10.s1 Soares_multiple_sclerosis_2NblHMS Homo sapiens cDNA clone IMAGE:279643 3' similar to contains Alu repetitive element;
6972	16849	27040	1.62	4.0E-04	N25507.1	EST_HUMAN	y339e12.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:264142 5'
7598	17439	27655	2.79	4.0E-04	A1025699.1	EST_HUMAN	ov87h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
7862	17612		1.44	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(at17) mRNA, alternatively spliced, complete cds
9526	19505		1.52	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
9677	19479		1.84	4.0E-04	Q05960	SWISSPROT	FORMIN (LIMB DEFORMITY PROTEIN)
150	10124	19942	3.04	3.0E-04	AL119426.1	EST_HUMAN	DKFZp761j221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761j221 5'
188	10160	19977	2.22	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
862	10788	20639	1.27	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1810	11707		1.16	3.0E-04	A1399674.1	EST_HUMAN	ht23a02.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2119082 3'
3268	13190	22998	3.37	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
3882	13793	23581	3.63	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
3969	13876		1.18	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4711	14597		4.5	3.0E-04	BE153778.1	EST_HUMAN	PMO-HT0339-190200-007.g12 HT0339 Homo sapiens cDNA
4784	14669	24456	0.85	3.0E-04	AW937723.1	EST_HUMAN	QV3-DT0045-221299-046-d09 DT0045 Homo sapiens cDNA
5052	14924		1.34	3.0E-04	Y11204.1	NT	V. carteri gene encoding volvoxopsin
5735	15643		4.82	3.0E-04	AL163291.2	NT	Homo sapiens chromosome 21 segment HS21C081
6091	16026	26166	5.88	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6906	16936	26875	3.49	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
7705	17555	27790	1.42	3.0E-04	AA454055.1	EST_HUMAN	zx48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762
							VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);
7977	17827	28098	3.66	3.0E-04	AA791201.1	EST_HUMAN	al24q05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S
							RIBOSOMAL PROTEIN L7A (HUMAN);
							nc38d04.r1 NCL_CGAP_P2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element ;
9118	19726	24908	2.33	3.0E-04	AA228301.1	EST_HUMAN	Homo sapiens mRNA for KIAA0749 protein, partial cds
9483	19576	25098	4.32	3.0E-04	AB018292.1	NT	Homo sapiens cDNA clone DKFZp547L185 5'
9874	19361		2.01	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547L185 5'
169	10141	19957	1.18	2.0E-04	AF217796.1	NT	Homo sapiens SGC10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
470	10413	20232	2.15	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
889	10815	20663	4.49	2.0E-04	M86524.1	NT	Human dystrophin gene
889	10815	20664	4.49	2.0E-04	M86524.1	NT	Human dystrophin gene
1162	11075		4	2.0E-04	AI286021.1	EST_HUMAN	q198e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1856052 3' similar to contains MER3.b2 MER3 repetitive element ;
1169	11081		1.99	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1791	11689		1.44	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Pitk3 gene
2136	12024		1.29	2.0E-04	AA478980.1	EST_HUMAN	zu39b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2528	12402	22293	4.15	2.0E-04	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV33S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,> am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
2958	12885	22683	1	2.0E-04	AI124529.1	EST_HUMAN	QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
3389	13307	23105	2.53	2.0E-04	BE082317.1	EST_HUMAN	Human tyrosine kinase TXK (btk) gene, exons 9 and 10
3417	13334	23138	0.98	2.0E-04	U34374.1	NT	EST390550 MAGe resequences, MAGP Homo sapiens cDNA
3837	13748	23541	0.78	2.0E-04	AW978441.1	EST_HUMAN	Phasolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4051	13953		4.61	2.0E-04	U01029.1	NT	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4569	14461	24249	1.27	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4569	14461	24250	1.27	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4689	14575		1.31	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
4991	14866	24630	1.7	2.0E-04	AB037997.1	NT	Danio rerio hagoromo gene, exons 1 to 6, partial cds
5403	15322	25371	1.63	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCDUH10 3'
5411	15331	25381	1.68	2.0E-04	AI690882.1	EST_HUMAN	tc03b11.x1 NCI_QGAP_U13 Homo sapiens cDNA clone IMAGE:2207709 3'
6291	16155		2.5	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
6493	16352		11.07	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6497	16356	26527	1.6	2.0E-04	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN- ASSOCIATED PROTEIN)
6638	16518	26708	1.33	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
6638	16518	26709	1.33	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
6819	16698	26890	1.19	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6819	16698	26891	1.19	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6982	18859	27054	2.29	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7729	17579	27801	1.46	2.0E-04	BE149303.1	EST_HUMAN	RC3-H20254-151099-011-b05 HT0254 Homo sapiens cDNA
7754	17604	27828	1.71	2.0E-04	AA405777.1	EST_HUMAN	zid6c11.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:742964 5'
8225	18107	28360	6.14	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAAA01 5'
8515	18387		1.88	2.0E-04	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
8625	18490	28762	5.57	2.0E-04	AI440282.1	EST_HUMAN	ij01f11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
8726	18582	28865	2.94	2.0E-04	AW136740.1	EST_HUMAN	UI-H-B11-adm-c-04-Q-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
750	10680	20516	0.98	1.0E-04	H99646.1	EST_HUMAN	y26c09.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262664 3' similar to contains L1.11 L1 repetitive element;
1059	10976	20819	2.43	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1098	11014	20855	3.87	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UI.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1098	11014	20856	3.87	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UI.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1310	11216		2.97	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
							Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1610	11515	21374	3.24	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1910	11515	21375	3.24	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1817	11714	21594	1.67	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2600	12469	22363	1.29	1.0E-04	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2600	12469	22364	1.29	1.0E-04	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2655	12522	22411	1.15	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
2655	12522	22412	1.15	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3247	13170	22969	1.04	1.0E-04	Q62203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3675	13589	23376	1.1	1.0E-04	AI440282.1	EST_HUMAN	ij01f11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
3971	13878	23654	1.78	1.0E-04	MI14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
3991	13898	23675	1.08	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLOBDB04.3'
4362	14258	24043	0.85	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5028	14901	24871	1.56	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5028	14901	24672	1.56	1.0E-04	7862015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5033	14905	24676	0.99	1.0E-04	A1357156.1	EST_HUMAN	q62h04.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2005975 3'
5148	15015		0.9	1.0E-04	Z72560.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL038c
5572	15487	25563	1.36	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6264	16129	26283	12.77	1.0E-04	A1251980.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
6468	16129	26283	14.47	1.0E-04	A1251980.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
7380	17249	27455	2.53	1.0E-04	A1806220.1	EST_HUMAN	wf26e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
7384	17253	27458	1.46	1.0E-04	O88969	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN8)
7562	17413	27628	1.75	1.0E-04	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
7848	17698		3	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8649	18513		2.17	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
8913	18721	29012	1.98	1.0E-04	AB032968.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
9035	18824		1.84	1.0E-04	BE696769.1	EST_HUMAN	CM0-CT0404-130700-475-h03 CT0404 Homo sapiens cDNA
9566	19158		1.65	1.0E-04	AW893325.1	EST_HUMAN	CM2-NN0010-220300-124-J08 NN0010 Homo sapiens cDNA
683	10616	20439	1.7	9.0E-05	AA718933.1	EST_HUMAN	ah45c11.x1 Soares_testis_NHT Homo sapiens cDNA clone 1292488 3'
3995	13902	23678	0.8	9.0E-05	A1762209.1	EST_HUMAN	wf54c11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394068 3' similar to contains MER6.11 MER6 repetitive element;
5628	15543	25632	1.47	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7455	17264		2.9	9.0E-05	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
7457	17266	27470	2.93	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
8479	18352	28617	2.6	9.0E-05	AW073078.1	EST_HUMAN	xa34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element;
8568	18436	28705	1.85	9.0E-05	A1287878.1	EST_HUMAN	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element;
8890	15543	25632	4.4	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
9329	19608		4.17	9.0E-05	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CS2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
804	10733	20576	1.46	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
846	10773		3.53	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
2920	12847		0.78	8.0E-05	M85575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4852	15080		1.15	8.0E-05	F28172.1	EST_HUMAN	HSPD16734 HM3 Homo sapiens cDNA clone s3000003H04
8491	18364	28630	1.87	8.0E-05	M69197.1	NT	Human haptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9911	19589		3.45	8.0E-05	AA279333.1	EST_HUMAN	zs88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
344	10303	20118	2.9	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
344	10303	20119	2.9	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
555	10496	20302	1.05	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
555	10496	20303	1.05	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1039	10957	20800	2.32	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2886	12551	22440	5.24	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3121	13046	22843	5.78	7.0E-05	AB009080.1	NT	Diclystetium discoidium gene for TRFA, complete cds
4276	14175	23953	1.27	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4344	14241	24023	0.82	7.0E-05	U60980.1	NT	Caenorhabditis elegans Skp1p homolog mRNA, complete cds
4842	14723	24506	0.84	7.0E-05	9845300	NT	Rat cytomegalovirus Maastfich1, complete genome
5202	15065		1.12	7.0E-05	AA367612.1	EST_HUMAN	EST178713 Placenta 1 Homo sapiens cDNA
7508	17296	27505	3.04	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBED60
8501	18374		2.89	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
1981	11874	21766	1.57	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1981	11874	21767	1.57	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
							wb54h06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb.J033250 DNA
2544	12418	22309	1.42	6.0E-05	A1655241.1	EST_HUMAN	TOPOISOMERASE I (HUMAN);
2652	12519	22409	0.89	6.0E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA28B10
2652	12519	22410	0.89	6.0E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA28B10
2783	10508	20415	2.45	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5905	15519	25596	3.33	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5905	15519	25600	3.33	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5955	15761	25879	1.49	6.0E-05	N72829.1	EST_HUMAN	yf50g11.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:246212 5'
6918	16796	26989	2.61	6.0E-05	AW896629.1	EST_HUMAN	PM4-NN0050-310300-001-110 NN0050 Homo sapiens cDNA
7330	17234	27437	1.37	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
7330	17234	27438	1.37	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
7484	17354	27558	1.28	6.0E-05	T94149.1	EST_HUMAN	ye28c12.1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119082 5'
8131	18019	28267	3.68	6.0E-05	R75639.1	EST_HUMAN	yf56d08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR1 repetitive element ;
8807	18621	28911	3.59	6.0E-05	AA044015.1	EST_HUMAN	zk58602.1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:487035 5'
9534	19587	25073	8.44	6.0E-05	AW890110.1	EST_HUMAN	MRO-NT0038-250400-001-109 NT0038 Homo sapiens cDNA

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9965	19427		1.54	6.0E-05	BE658403.1	EST_HUMAN	7g28a08.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3307766 3'
1382	11287	21141	14.37	5.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241199-040-111 ST0234 Homo sapiens cDNA
1819	11716		1.63	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
2831	12760	22550	0.88	5.0E-05	AJ251058.1	NT	Homo sapiens MEP1A gene, promoter region and exon 1
3897	13807	23593	2.99	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5392	15311	25165	9.01	5.0E-05	X58655.1	NT	Human ML C1emb gene for embryonic myosin alkaline light chain, 3'UTR
5648	15559	25652	3.46	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLODMA06 3'
9326	19173		2.96	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
9590	19173		3.47	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2776	10193		4.58	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
7486	17356		7.17	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
8150	18038	28286	4.6	4.0E-05	AW627946.1	EST_HUMAN	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element;
9287	18989		2.17	4.0E-05	AW117580.1	EST_HUMAN	xd93e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805192 3'
665	10599	20417	0.84	3.0E-05	A1248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
1043	10961	20804	1.36	3.0E-05	AW273851.1	EST_HUMAN	xv24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1115	11030	20870	1.28	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1115	11030	20871	1.28	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
2888	12553	22442	0.91	3.0E-05	Q62234	SWISSPROT	SKELEMIN
4285	14184	23964	6.89	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4285	14184	23965	6.89	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4365	14261	24045	1.19	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4365	14261	24046	1.19	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4519	14412	24197	0.85	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4731	10599	20417	0.84	3.0E-05	A1248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
5151	15018	24786	0.97	3.0E-05	AV726630.1	EST_HUMAN	AV726630 HTC Homo sapiens cDNA clone HTCCEA01 5'
5412	15332	25382	1.54	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylic2p), mRNA
6611	16491	26677	2.23	3.0E-05	BE733157.1	EST_HUMAN	601557451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842262 5'
6863	16742	26935	1.62	3.0E-05	AA284049.1	EST_HUMAN	z86b05.s1 S'tratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
7154	17031	27225	1.65	3.0E-05	AW770982.1	EST_HUMAN	h1p4e08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
7158	17035	27228	1.5	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
7373	17242	27447	1.33	3.0E-05	AA372562.1	EST_HUMAN	EST844475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end

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7570	17421		3.15	3.0E-05	AJ769331.1	EST_HUMAN	ig36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367206 3'
2276	12160	22058	1.76	2.0E-05	AJ286021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2538	12412	22302	3.02	2.0E-05	M13792.1	NT	MER3 b2 MER3 repetitive element;
2681	12546						Human adenosine deaminase (ADA) gene, complete cds
3098	13025	22821	7.21	2.0E-05	AA160562.1	EST_HUMAN	zq46a12.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632734 5' similar to
3304	13225	23027	0.94	2.0E-05	BE066036.1	EST_HUMAN	contains Alu repetitive element; contains element L1 repetitive element;
3323	13243	23050	1.14	2.0E-05	AF184614.1	NT	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3449	13366		1	2.0E-05	X8921.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3737	13649		0.85	2.0E-05	X95465.1	NT	H. sapiens DNA for endogenous retroviral like element
4510	14403	24191	0.99	2.0E-05	AL039107.1	EST_HUMAN	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
4592	14480		1.06	2.0E-05	BE378471.1	EST_HUMAN	DKFZp5681084_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp5681064 5'
4782	14666	24453	0.81	2.0E-05	AJ131016.1	NT	q013a08.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1932374 3' similar to contains
5520	15438	25502	1.42	2.0E-05	AJ011712.1	NT	MER18 b3 MER18 repetitive element;
5993	15998	26022	2.19	2.0E-05	AA714330.1	EST_HUMAN	601230455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
6125	15972	26108	2.19	2.0E-05	Y08926.1	NT	Homo sapiens SCL gene locus
6136	15963		8.04	2.0E-05	AI991025.1	EST_HUMAN	Homo sapiens TNNI1 gene, exons 1-11 (and joined CDS)
							mw06d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
							P. falciparum mRNA for AARP1 protein, partial
							wu35h07.x1 Soares_Dieckgraeft_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
6243	16109	26280	2.21	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
6243	16109	26281	2.21	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
6803	16483	26671	2.3	2.0E-05	AI381040.1	EST_HUMAN	ig20h05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
8024	17874	28116	2.45	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:259570 5'
8024	17874	28117	2.45	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:259570 5'
8039	15983		2.42	2.0E-05	AI991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraeft_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
8748	17897	28141	2.93	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
9335	19514		2.98	2.0E-05	BE346229.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832
							Q12832 GLYCOPHORIN HEP2;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9442	19677		3.73	2.0E-05	AW074604.1	EST_HUMAN	xe89a03.x1 NCL_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1 repetitive element ;
9486	19503		2.25	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
9637	19208	25257	1.81	2.0E-05	AU131513.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
2663	12729	22417	1.61	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3599	13513	23301	1.67	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lairto 120 Suppressor of Hairless (Su(H)) gene, partial cds
3886	13797	23583	9.24	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4082	13984	23761	1.09	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4180	14080	23853	2.01	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4742	14627	24413	2.15	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCL_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856518 3'
4882	14763	24539	4.46	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6049	15952	26082	1.42	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
6211	15993	26128	3.54	1.0E-05	AA641846.1	EST_HUMAN	hs19g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 repetitive element ;
6213	16079	26228	6.45	1.0E-05	4505844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
6572	16430		1.8	1.0E-05	P19474	SWISSPROT	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
7168	17045		2.18	1.0E-05	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7240	17117	27312	2.48	1.0E-05	AA452578.1	EST_HUMAN	z35h12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb.L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
7352	17220	27420	11.8	1.0E-05	AA236110.1	EST_HUMAN	zs05e11.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element ;
7704	17554	27778	1.2	1.0E-05	AW291521.1	EST_HUMAN	UI-H-B12-agk-a-08-Q-U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
7704	17554	27779	1.2	1.0E-05	AW291521.1	EST_HUMAN	UI-H-B12-agk-a-08-Q-U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
7851	17701		1.78	1.0E-05	AW466995.1	EST_HUMAN	ha07c10.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.t2 L1 repetitive element ;
8291	18170	28414	2.2	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRei gene, and sodium phosphate transporter (NPT3) gene, complete cds
8291	18170	28415	2.2	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRei gene, and sodium phosphate transporter (NPT3) gene, complete cds
2637	12504	22398	6.59	9.0E-06	AI583811.1	EST_HUMAN	h73a06.x1 NCL_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3057	12984	22775	3.66	9.0E-06	AI218983.1	EST_HUMAN	qg11.b08.x1 Soares_placenta_8to9weeks_2Nb1P81c9w Homo sapiens cDNA clone IMAGE:1759191 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3559	13473		2.94	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
5599	15513	25591	2.58	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6570	16428	26611	10.24	9.0E-06	A034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element;
6931	16809	27004	1.16	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7192	17069	27257	2.81	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7192	17069	27258	2.81	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7317	17193	27394	4.58	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
8309	18186	28434	3.35	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2483	12722	22251	1.55	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA
8992	18796	29087	2.24	8.0E-06	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
8992	18796	29088	2.24	8.0E-06	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
963	10886		1.7	7.0E-06	AA699729.1	EST_HUMAN	ab9010.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.t1 MER20 repetitive element;
1420	11326	21191	3.19	7.0E-06	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2844	12772		6.66	7.0E-06	A1368252.1	EST_HUMAN	qw16g09.x1 NC1_OGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element;
3516	13432		0.85	7.0E-06	AA385542.1	EST_HUMAN	EST99205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5493	15412		5.73	7.0E-06	AW883141.1	EST_HUMAN	QV2-QT0062-250400-173-h01 OT0062 Homo sapiens cDNA
9072	19698	24900	5.39	7.0E-06	BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083972 5'
2887	12814	22607	1.09	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3635	13549	23336	1.02	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4847	12838	22637	1.77	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4853	14539	24328	2.01	6.0E-06	A1040099.1	EST_HUMAN	ox08e02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element;
5281	15203	24979	1.46	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
7670	17520		1.88	6.0E-06	AW801912.1	EST_HUMAN	IL5-UJM0070-110400-063-g02 UJM0070 Homo sapiens cDNA
9900	19377	25195	1.8	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
5865	15604	25706	3.58	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5825	15731	25843	1.98	5.0E-06	U07581.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7817	17667	27907	6.9	5.0E-06	AA313820.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9795	19311	25204	4.74	5.0E-06	A1065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
631	10568	20380	4.41	4.0E-06	R16267.1	EST_HUMAN	ye48c03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element;
828	10755	20605	9.3	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2588574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element;
1312	11218	21074	5.18	4.0E-06	A1334928.1	EST_HUMAN	fb39e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1312	11218	21075	5.18	4.0E-06	A1334928.1	EST_HUMAN	fb39e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1458	11363	21227	2.23	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
2218	12104	22008	1.22	4.0E-06	AW015401.1	EST_HUMAN	UI-H-B10-eat-f-05-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3025	12953	22746	1.39	4.0E-06	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3819	13731	23520	1.78	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4702	14588	24378	1.58	4.0E-06	A1888939.1	EST_HUMAN	wl94c10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;
4940	14721	24504	1.02	4.0E-06	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7109	16986	27177	3.1	4.0E-06	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8745	17895	28139	3.74	4.0E-06	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0496
2117	12006	21904	1.27	3.0E-06	AA700562.1	EST_HUMAN	zi34b08.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element;
2117	12006	21905	1.27	3.0E-06	AA700562.1	EST_HUMAN	zi34b08.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element;
2220	12105		1.37	3.0E-06	AF202635.1	NT	Homo sapiens PF1200 mRNA, complete cds
2891	12818	22610	0.95	3.0E-06	AA888218.1	EST_HUMAN	ak48q11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element;
3228	13152		2.14	3.0E-06	A1857779.1	EST_HUMAN	wl22a05.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ; contains L1.12 L1 repetitive element ;
3716	13628	23412	1.26	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3716	13628	23413	1.26	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4376	14272	24053	0.9	3.0E-06	T50266.1	EST_HUMAN	y678b10.r1 Stratiogene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4461	14355	24146	4.31	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
6290	16154		1.92	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9494	19110		4.17	3.0E-06	AW385252.1	EST_HUMAN	RC0-L T0001-261199-011-A03 L T0001 Homo sapiens cDNA
195	10167		3.28	2.0E-06	P54366	SWISSPROT	HOMEBOX PROTEIN GOOSECOID

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1550	11455		6.27	2.0E-06	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE, REVERSE TRANSCRIPTASE; ENDONUCLEASE] wa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 MER30 repetitive element;
2326	12207	22106	2.95	2.0E-06	A1672138.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2418	12295	22192	2.14	2.0E-06	P04929	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
2519	12393	22285	2.69	2.0E-06	P06719	SWISSPROT	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3475	13391	23196	1.11	2.0E-06	AV657555.1	EST_HUMAN	z02e05.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3700	13614	23398	1.5	2.0E-06	AA173518.1	EST_HUMAN	Mus musculus gene for odorant receptor A16, complete cds
3710	13623	23406	1.5	2.0E-06	AB030896.1	NT	w90b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
5878	15784	25904	5.08	2.0E-06	A1819424.1	EST_HUMAN	yu37c04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb.X74929 KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN); PROTEIN MOV-10
7136	17013	27206	1.65	2.0E-06	H62051.1	EST_HUMAN	hs92f02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.12 L1 repetitive element;
9403	19699	24901	1.35	2.0E-06	P23249	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH- AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
9548	19148		2.46	2.0E-06	BE328232.1	EST_HUMAN	Mus musculus D6Mm5E protein (D6Mm5e) mRNA, complete cds
31	10018	19813	1.9	1.0E-06	O76082	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
641	10578	20394	1.61	1.0E-06	AF084364.1	NT	Homo sapiens chromosome 21 segment HS21C078
1435	11340	21206	2.22	1.0E-06	P09125	SWISSPROT	z06a12.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1507	11412	21271	1.09	1.0E-06	AL163278.2	NT	z06a12.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1554	11459	21317	0.93	1.0E-06	AA034141.1	EST_HUMAN	z06a12.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1554	11459	21317	0.93	1.0E-06	AA034141.1	EST_HUMAN	z06a12.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1565	11470		1.2	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1949	11844	21729	4.74	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1949	11844	21730	4.74	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4273	14172	23949	11.11	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5043	14915	24698	1.38	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5043	14915	24699	1.38	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5233	15157	24925	4.69	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
6107	16001	26139	6.11	1.0E-06	P02971	SWISSPROT	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
6813	16692	26881	1.16	1.0E-06	A1347010.1	EST_HUMAN	qp54e02.x1 NCI_CGAP_Cc8 Homo sapiens cDNA clone IMAGE:1928842 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6944	16822	27013	1.53	1.0E-06	A1287878.1	EST_HUMAN	q23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982485 3' similar to contains element
7582	17433	27647	3.72	1.0E-06	U82668.1	NT	MIR repetitive element;
7582	17433	27648	3.72	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
7609	17460	27676	4.86	1.0E-06	AA132611.1	EST_HUMAN	Homo sapiens shox gene, alternatively spliced products, complete cds
7637	17488		3.73	1.0E-06	AA449257.1	EST_HUMAN	z017e08.r1 Stratagene cdon (#837204) Homo sapiens cDNA clone IMAGE:587174 5'
7989	17839		1.52	1.0E-06	AL163203.2	NT	z04d11.s1 Soares, total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785483 3' similar to
8912	18720		4.81	1.0E-06	AW890941.1	EST_HUMAN	gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
9410	19077	25280	2.98	1.0E-06	L78810.1	NT	Homo sapiens chromosome 21 segment HS21C003
9536	11844	21729	1.84	1.0E-06	AF184614.1	NT	RC4-NT0054-120500-012-503 NT0054 Homo sapiens cDNA
9536	11844	21730	1.84	1.0E-06	AF184614.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
357	10314	20134	1.49	9.0E-07	AF003529.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
357	10314	20135	1.49	9.0E-07	AF003529.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
8572	18440	28708	2.38	9.0E-07	AL163281.2	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4661	14547	24336	4.49	8.0E-07	A1288596.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4661	14547	24337	4.49	8.0E-07	A1288596.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
5589	15504		7.45	8.0E-07	P21414	SWISSPROT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
6667	16547		7.89	8.0E-07	AF135416.1	NT	Homo sapiens chromosome 21 segment HS21C081
8893	18703		7.2	8.0E-07	T07770.1	EST_HUMAN	q182g07.x1 Soares, NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
9055	18838		4.15	8.0E-07	AL163280.2	NT	q182g07.x1 Soares, NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
1822	11719	21599	0.94	7.0E-07	AF167941.1	NT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1870	11766	21641	2.36	6.0E-07	AW855558.1	EST_HUMAN	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
							EST056660 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBEN89
							Homo sapiens chromosome 21 segment HS21C080
							Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
							CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
2442	12319	22217	2.41	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-
3891	13802		1.65	6.0E-07	P41479	SWISSPROT	hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B
							(Bf), and complement component C2 (C2) genes;>
7279	17156	27351	1.35	6.0E-07	BF001867.1	EST_HUMAN	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
9303	19653		1.81	6.0E-07	AW903222.1	EST_HUMAN	Tg94f07.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920
323	10284		3.55	5.0E-07	A1831893.1	EST_HUMAN	4F5L.;
1041	10959		2.9	5.0E-07	AA380830.1	EST_HUMAN	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
2995	12923		0.87	5.0E-07	A1831893.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
							EST193615 Supt cells Homo sapiens cDNA 5' end
							wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4547	14440	24223	1.44	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6203	15963	26096	1.71	5.0E-07	A1393981.1	EST_HUMAN	ig06b05.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
6203	15963	26097	1.71	5.0E-07	A1393981.1	EST_HUMAN	ig06b05.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
6348	16211	26373	15.93	5.0E-07	AW070885.1	EST_HUMAN	xa31a02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gbX15341
7932	17782	28021	4.11	5.0E-07	A1908587.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8805	18619	28909	4.31	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
8863	18675		2.06	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9712	19556		2.02	5.0E-07	AW62537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
3918	13827	23608	1.98	4.0E-07	AW009602.1	EST_HUMAN	ws94h05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3'
7235	17112	27305	5.29	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
8308	18185	28432	3.84	4.0E-07	A1765528.1	EST_HUMAN	w181b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
8308	18185	28433	3.84	4.0E-07	A1765528.1	EST_HUMAN	w181b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
8552	18422		2.05	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
434	10379	20200	5.01	3.0E-07	U19719.1	NT	Human microfilament-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
558	10507	20314	2.38	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1352	11258	21114	2.19	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1608	11513		2.23	3.0E-07	M64857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2000	11893		1.01	3.0E-07	AA526763.1	EST_HUMAN	ni56b09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1; L3 L1 repetitive element;
2242	12126	22026	1.15	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2420	12297	22194	17.25	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2420	12297	22195	17.25	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2696	12926	22718	0.85	3.0E-07	T84704.1	EST_HUMAN	yc50f12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:111695 5'
3122	13047	22844	1.82	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4624	14512	24302	7.05	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01 3'
4654	14540	24329	0.89	3.0E-07	A1797236.1	EST_HUMAN	we86b12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347987 3'
4996	14871	24634	1.47	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gbM62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
4996	14871	24635	1.47	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gbM62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5476	15396	25482	10.26	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6026	15930		5.32	3.0E-07	AA815175.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6433	16294	26456	3	3.0E-07	AW797168.1	EST_HUMAN	oc04c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
8918	18726		3	3.0E-07	AF029308.1	NT	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
9339	19408		2.76	3.0E-07	AJ132352.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
26	10013	19807	2.62	2.0E-07	AF262988.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
148	10122	19940	4.75	2.0E-07	L77569.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
148	10122	19941	4.75	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
175	10146	19962	116.1	2.0E-07	U38849.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
731	10663	20495	1.71	2.0E-07	AF003530.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
731	10663	20496	1.71	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
928	10853	20701	3.11	2.0E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:560869 3' similar to gb:U31860 GLYCOPHORIN A PRECURSOR (HUMAN);contains Alu repetitive element;
929	10854	20702	3.38	2.0E-07	T63042.1	EST_HUMAN	ye15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element;
1147	11060	20903	1.28	2.0E-07	Q26768	SWISSPROT	I/G AUTOANTIGEN
1582	11486	21347	1.84	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I
3633	13547	23334	14.74	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5078	14948	24723	0.97	2.0E-07	AW070995.1	EST_HUMAN	xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1
5078	14948	24724	0.97	2.0E-07	AW070995.1	EST_HUMAN	CE00923 PROBABLE RABGAP DOMAINS ;
5198	15061	24826	0.95	2.0E-07	AL163301.2	NT	CE00923 PROBABLE RABGAP DOMAINS ;
5277	15199	24975	1.73	2.0E-07	AW898066.1	EST_HUMAN	xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1
6009	15914	26041	1.89	2.0E-07	AI208715.1	EST_HUMAN	CE00923 PROBABLE RABGAP DOMAINS ;
6834	16812		3.91	2.0E-07	AV729390.1	EST_HUMAN	CE00923 PROBABLE RABGAP DOMAINS ;
7627	17478		1.61	2.0E-07	AL163303.2	NT	CE00923 PROBABLE RABGAP DOMAINS ;
7891	17741	27984	6.48	2.0E-07	AW892507.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
9094	19557		1.48	2.0E-07	AI732462.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
1086	11002		1.21	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2331	12212	22110	0.94	1.0E-07	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2403	12280	22177	0.94	1.0E-07	7549818	NT	Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript variant 2, mRNA
2797	11410	21269	1.75	1.0E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3684	11002		1.33	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4195	14095	23874	2.37	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GI:CFNF04 5'
4195	14095	23875	2.37	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
6103	15997	26132	5.2	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291339 5'
6103	15997	26133	5.2	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291339 5'
6424	16285	26447	9.04	1.0E-07	N56081.1	EST_HUMAN	y43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
6782	16661	26850	2.81	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
6782	16661	26851	2.81	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
7180	17057	27246	3.24	1.0E-07	AA693576.1	EST_HUMAN	zif51e10.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:434346 3'
7714	17564	27790	2.37	1.0E-07	BF674524.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
7716	17566	27792	1.28	1.0E-07	AA386311.1	EST_HUMAN	EST180354 Brain IV Homo sapiens cDNA
7980	17830		1.56	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
9364	19533	25080	3.66	1.0E-07	BE048770.1	EST_HUMAN	hr53c11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722
9497	19113		1.37	1.0E-07	X64467.1	NT	DJ1163J1.1 ;
9661	19222		4.61	1.0E-07	X51755.1	NT	H sapiens ALAD gene for porphobilinogen synthase
7689	17539	27765	1.67	9.0E-08	AV734819.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
8520	18392	28656	2.91	9.0E-08	AI891052.1	EST_HUMAN	AV734819 cda Homo sapiens cDNA clone cdABFB06 5'
8922	18730	29025	3.91	9.0E-08	AL163301.2	NT	wn30a07.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
9316	19008		3.09	9.0E-08	AJ251973.1	NT	OFR repetitive element ;
591	12671		2.65	8.0E-08	AI911352.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
1034	10952		0.88	8.0E-08	BE795469.1	EST_HUMAN	Homo sapiens partial steerin-1 gene
3498	13415		1.43	8.0E-08	BE795469.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
7074	16951	27144	3.38	8.0E-08	AI752367.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
7074	16951	27145	3.38	8.0E-08	AI752367.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
7551	17402	27616	2.89	8.0E-08	AW970693.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
8570	18438		2.39	8.0E-08	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
73	10657	19874	3.27	7.0E-08	Q02957	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1338	11244	21102	12.71	7.0E-08	X04909.1	NT	Rat mRNA for ribosomal protein L31
3528	13444	23240	1.09	7.0E-08	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3528	13444	23241	1.09	7.0E-08	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
8189	18075		4.63	7.0E-08	AI535743.1	EST_HUMAN	cong3.P11.A5 conorm Homo sapiens cDNA 3'
8926	18734	29027	5.6	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
9770	13444	23240	4.54	7.0E-08	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
9770	13444	23241	4.54	7.0E-08	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
9834	19334		1.89	7.0E-08	AJ131016.1	NT	Homo sapiens SOL gene locus
800	10729	20569	2.84	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
800	10729	20570	2.84	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2312	12193	22092	1.73	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0166-191199-004-g09 HT0166 Homo sapiens cDNA
4155	14055	23829	0.99	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8717	18534	28818	2.26	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8819	18632		1.74	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
79	10063	19880	3.06	6.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2189	12076	21981	1.97	5.0E-08	AA493851.1	EST_HUMAN	rh03b09.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element
5178	15042	24809	1.12	5.0E-08	Q06278	SWISSPROT	ALDEHYDE OXIDASE
9057	18839		4.36	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
9245	18958	25317	1.94	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131099-034-at12 CT0225 Homo sapiens cDNA
1724	11825	21493	1.1	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1724	11825	21494	1.1	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
7278	17155	27350	1.41	4.0E-08	L42571.1	NT	Cricetus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
7938	17788	28030	4.17	4.0E-08	AJ050027.1	EST_HUMAN	an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
8274	18154		1.79	4.0E-08	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
8439	18313	28570	3.66	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
8439	18313	28571	3.66	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
9061	19880		1.54	4.0E-08	W76159.1	EST_HUMAN	z656g03.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
9703	19252		1.46	4.0E-08	AJ343353.1	EST_HUMAN	tb95a11.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 MER13 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5184	15048	24812	7.24	3.0E-08	AA191195.1	EST_HUMAN	zq45d05.r1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632649 5'
5184	15048	24813	7.24	3.0E-08	AA191195.1	EST_HUMAN	zq45d05.r1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632649 5'
5446	15367	25423	1.99	3.0E-08	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
6163	15120	24864	3.58	3.0E-08	AI792737.1	EST_HUMAN	SYNTAXIN 17.1
6451	16312	26478	1.41	3.0E-08	AL163246.2	NT	qs76f11.y5 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:1944045 5'
						NT	Homo sapiens chromosome 21 segment HS21C046
6558	16416		2.97	3.0E-08	AI436352.1	EST_HUMAN	th93h09.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9027	18819		11.6	3.0E-08	R18420.1	EST_HUMAN	y902f04.r1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element;
199	10171		15.76	2.0E-08	AW302996.1	EST_HUMAN	xt87f06.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2787139 3'
223	10194		7.97	2.0E-08	AA425598.1	EST_HUMAN	zw48f07.r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element ;
488	10431	20245	1.48	2.0E-08	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
644	10581	20396	10.93	2.0E-08	AW886438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
644	10581	20397	10.93	2.0E-08	AW886438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
874	10898		37.42	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1319	11226	21082	1.93	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1707	11608		1.03	2.0E-08	BE794871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5'
1811	11708		3.99	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2388	12248	22140	1.42	2.0E-08	AA731948.1	EST_HUMAN	rw64h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1251409 3' similar to contains L1.t3 L1 repetitive element ;
2496	12371		2.16	2.0E-08	K00216.1	NT	Sheep H1s-rRNA-GUG
3171	13096	22901	6.02	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3171	13096	22902	6.02	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3783	13695		1.66	2.0E-08	AW813620.1	EST_HUMAN	RC3-S10197-161099-012-b03 ST0197 Homo sapiens cDNA
3986	13693	23669	0.78	2.0E-08	UB2688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4305	14203		3.35	2.0E-08	AA459040.1	EST_HUMAN	aa26c07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.t2 L1 repetitive element ;
4876	14756		2.89	2.0E-08	AW572881.1	EST_HUMAN	he17h06.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
6722	16602	26791	1.31	2.0E-08	AA490121.1	EST_HUMAN	ab02g06.s1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
8995	18799	29092	11.62	2.0E-08	BF589004.1	EST_HUMAN	naa32e09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3257969 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1493	12896	21257	1.13	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
2005	11897		2.92	1.0E-08	BE141958.1	EST_HUMAN	PM2-HT0130-150999-001-F12 HT0130 Homo sapiens cDNA
3155	13080	22881	1.24	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3155	13080	22882	1.24	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
5191	15054	24818	1.43	1.0E-08	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5438	15358	25414	4.05	1.0E-08	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
6975	16852	27045	1.84	1.0E-08	AJ015304.1	EST_HUMAN	c35a05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
8633	18498	28773	3.66	1.0E-08	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
9434	19074		2.01	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9804	19316		6.3	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9894	19518		1.76	1.0E-08	BF375398.1	EST_HUMAN	MR4-S10240-240700-013-g04 ST0240 Homo sapiens cDNA
4149	14049	23823	2.98	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4149	14049	23824	2.98	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3444	13361		1.07	8.0E-09	BE012076.1	EST_HUMAN	RC5-BN1058-270400-031-C06 BN1058 Homo sapiens cDNA
6307	16171	26328	6.12	8.0E-09	AJ183500.1	EST_HUMAN	q42a07.x1 Soares fetal heart_Nb-HH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1 t1 MSR1 repetitive element ;
6666	16546	26743	2.71	8.0E-09	AW900159.1	EST_HUMAN	CM0-NN1004-100300-273-e06 NN1004 Homo sapiens cDNA
7196	17073		3.06	8.0E-09	AA938892.1	EST_HUMAN	op74408.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
3555	13469		1.68	7.0E-09	D68842.1	NT	Homo sapiens DNA for 3-ketocyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4558	14450	24236	0.99	7.0E-09	D00649.1	NT	Homo sapiens gene for enteric smooth muscle gamma-actin, exon 2, 3
7335	17203	27403	3.27	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
7850	17700	27945	1.84	7.0E-09	BE254850.1	EST_HUMAN	60111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
2107	11996		1.06	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514.t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0514 5'
3941	13849	23625	1.06	6.0E-09	AA557940.1	EST_HUMAN	nl17a11.s1 NCI_CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.12 L1 repetitive element ;
4906	14786	24562	4.44	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA
5305	15226	25030	8.19	6.0E-09	AW195784.1	EST_HUMAN	xr85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
7294	17170	27370	2.26	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
7896	17746		4.06	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
1394	11299	21157	3.09	5.0E-09	BE149264.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5858	15764	25881	1.92	5.0E-09	AA359454.1	EST_HUMAN	EST168746 Fetal lung II Homo sapiens cDNA 5' end
7811	17661	27901	2.69	5.0E-09	AW799667.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
510	10452		1.68	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
949	10873		2.31	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1453	11358	21222	0.96	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2379	12259	22151	6.36	4.0E-09	AA350378.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
							hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2303	12184	22082	3.82	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element ;
2506	12380	22270	1.25	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2614	12482	22371	1.1	3.0E-09	P23249	SWISSPROT	MER18 repetitive element ;
							PROTEIN MOV-10
3287	13208	23008	1.1	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
4329	14226	24008	3.22	3.0E-09	AF175325.1	NT	MER18 repetitive element ;
4411	14305	24088	1.54	3.0E-09	Q9Y3R5	SWISSPROT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
7884	17734	27978	1.73	3.0E-09	AL163247.2	NT	258.1 KDA PROTEIN C21ORF5 (K1AA0933)
8384	18261	28510	3.8	3.0E-09	BF109943.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
8384	18261	28511	3.8	3.0E-09	BF109943.1	EST_HUMAN	772c08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
795	10724		0.93	2.0E-09	X16674.1	NT	772c08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1237	11144	20995	5.23	2.0E-09	AL163284.2	NT	H. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
1637	11541		10.52	2.0E-09	AL118573.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
2278	12162	22059	2.25	2.0E-09	Q9Y3R5	SWISSPROT	DKFZp761B1710_j1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
3858	13769	23561	3.65	2.0E-09	O60241	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (K1AA0933)
							BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
6405	16266	26428	8.9	2.0E-09	AA461430.1	EST_HUMAN	z63h08.r1 Soares total fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains
7055	16932	27122	1.37	2.0E-09	AJ271735.1	NT	Alu repetitive element;
8589	18457	28726	2.11	2.0E-09	AL163248.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9576	10724		11.53	2.0E-09	X16674.1	NT	Homo sapiens chromosome 21 segment HS21C048
							H. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
9640	19749		1.62	2.0E-09	AA226070.1	EST_HUMAN	nc11c02.1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive
1093	11009	20850	2.48	1.0E-09	5031624	NT	element;
1093	11009	20851	2.48	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1616	11520		0.95	1.0E-09	AJ228041.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
							Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2453	12330		0.94	1.0E-09	A1359086.1	EST_HUMAN	qy64e11.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER1212 MER12 repetitive element;
2860	12788	22580	1.51	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p-44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2895	12822	22614	3.25	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2895	12822	22615	3.25	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2949	12876	22674	1.23	1.0E-09	P11799	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) [CONTAINS: TELOKIN]
3002	12930	22722	0.78	1.0E-09	BE35440.1	EST_HUMAN	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5' zh35b03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4692	14578		4.26	1.0E-09	AA719297.1	EST_HUMAN	Human breakpoint cluster region (BCR) gene, complete cds
5550	15476	25549	1.37	1.0E-09	U07000.1	NT	CIRCUMSPOROZITE PROTEIN PRECURSOR (CS)
5736	15644	25749	3.21	1.0E-09	P28694	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
7911	17761		3.1	1.0E-09	AL163283.2	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
9478	19689	24995	2.14	1.0E-09	11418127	NT	MR0-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
1287	11195	21048	1.8	9.0E-10	AW867740.1	EST_HUMAN	
2803	12733	22532	6.03	9.0E-10	A1870071.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW_RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element PTR5 repetitive element ;
6087	16032	26172	4.63	9.0E-10	A1452982.1	EST_HUMAN	ij46509.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR:O00372 O00372 PUTATIVE P150. ;
141	10115	19935	9.43	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3300	13222	23022	0.87	8.0E-10	BE080748.1	EST_HUMAN	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
4106	14006	23782	2.82	8.0E-10	AA376932.1	EST_HUMAN	EST89564 Small Intestine I Homo sapiens cDNA 5' end
7725	17575		2.32	8.0E-10	U36308.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
9005	18808	29100	2.31	8.0E-10	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
696	10619	20444	12.45	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
686	10619	20445	12.45	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1605	11510	21371	1.87	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
1974	11867		1.01	7.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2512	12386		16.88	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3049	12976	22768	2.65	7.0E-10	X00856.1	NT	H. sapiens DHFR gene, exon 3
5754	15662	25769	3.98	7.0E-10	AA345220.1	EST_HUMAN	EST151247 Gall bladder II Homo sapiens cDNA 5' end
6514	16373		1.39	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT

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895	10821	20866	2.81	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2644	12511	22402	1.47	6.0E-10	A1424405.1	EST_HUMAN	t02407.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3'
4634	14522		2.51	6.0E-10	AW853719.1	EST_HUMAN	RC3-C70254-031089-012-g12 C70254 Homo sapiens cDNA
9092	18865		1.79	6.0E-10	AW971923.1	EST_HUMAN	EST384012 MAGe resequences, MAGL Homo sapiens cDNA
9947	19597		3.54	6.0E-10	BE598410.1	EST_HUMAN	RC3-NN0070-110800-074-h07 NN0070 Homo sapiens cDNA
744	10675		4.5	5.0E-10	AL046904.1	EST_HUMAN	DKFZp434N219_t1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434N219 5'
3430	13347	23152	1.48	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
6334	16197		1.82	5.0E-10	BF105159.1	EST_HUMAN	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
7496	17366	27570	1.79	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
7496	17366	27571	1.79	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
106	10087		0.99	4.0E-10	A1221083.1	EST_HUMAN	qg09f09.x1 Soares_piacenta_8b9weeks_2NbhP8tc9W Homo sapiens cDNA clone IMAGE:1759049 3' similar to contains LTR8.b2 LTR8 repetitive element ;
1951	11846	21732	1.4	4.0E-10	AW594709.1	EST_HUMAN	hg58g03.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;
2527	12401	22582	6.09	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6259	16125	26278	19.23	4.0E-10	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8436	18310		7.7	4.0E-10	AF003528.1	NT	Homo sapiens X-linked anthriloitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
897	10822	20668	1.72	3.0E-10	N36113.1	EST_HUMAN	y92706.s1 Soares_melanocyte 2NbhM1 Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.11 L1 repetitive element ;
1329	11236		6.63	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
4435	14330	24117	1.1	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4435	14330	24118	1.1	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5765	15672	25779	2.83	3.0E-10	P20350	SWISSPROT	RHOMBOD PROTEIN (VEINLET PROTEIN)
5833	15739	25851	3.27	3.0E-10	BE302970.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
5562	16420	26599	1.31	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
5562	16420	26500	1.31	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7067	16944	27136	1.58	3.0E-10	H87208.1	EST_HUMAN	y674b12.s1 Soares_retina N2b1HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element ;
7233	17110	27302	1.47	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
7233	17110	27303	1.47	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
7079	17826		2.56	3.0E-10	U65894.1	EST_HUMAN	uc11e12.r1 Strakapeje_humo (#8337210) Homo sapiens cDNA clone IMAGE:80398 5'

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8026	17876		1.54	3.0E-10	AA769294.1	EST_HUMAN	nz36g03.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:128908 3'
9737	19271	25227	2.03	3.0E-10	BE179517.1	EST_HUMAN	IL3-H10618-110500-136-E07 HT0618 Homo sapiens cDNA
32	10019	19814	1.43	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
32	10019	19815	1.43	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1855	11751		5.91	2.0E-10	U30017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (hnp) and survival motor neuron protein (smn) genes, complete cds
5547	15463		2.41	2.0E-10	Q28640	SWISSPROT	(HPRG)
5787	15693	25801	1.71	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6367	16230	26389	5.79	2.0E-10	BE791082.1	EST_HUMAN	6071586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
1492	11397		3.56	1.0E-10	AW867767.1	EST_HUMAN	MR0-SN0038-290300-001-f01 SN0038 Homo sapiens cDNA
1589	11493	21353	3.14	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
2537	12411		2.4	1.0E-10	AW852001.1	EST_HUMAN	QV0-C10225-191199-058-e08 C10225 Homo sapiens cDNA
3456	13372	23178	0.89	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA
3770	13411		0.91	1.0E-10	AL041865.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3833	13842		5.44	1.0E-10	AF213984.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4036	13939	23716	4.51	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4036	13939	23717	4.51	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4042	13945	23724	2.25	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4079	13981		2.06	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5145	15012		0.93	1.0E-10	X87344.1	NT	H sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
7859	17709		4.59	1.0E-10	AA081868.1	EST_HUMAN	zt23g06.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
8286	13165	28408	3.4	1.0E-10	AJ038280.1	EST_HUMAN	cy85h03.x1 Scores fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
9037	15012		1.43	1.0E-10	X87344.1	NT	H sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
9084	18859		1.3	1.0E-10	AA397885.1	EST_HUMAN	zt86b10.r1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:729211 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
261	10226	20042	1.2	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2057	11947	21843	5.43	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5'
2057	11947	21844	5.43	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5'
3337	13257	23084	2.25	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5'
3337	13257	23065	2.25	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5'
4400	14295	24079	1.09	9.0E-11	AA775985.1	EST_HUMAN	ae78i01.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5421	15342		4	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
9410	19062	25312	2.69	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-506B08 5'
3078	13005		9.97	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
3381	13792	23580	0.83	8.0E-11	AJ478617.1	EST_HUMAN	tm54c09.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
3957	13865	23641	4.03	8.0E-11	N23712.1	EST_HUMAN	ym46a06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
1431	11336	21202	2.11	7.0E-11	AA330642.1	EST_HUMAN	EST34392 Embryo, 6 week I Homo sapiens cDNA 5' end
6949	16827	27020	2.55	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
7873	17723		1.22	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9545	19145		1.31	7.0E-11	AV701656.1	EST_HUMAN	AV701656 ADB Homo sapiens cDNA clone ADBABC09 5'
406	10352	20180	5.16	6.0E-11	M56270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
406	10352	20181	5.16	6.0E-11	M56270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6529	16388	26588	3.58	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6871	16750	26945	6.49	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTG Homo sapiens cDNA clone HTCASC06 5'
11	9997	19788	0.92	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3320	9997	19788	1.48	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4135	14035	23811	1.49	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
5926	15831	25954	1.69	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
6446	16307	26472	14.59	5.0E-11	11416799	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
8975	18780	29072	1.79	5.0E-11	AJ289880.1	NT	Homo sapiens KIAA0351 gene (partial), X13 gene and LZTFL1 gene
1380	11285		1.4	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2760	12622	22514	8.45	4.0E-11	BE885900.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295 5'
4518	14411	24196	1.37	4.0E-11	D44666.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
5997	15803	25927	2.94	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
6362	16225		3.65	4.0E-11	AF224669.1	NT	Homo sapiens mannosidase; beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
7405	17272		1.59	4.0E-11	BE149425.1	EST_HUMAN	RC1-HT0256-210100-013-08 HT0256 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9611	19190	25252	1.93	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1476	11381	21245	2.15	3.0E-11	6670077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4179	14079		1.45	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
944	10869	20716	1.58	2.0E-11	AI150502.1	EST_HUMAN	qf38c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1168	11080	20926	3.64	2.0E-11	R24807.1	EST_HUMAN	y943e12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5'
1168	11080	20927	3.64	2.0E-11	R24807.1	EST_HUMAN	y943e12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5'
1596	11500	21359	3.91	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
1596	11500	21360	3.91	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
							COR3/beta (COR3/beta) genes, complete cds
1600	11505	21365	1.04	2.0E-11	AI128374.1	EST_HUMAN	qc51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to
2737	12599	22493	1.11	2.0E-11	AF087913.1	NT	gb1.02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.t1
3160	13085	22889	4.23	2.0E-11	P10263	SWISSPROT	L1 repetitive element;
3284	13205	23005	0.87	2.0E-11	AI478617.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T47D
							RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3452	13368		0.95	2.0E-11	AF020503.1	NT	tm54c09.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161636 3'
4501	14395		0.97	2.0E-11	AL163227.2	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4851	14732		5.46	2.0E-11	BE062558.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
							QV2-BT0258-261099-014-s01 BT0258 Homo sapiens cDNA
4961	14836	24604	1.32	2.0E-11	AA307331.1	EST_HUMAN	EST178226 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2-
							macroglobulin
5810	15715	25828	1.83	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.r1 NCJ_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW.PR16_YEAST
							P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16. ;
7318	17194		1.43	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7900	17750	27989	4.61	2.0E-11	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
8457	18330	28591	2.07	2.0E-11	AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
8457	18330	28592	2.07	2.0E-11	AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
9160	19679		1.29	2.0E-11	AA704195.1	EST_HUMAN	zj77e03.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
9192	18927		2.25	2.0E-11	AW842143.1	EST_HUMAN	RCO-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
9216	18943	25356	1.98	2.0E-11	BF37859.1	EST_HUMAN	GM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
9477	19103		1.89	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9827	19201		2.38	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9930	19401		2.38	2.0E-11	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
660	10594	20412	1.24	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
1199	11109	20954	2.58	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1483	11388		1.94	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2079	11969	21862	3.12	1.0E-11	AF000573.1	NT	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds
3454	13370	23174	1.32	1.0E-11	BE004315.1	EST_HUMAN	CMO-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
5269	15191	24966	14.34	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6773	16852	26840	3.25	1.0E-11	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
6989	16866	27080	5.41	1.0E-11	R13174.1	EST_HUMAN	yf73d08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28166 5'
7232	17109	27300	1.32	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
7232	17109	27301	1.32	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
8607	18474	28747	1.9	1.0E-11	BF680078.1	EST_HUMAN	602154807F1.NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5'
9702	19483		1.29	1.0E-11	Z20377.1	EST_HUMAN	HSAAAACADH P. Human foetal Brain Whole tissue Homo sapiens cDNA
2922	12849	22649	0.82	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
7641	17491	27712	1.22	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7641	17491	27713	1.22	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9270	18974		3.57	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4562	14454	24241	2.75	7.0E-12	Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
8656	18545	28828	11.23	7.0E-12	AA704735.1	EST_HUMAN	z23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
3500	13417		0.92	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5'
4252	14151	23925	7.85	6.0E-12	AA732516.1	EST_HUMAN	nz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
7201	17078	27263	1.19	6.0E-12	AF003249.1	NT	Marone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
7453	17262		1.86	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367688 similar to contains MER29.12
1027	10945	20790	2.88	5.0E-12	T06573.1	EST_HUMAN	MER29 repetitive element;
3344	13264	23070	1.18	5.0E-12	BE047779.1	EST_HUMAN	EST04462 Fetal brain, Stragene (cat#936206) Homo sapiens cDNA clone HFBDV33
3666	13580	23367	5.93	5.0E-12	AJ271736.1	NT	tz2b05.y1 NCI_CGAP_Birm52 Homo sapiens cDNA clone IMAGE:2291217 5'
5171	15037		0.84	5.0E-12	AA720661.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
5667	15578	25676	4.75	5.0E-12	AL163278.2	NT	nw24b11.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241373 3'
5667	15578	25677	4.75	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5909	15815	25940	9.12	5.0E-12	AW974760.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
7268	17145	27339	2.15	5.0E-12	AJ271735.1	NT	EST386850 IMAGE resequences, MAGN Homo sapiens cDNA
							Homo sapiens Xq pseudautosomal region; segment 1/2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7895	17745		4.67	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
244	10211	20027	3.42	4.0E-12	AA700326.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
245	10211	20027	3.55	4.0E-12	AA700326.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4520	14413	24198	0.85	4.0E-12	A1689984.1	EST_HUMAN	bx28h05.x1 NCLCGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13839 Q13539 MARINER TRANSPOSASE. ;
6797	16676		2.89	4.0E-12	AF109097.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
8431	18305	28561	3.51	4.0E-12	AJ229043.1	NT	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22, segment 3/3
9520	19131		1.9	4.0E-12	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
600	10536	20345	3.81	3.0E-12	AW341683.1	EST_HUMAN	hd13401.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP. ;
600	10536	20346	3.81	3.0E-12	AW341683.1	EST_HUMAN	hd13401.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP. ;
8047	17938	28187	3.08	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
8047	17938	28188	3.08	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
3421	13338	23143	1.03	2.0E-12	67544495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4025	13928	23704	1.04	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4025	13928	23705	1.04	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4324	14221		1.8	2.0E-12	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
4804	14688	24473	0.78	2.0E-12	O70306	SWISSPROT	TX15 PROTEIN (T-BOX PROTEIN 15)
4804	14688	24474	0.78	2.0E-12	O70306	SWISSPROT	TX15 PROTEIN (T-BOX PROTEIN 15)
5898	15804		2.22	2.0E-12	AW971857.1	EST_HUMAN	EST383946 MAGe resequences; MAGL Homo sapiens cDNA
6258	16124	26277	3.34	2.0E-12	T08169.1	EST_HUMAN	EST06060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
6516	16375	26562	2.07	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
7367	17345		1.68	2.0E-12	AF196864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7737	17587		8.13	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9175	18916		1.71	2.0E-12	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
9377	19041		1.52	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
117	10095	19914	1.82	1.0E-12	AW627674.1	EST_HUMAN	hh90a09.x1 NCLCGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11 MER18 repetitive element ;
1944	11839		2.03	1.0E-12	AJ871726.1	EST_HUMAN	wm5f07.x1 NCLCGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element ;
3032	12960	22752	1.16	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds

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3032	12960	22753	1.16	1.0E-12	AF000691.1	NT	Homo sapiens testis-specific Testis Transcript Y2 (TTY2) mRNA, partial cds
3798	13710	23496	27.7	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3798	13710	23497	27.7	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
5630	15544		1.73	1.0E-12	U82828.1	NT	Homo sapiens alaxia telangiectasia (ATM) gene, complete cds
5682	15591		1.82	1.0E-12	O9Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
6224	16090	26240	1.72	1.0E-12	AF196964.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
6240	16106	26256	9.11	1.0E-12	A1248533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element;
6240	16106	26257	9.11	1.0E-12	A1248533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element;
7051	16928	27119	1.31	1.0E-12	AA782323.1	EST_HUMAN	ac26d05.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:857577 3'
9085	18860	29118	3.36	1.0E-12	AW962164.1	EST_HUMAN	ES1374237 MAGE resequences, MAGG Homo sapiens cDNA
9605	19728		2.2	1.0E-12	P44836	SWISSPROT	PROBABLE TONB-DEPENDENT RECEPTOR HI0712 PRECURSOR
9963	19426		2.72	1.0E-12	X85949.1	NT	M.setulosus mitochondrial 12S rRNA gene
3575	13489		1.13	9.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3865	13776	23570	1.16	9.0E-13	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
7537	17388		2.37	9.0E-13	N69653.1	EST_HUMAN	za26b05.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:263651 3'
700	10633	20458	5.05	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
700	10633	20459	5.05	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1796	11694	21570	1.36	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
7838	17688		2.13	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8984	18789	23079	2.49	8.0E-13	U69060.1	NT	Human germline T-cell receptor beta chain TORBV13S1, TORBV6S8A2T, TORBV6S6A3N2T, TORBV13S6A2T, TORBV6S9P, TORBV6S3A2T, TORBV13S8P, TORBV6S3A1N1T, TORBV5S2, TORBV6S6A2T, TORBV6S7P, TORBV13S4, TORBV6S2A1N1T, TORBV6S4A2T, TORBV6S4A1, TORBV23S1A2T, TORBV12>
9550	19149		10.33	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865613 5'
9768	19287		1.33	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
2054	11944	21840	18.51	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3260	13201		1.05	5.0E-13	R78338.1	EST_HUMAN	y82704.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3351	13271		1.45	5.0E-13	AA435773.1	EST_HUMAN	z177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
8234	18115	28367	2.75	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1824	11721		2.96	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221039-001-e11 HT0224 Homo sapiens cDNA
2411	12288		1.58	4.0E-13	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
5430	15350	25404	4.86	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
6278	18142	26298	1.92	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
6542	16400		1.52	4.0E-13	N44291.1	EST_HUMAN	yv33g05.r1 Soares melanocyte 2Nb1HM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR-A32995 A32995 t complex sterility protein - mouse;
7757	17607	27831	4.57	4.0E-13	AI289831.1	EST_HUMAN	qn32d05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1898945 3' similar to contains Alu repetitive element;
8507	18379	28845	1.83	4.0E-13	AA435819.1	EST_HUMAN	z178g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
8507	18379	28846	1.83	4.0E-13	AA435819.1	EST_HUMAN	z178g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
173	10144		3.8	3.0E-13	AF003528.1	NT	Homo sapiens X-linked antihydrolytic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
847	10774		1.37	3.0E-13	AA430310.1	EST_HUMAN	zw88g08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
2319	12200	22099	1.25	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2429	12306		2.63	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2629	12497	22387	4.23	3.0E-13	BF372962.1	EST_HUMAN	CM3-FT0100-140700-242-h08 FT0100 Homo sapiens cDNA
3150	13075		2.86	3.0E-13	AA745844.1	EST_HUMAN	ob18d02.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
6601	16481	26669	5.92	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
8084	17955		4.03	3.0E-13	AI064768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
8403	18279	28531	3.86	3.0E-13	BE083509.1	EST_HUMAN	GM0-BT0281-031196-087-a03 BT0281 Homo sapiens cDNA
8876	18688	28980	2.6	3.0E-13	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
144	10118	19938	2.77	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
239	10207	20024	1.31	2.0E-13	U23839.1	NT	Danto rario fibroblast growth factor receptor 4 mRNA, complete cds
1249	11158	21005	4.71	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3244	13167	22966	1.08	2.0E-13	BF431899.1	EST_HUMAN	nab7605.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4019	13923		1.72	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5722	15629	25732	3.87	2.0E-13	Q06952	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6378	16061	26209	6.32	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7976	17826	28067	3.97	2.0E-13	5031896	NT	Homo sapiens mab-21 [C. elegans]-like 1 (MAB21L1) mRNA
9251	18931		7.42	2.0E-13	AW892155.1	EST_HUMAN	OM0-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
288	10252	20072	1.37	1.0E-13	S74129.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
870	10796	20646	4.39	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1314	11220	21077	1.27	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
1976	11869	21761	2.16	1.0E-13	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
4488	14382	24169	1.48	1.0E-13	BF340987.1	EST_HUMAN	THR repetitive element;
							602038009F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4185866 5'
8684	18572	28855	13.83	1.0E-13	BF108755.1	EST_HUMAN	745e10.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
9076	18853		1.62	1.0E-13	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIED3 5'
9714	19255		1.6	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
							aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
330	10289	20105	2.92	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
331	10290	20106	2.85	9.0E-14	AA781159.1	EST_HUMAN	repetitive element;
2451	12328		4.04	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2725	12587	22482	4.62	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3073	13000	22790	3.74	9.0E-14	AW513296.1	EST_HUMAN	xc64h05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833 3'
							aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
3200	10289	20105	0.98	9.0E-14	AA781159.1	EST_HUMAN	repetitive element;
3728	13640	23426	5.22	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4550	14536	24325	1.93	9.0E-14	AJ002153.1	NT	Saguinus oedipus gene for seminal vesicle secreted protein semenogelin I
3453	13359		1.57	8.0E-14	BE468263.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
3872	13783		2.77	8.0E-14	R76269.1	EST_HUMAN	y72e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
7434	16447	26637	60.69	8.0E-14	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
7515	17303	27510	3.49	8.0E-14	AA219316.1	EST_HUMAN	zq17c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629670 3'
8732	18588		4.39	8.0E-14	BE062558.1	EST_HUMAN	QV2-BT0288-261099-014-a01 BT0258 Homo sapiens cDNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1611	12699		3.07	7.0E-14	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element;
363	10319	20140	10.2	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
5114	14982	24756	1.02	6.0E-14	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
5114	14982	24757	1.02	6.0E-14	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
7652	17502	27725	2.56	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7652	17502	27726	2.56	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
602	10538	20348	3.92	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
4985	14860	24628	1.09	5.0E-14	AW073791.1	EST_HUMAN	x603b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1 repetitive element;
5397	15316	25363	5.12	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1107	12685		1.77	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1835	11732	21608	6.5	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3693	13607		0.94	4.0E-14	AA046502.1	EST_HUMAN	z667a06.r1 Soares_pregnant_uterus_NbHPJ Homo sapiens cDNA clone IMAGE:487858 5'
4194	14094	23873	1	4.0E-14	N46328.1	EST_HUMAN	y773c12.s1 Soares_multiple_sclerosis_2NBHWP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element;
9777	19760		2.31	4.0E-14	AI886224.1	EST_HUMAN	w708c03.x1 NCI_CGAP_Uk4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element;
934	10859	20705	2.13	3.0E-14	X95466.1	NT	R.norvegicus mRNA for CPG32 protein
4841	14722	24505	0.82	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
4844	14725	24507	1.1	3.0E-14	7656964	NT	Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM29), mRNA
5104	14972		1.23	3.0E-14	BE466372.1	EST_HUMAN	h9d4f11.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3195501 3' similar to contains MER4.b2 MER4 repetitive element;
5157	15024	24791	1.5	3.0E-14	P02894	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8563	14722	24505	7.59	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
384	10331	20154	3.98	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
384	10331	20155	3.98	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
675	12673	20428	6.35	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
2339	12219		1.36	2.0E-14	AW372868.1	RC5-BT0377-091298-031-D12 BT0377 Homo sapiens cDNA
2416	12293		1.09	2.0E-14	7657629	Homo sapiens thabdooid tumor deletion region protein 1 (RTDR1), mRNA
2479	12355	22246	1.24	2.0E-14	AL163209.2	Homo sapiens chromosome 21 segment HS21C009
2640	12507		0.95	2.0E-14	P08548	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5505	15423	25485	2.96	2.0E-14	J01317.1	Human beta globin region on chromosome 11
6114	16008		2.18	2.0E-14	BE000550.1	RC3-BN0072-240200-011-a05 BN0072 Homo sapiens cDNA
6432	16293	26454	19.91	2.0E-14	BE168761.1	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
6432	16293	26455	19.91	2.0E-14	BE168761.1	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
8180	18048	28300	4.76	2.0E-14	AW139800.1	UI-H-B11-adw-a-10-0-UJ1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
8791	15423	25485	1.81	2.0E-14	J01317.1	Human beta globin region on chromosome 11
1051	10968	20610	1.31	1.0E-14	AL163246.2	Homo sapiens chromosome 21 segment HS21C046
1384	11289	21143	7.67	1.0E-14	AL163268.2	Homo sapiens chromosome 21 segment HS21C068
1384	11289	21144	7.67	1.0E-14	AL163268.2	Homo sapiens chromosome 21 segment HS21C068
1956	11851	21738	21.54	1.0E-14	L44140.1	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2137	12025	21921	6.17	1.0E-14	AL163303.2	Homo sapiens chromosome 21 segment HS21C103
2358	12238	22134	6.43	1.0E-14	AF001699.1	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2914	12841	22641	1.38	1.0E-14	P05227	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3130	13055	22854	4.67	1.0E-14	BF335227.1	RC2-CT0492-310700-013-a09_1 CT0432 Homo sapiens cDNA
3130	13055	22855	4.67	1.0E-14	BF335227.1	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3811	13723	23512	2	1.0E-14	AA682994.1	ae89c12.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4374	14270	24051	1.74	1.0E-14	AW275852.1	xq39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5550	15486	25536	1.97	1.0E-14	AF126145.1	Bos taurus xenobiotol/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6012	19457	26045	10.41	1.0E-14	11437150	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6012	19457	26046	10.41	1.0E-14	11437150	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1558	11463	21320	2.85	9.0E-15	7427522	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2126	12014		1.64	9.0E-15	AF196779.1	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
6427	16288	26449	4.28	9.0E-15	P21416	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
6673	16563	26748	1.53	9.0E-15	BE903559.1	60167750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5'
2780	10415		1	8.0E-15	BE261482.1	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7963	17813		2.83	7.0E-15	AW241958.1	EST_HUMAN	xn77402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains
978	10901	20748	6.12	6.0E-15	AJ271736.1	NT	THR12 THR repetitive element;
8622	19770		1.86	6.0E-15	AW838643.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
9948	19415		1.57	6.0E-15	BF432200.1	EST_HUMAN	QV1_L T0036-160200-070-c10 L T0036 Homo sapiens cDNA
404	10350	20177	5.79	5.0E-15	AL163208.2	NT	nab81c12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
							Homo sapiens chromosome 21 segment HS21C008
2733	12595	22490	1.38	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NP73) gene, complete cds
3423	13340		1	5.0E-15	AW296817.1	EST_HUMAN	UI-H-BW0-ajp-g-10-c-J1 s1 NCI_CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2731219 3'
8063	17954		2.22	5.0E-15	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
421	9988	19779	2.6	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4039	13942	23720	0.78	4.0E-15	AL118596.1	EST_HUMAN	DKFZp761C0810_r1_761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761C0810 5'
8414	16438	26623	2.38	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
8414	16438	26624	2.38	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
							LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to
4123	14023		5.93	3.0E-15	N89452.1	EST_HUMAN	ANF(CARDIODILATIN)
4843	14724		1.41	3.0E-15	P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
4955	14832	24599	0.88	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
4955	14832	24600	0.88	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6314	16177	26335	2.86	3.0E-15	M27585.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6314	16177	26336	2.86	3.0E-15	M27585.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
							oc36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11
7709	17559		1.87	3.0E-15	AA807128.1	EST_HUMAN	MER19 repetitive element;
8173	18061	28311	2.71	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
250	10216	20033	3.29	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
364	10320	20141	3.23	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
364	10320	20142	3.23	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1512	11417		1.14	2.0E-15	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3465	13381	23186	1.04	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3465	13381	23187	1.04	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4522	14415		2.07	2.0E-15	AI060335.1	EST_HUMAN	wf07f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN. ;
5097	14966	24741	1.33	2.0E-15	P13993	SWISSPROT	REPEATITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
5097	14966	24742	1.33	2.0E-15	P13993	SWISSPROT	REPEATITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
6223	16089		1.71	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6310	16173	26331	2.2	2.0E-15	AA704195.1	EST_HUMAN	z177e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
6375	16237	26397	5.13	2.0E-15	W05064.1	EST_HUMAN	za78d10.1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:298675 5' similar to WP:F44F4.8 CE02227 TRANSPPOSASE ;
7163	17040	27232	2.72	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
7410	17277	27484	1.26	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-at12 HT0244 Homo sapiens cDNA
7410	17277	27485	1.26	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-at12 HT0244 Homo sapiens cDNA
8212	18096		3.01	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9799	13381	23186	2.22	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9799	13381	23187	2.22	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2747	12609		1.84	1.0E-15	AI680984.1	EST_HUMAN	b28h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPPOSASE. ;
2979	12906	22705	0.8	1.0E-15	BE043584.1	EST_HUMAN	hk40e02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999162 5'
3103	13029	22825	0.99	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4262	14161	23939	0.8	1.0E-15	BE182696.1	EST_HUMAN	RC3-HT0649-100500-022-b05 HT0649 Homo sapiens cDNA
5096	14966	24731	1.15	1.0E-15	AI984928.1	EST_HUMAN	wf86e04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494590 3'
5844	15750	25864	1.83	1.0E-15	T95763.1	EST_HUMAN	ye40e10.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element ;
6182	16088		1.96	1.0E-15	BE074217.1	EST_HUMAN	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
6791	16670	26862	1.28	1.0E-15	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6905	16783	26976	4.57	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
6905	16783	26977	4.57	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
7227	17104	27293	1.44	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8193	19079	28331	6.81	1.0E-15	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region fr31c05.x1 NCI_OGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive element;
9867	19492	25131	3.71	1.0E-15	AI783944.1	EST_HUMAN	
4404	14298	24082	1.03	9.0E-16	4503168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
8361	18238	28486	2.6	9.0E-16	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
6343	16206	26368	1.5	7.0E-16	Q88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6343	16206	26369	1.5	7.0E-16	Q88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
9816	19585		6.8	7.0E-16	T94149.1	EST_HUMAN	ye28c12.11 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'
2094	11983		8.32	6.0E-16	AW972611.1	EST_HUMAN	EST384702 IMAGE resequences, MAGL Homo sapiens cDNA
1477	11382	21246	1.09	5.0E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene d80c04.s1 Sceres. total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element;
2647	12514	22404	1.79	5.0E-16	AA982176.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
7784	17634	27867	1.69	5.0E-16	AL163246.2	NT	
8809	18623	28914	3.33	5.0E-16	BF217388.1	EST_HUMAN	601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
9904	19381		8.34	5.0E-16	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2192	12079		1.27	4.0E-16	AB001523.1	NT	Homo sapiens gene for TMEIMT and PWP2, complete and partial cds
2328	12209	22107	1.32	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
2328	12209	22108	1.32	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3411	13328	23129	3.95	4.0E-16	Q16863	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4050	13982	23728	3.55	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4050	13952	23729	3.55	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
5092	14962	24737	1	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6538	16396	26575	33.8	4.0E-16	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7398	17226	27425	1.22	4.0E-16	11423191	NT	Homo sapiens hypothetical protein FLJ170024 (FLJ170024), mRNA
8551	18421	28591	1.74	4.0E-16	AV730030.1	EST_HUMAN	AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'
9156	18906		1.64	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9244	18957		5.94	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355
9255	18984	26319	2.04	4.0E-16	6912459	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
128	10102	19924	1.59	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
128	10102	19925	1.59	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
458	10402		1.47	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434P037 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
487	10410		1.6	3.0E-16	AF136446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1436	11341	21207	2.01	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2946	12873	22670	4.05	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3874	13785		8.18	3.0E-16	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3875	13786		0.99	3.0E-16	U03887.1	NT	Human BXP20 gene
4861	14741	24521	1.01	3.0E-16	AV661393.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLCGSA01 3'
5452	15373	25431	1.41	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
7031	16908	27098	4.72	3.0E-16	AI002836.1	EST_HUMAN	am98h05.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;
7691	17541		1.27	3.0E-16	BF690617.1	EST_HUMAN	602246338F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
7828	17678	27922	3.08	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
956	10880		1.18	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2337	12217		0.96	2.0E-16	AA621761.1	EST_HUMAN	af06404.s1 Soares_leslis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2657	12524		1.71	2.0E-16	J03061.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4087	13987	23764	1.33	2.0E-16	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
6646	16526	26720	1.63	2.0E-16	AI732837.1	EST_HUMAN	nz47f06.x6 NCI_CGAP_Pri12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 contains MER7.t1 MER7 repetitive element;
178	10149	19963	2.55	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
377	10361		22.41	1.0E-16	AA628592.1	EST_HUMAN	af39g11.s1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element;
1928	11823	21704	2.44	1.0E-16	BF327942.1	EST_HUMAN	QVO-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5877	15783		23.72	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
5960	15865	25987	2.81	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
6458	15783		6.59	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
7349	17217	27416	1.31	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
3679	13593	23379	2.54	9.0E-17	AW900048.1	EST_HUMAN	QV1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
6035	15938		2.02	9.0E-17	AI392964.1	EST_HUMAN	ig22c11.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.t2 MER28 repetitive element;
6720	16600		4.87	9.0E-17	AW150257.1	EST_HUMAN	xg49g12.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2680950 3' similar to contains OFR.12 OFR repetitive element;

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7870	17720		2.18	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1001	10919		1.7	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-001 OT0032 Homo sapiens cDNA
3817	13729		0.87	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5427	19444	25402	3.56	8.0E-17	BE172081.1	EST_HUMAN	MRO-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
6311	16174		1.36	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1442	11347		3.18	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5262	15184		3.05	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6017	15921	26052	6.83	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
196	10168	19886	4.78	6.0E-17	AW983880.1	EST_HUMAN	RC1-HIN0003-220300-021-b04 HIN0003 Homo sapiens cDNA
5812	15717	25830	1.61	6.0E-17	AW662772.1	EST_HUMAN	hi81c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12
415	9982	19773	2.31	5.0E-17	T64110.1	EST_HUMAN	L1 repetitive element;
6476	16335	26502	2.07	5.0E-17	T81043.1	EST_HUMAN	yc05h08.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
8783	18598	28887	2.12	4.0E-17	AL163247.2	NT	yd28b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
							Homo sapiens chromosome 21 segment HS21C047
9171	18914		1.98	4.0E-17	AI073546.1	EST_HUMAN	ov45e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530
2051	11941	21836	1.35	3.0E-17	AW119123.1	EST_HUMAN	Q16530 PMS3 MRNA; contains MER10.t2 MER10 repetitive element;
3157	13082		1.31	3.0E-17	P35410	SWISSPROT	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3590	13504	23293	1.14	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3590	13504	23294	1.14	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
							hw05b04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
7594	17445	27660	4.72	3.0E-17	AB026898.1	NT	
9134	18890		3.16	3.0E-17	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
9909	19386		15.82	3.0E-17	AV720204.1	EST_HUMAN	AV720204 GLC Homo sapiens cDNA clone GLC01F08 5'
							qt63a06.x1 NCL CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
350	10309	20127	2.81	2.0E-17	AI270080.1	EST_HUMAN	qt63a06.x1 NCL CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
351	10309	20127	2	2.0E-17	AI270080.1	EST_HUMAN	
972	10896		1.27	2.0E-17	AA722932.1	EST_HUMAN	zg81c04.s1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:399751 3'
2397	12275	22170	2.6	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2397	12275	22171	2.6	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2899	12826	22621	5.62	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET-H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5295	15216	25017	1.95	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5295	15216	25018	1.95	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5790	15696		2.07	2.0E-17	AF055066.1	NT	Homo sapiens MHC class I region
6711	16591	26779	1.44	2.0E-17	Q95156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
6925	16803	26997	1.38	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
7699	17549	27772	2.72	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7699	17549	27773	2.72	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7887	17737	27981	5.3	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
733	10665	20499	3.37	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1729	11630	21499	2.45	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2069	11959	21853	1.68	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2287	12170	22087	1.46	1.0E-17	U79410.1	NT	Homo sapiens fibronectin 2 (THBS2) gene, promoter region and exons 1A and 1B
3519	13435		1.01	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
4045	13947		7.17	1.0E-17	R09942.1	EST_HUMAN	(UBE2D3) genes, complete cds
5885	15792		4.7	1.0E-17	AW468468.1	EST_HUMAN	yf30e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'
6006	15911	26037	1.44	1.0E-17	A1185642.1	EST_HUMAN	he38e05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921312 3' similar to contains Alu repetitive element; contains LTR8.1 LTR8 repetitive element;
6006	15911	26038	1.44	1.0E-17	A1185642.1	EST_HUMAN	qe65b05.x1 Soares fetal_lung NBHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6216	16082	26232	1.32	1.0E-17	Q16831	SWISSPROT	qe65b05.x1 Soares fetal_lung NBHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
8719	18536	28821	2.01	1.0E-17	Q28824	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
2422	12299	22196	0.96	9.0E-18	AA174078.1	EST_HUMAN	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
7468	17328		3.26	9.0E-18	AJ472167.1	EST_HUMAN	zp18g12.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609862 3'
3718	13630	23415	1.75	8.0E-18	4758977	NT	q86d03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
346	10305	20121	8.39	7.0E-18	AW316976.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
346	10305	20122	8.39	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
5136	15003	24774	0.85	7.0E-18	R18220.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); xx10b04.x1 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN); ye49c07.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53285 3' similar to contains L1 repetitive element;

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9638	10305	20121	5.73	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
9638	10305	20122	5.73	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
3255	13178	22976	1.16	6.0E-18	X71791.2	NT	Rattus norvegicus partial Gdn/Pn-1 gene for gila-derived nexin/protease nexin I, enhancer region
4641	14529		3.37	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
6799	16678		2.69	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8476	18349	28614	1.75	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8642	18506	28784	1.78	6.0E-18	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
9394	19052	25308	3.66	6.0E-18	U87929.1	NT	Human aconitate hydratase (ACO2) gene, exon 4
1130	11044	20886	14.74	5.0E-18	AI280214.1	EST_HUMAN	qm65g11.x1 Soares_placenta_8tc9weeks_2NbpHP8c9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element
4217	14115	23893	0.92	5.0E-18	10946665	NT	Mus musculus gasdermin (Gsdm), mRNA
5058	14928	24700	1.76	5.0E-18	D01517.1	EST_HUMAN	HUM411F05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-411F05 5'
5224	15147	24914	1.38	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
7061	16938	27128	4.26	5.0E-18	BE143312.1	EST_HUMAN	MR0-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA
8346	18223	28474	4.33	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
8346	18223	28475	4.33	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
9512	19125		5.3	5.0E-18	AW867182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
9837	19336		13	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCCGA02 3'
119	10096	19915	1.36	4.0E-18	BE044076.1	EST_HUMAN	ho36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
119	10096	19916	1.36	4.0E-18	BE044076.1	EST_HUMAN	ho36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
1846	11742		1.08	4.0E-18	AI738592.1	EST_HUMAN	wi33h08.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2392095 3'
2154	12042	21940	0.98	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
2154	12042	21941	0.98	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
5293	15214	25014	2.55	4.0E-18	AI017565.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5293	15214	25015	2.55	4.0E-18	AI017565.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
8370	18247	28499	7.12	4.0E-18	AA371807.1	EST_HUMAN	EST83633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
831	10758	20609	2.38	3.0E-18	AA814196.1	EST_HUMAN	ob23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN
914	10838	20686	2.41	3.0E-18	BE086634.1	EST_HUMAN	P46782 40S RIBOSOMAL PROTEIN S5 ;
3867	13778	23571	1.19	3.0E-18	AL163247.2	NT	CM0-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA
6084	16029	26169	5.2	3.0E-18	BE001671.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
9642	19210		4.92	3.0E-18	AW022015.1	EST_HUMAN	PM0-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
261	10217	20034	2.83	2.0E-18	AW836820.1	EST_HUMAN	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485128 5'
1135	11049		47.22	2.0E-18	BE256097.1	EST_HUMAN	QV1-LT0036-150200-070-e07 LT0036 Homo sapiens cDNA
							601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
							ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577
5322	15242		3.2	2.0E-18	AA868610.1	EST_HUMAN	O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE. ;
5380	15299	25149	3.04	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5380	15299	25150	3.04	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5585	15500		1.67	2.0E-18	BF347229.1	EST_HUMAN	802021164F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156670 5'
5814	15720	25834	3.53	2.0E-18	AW665853.1	EST_HUMAN	h194g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains MER19.t2 MER19 repetitive element ;
7779	17629	27861	1.53	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element ;
							x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element ;
7779	17629	27862	1.53	2.0E-18	AW151673.1	EST_HUMAN	MER10 repetitive element ;
8340	18217	28469	5.32	2.0E-18	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
8968	18774	29065	4.44	2.0E-18	AW151299.1	EST_HUMAN	xg47e09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element ;
9325	11049		3.15	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
4318	14215		1.02	1.0E-18	T95406.1	EST_HUMAN	ye43g05.r1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element ;
5286	15208	24985	2.38	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLCKE11 3'
5419	15340	25394	1.97	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5419	15340	25395	1.97	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5883	15790	25912	1.32	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rctet gene, and sodium phosphate transporter (NP13) gene, complete cds
7696	17546	27769	4.4	1.0E-18	U91328.1	NT	
9277	18980	26324	2.53	1.0E-18	AF003529.1	NT	Homo sapiens glycocal 3 (GPC3) gene, partial cds and flanking repeat regions
533	10475	20289	4.28	9.0E-19	AA281961.1	EST_HUMAN	z11406.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
534	10475	20289	3.19	9.0E-19	AA281961.1	EST_HUMAN	z11406.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
6584	16484		5.21	9.0E-19	F08688.1	EST_HUMAN	MER19 repetitive element;
7042	16919	27110	2.46	9.0E-19	AL163203.2	NT	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
7042	16919	27111	2.46	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8470	18343	28608	3.88	9.0E-19	AB032969.1	NT	Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens mRNA for KIAA1143 protein, partial cds
9042	10475	20289	8.69	9.0E-19	AA281961.1	EST_HUMAN	z11406.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
1032	10950		1.54	8.0E-19	AW974902.1	EST_HUMAN	MER19 repetitive element;
							EST387007 MAGE resequences, MAGN Homo sapiens cDNA
2198	12085	21987	1.58	7.0E-19	4758139	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
5884	15791	25913	2.15	7.0E-19	AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
9179	19742		2.95	7.0E-19	AA705684.1	EST_HUMAN	z160b01.s1 Soares fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3713	13526		1.02	6.0E-19	AW852930.1	EST_HUMAN	PMO-CTC248-131099-001-g01 CT0248 Homo sapiens cDNA
4360	14256	24041	1.36	6.0E-19	P34986	SW/ISSPROT	OLFACTORY RECEPTOR 6 (N50)
4360	14256	24042	1.36	6.0E-19	P34986	SW/ISSPROT	OLFACTORY RECEPTOR 6 (N50)
4694	14580		1.16	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4952	14829	24595	1.09	6.0E-19	AL120817.1	EST_HUMAN	DKFZp762F192.t1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762F192 5'
							ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC56)
5571	15486	25562	5.24	5.0E-19	Q00193	SW/ISSPROT	X87b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element MSR1 repetitive element;
8824	18637	28921	7.19	5.0E-19	AW183725.1	EST_HUMAN	
							Human germline T-cell receptor beta chain TCRBV:3S1, TCRBV6S8A2T, TCRBV6S3A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV6S2, TCRBV6S6A2T, TCRBV6S7P, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
9849	19495		1.52	5.0E-19	U66080.1	NT	
542	10483	20293	1.45	4.0E-19	AE007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2649	12516	22406	1.39	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3778	13690	23475	1.74	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3778	13690	23476	1.74	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4345	14242	24024	1.18	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
6370	16232		2.47	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
7443	16456	26645	1.23	3.0E-19	X89885.1	NT	M.musculus mRNA for TPCR33 protein
9416	19068		7.38	3.0E-19	AF165520.1	NT	Homo sapiens porbabin 1 protein (PB1) mRNA, complete cds
2513	12387	22279	17.57	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
6849	16728	26923	8.96	2.0E-19	AA012854.1	EST_HUMAN	zs34c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
473	10417		1.6	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2118	12007	21906	1.4	1.0E-19	H30795.1	EST_HUMAN	yo79g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2685	12550		2.88	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2817	12746		5.03	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3355	13274	23075	1.27	1.0E-19	AA834967.1	EST_HUMAN	aj49b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12
5701	15609	25711	2.37	1.0E-19	U12186.1	NT	MER37 repetitive element;
6919	16797	26990	1.79	1.0E-19	M64657.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
7076	16953		2.83	1.0E-19	T99920.1	EST_HUMAN	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
7853	17703	27948	25.21	1.0E-19	AW812259.1	EST_HUMAN	ye72b02.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains ORF repetitive element;
7857	17707	27953	1.79	1.0E-19	N44631.1	EST_HUMAN	RCO-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA
6005	15910	26035	2.22	8.0E-20		NT	yy31e09.r1 Soares melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:272872 5'
6005	15910	26036	2.22	8.0E-20		NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6439	16300	26462	1.31	8.0E-20	A1221371.1	EST_HUMAN	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6439	16300	26463	1.31	8.0E-20	A1221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3238	13161	22981	0.88	7.0E-20	BF326455.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
6176	15133	24852	5.53	7.0E-20	AL138120.1	EST_HUMAN	PMA4-AN0096-050900-003-ac04 AN0096 Homo sapiens cDNA
6947	16825	27018	10.99	7.0E-20	AA557657.1	EST_HUMAN	DKFZp547D092_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D092 5'
6947	16825	27019	10.99	7.0E-20	AA557657.1	EST_HUMAN	n146c04.s1 NCL_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
8952	18759		10.45	7.0E-20	6912633	NT	MER29 repetitive element;
3508	13424	23227	3.85	6.0E-20	P39188	SWISSPROT	n146c04.s1 NCL_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
							Homo sapiens ribosomal protein L13a (RPL13a), mRNA
							ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4175	14075	23850	2.55	6.0E-20	BE622434.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4491	14385		1.17	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTCBTA01 5'
6634	16514	26704	4.66	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;
6634	16514	26705	4.66	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;
7128	17005	27197	1.44	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
7128	17005	27198	1.44	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
6624	16504		6.03	4.0E-20	AI874352.1	EST_HUMAN	tz64g03.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2293396 3'
7995	17845	28087	1.17	4.0E-20	AW937469.1	EST_HUMAN	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA
2092	11981	21876	1.04	3.0E-20	U03888.1	NT	Human BXP21 gene
4115	14015	23795	1.69	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I14
4524	14417	24201	0.86	3.0E-20	AA037616.1	EST_HUMAN	zk36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;
7172	17049		3.26	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
8065	17946		2.08	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9195	18929	25352	5.37	3.0E-20	BE888422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915622 5'
813	10741		4.52	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5;
1095	11011	20852	2.03	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN;
1095	11011	20853	2.03	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN;
2796	10741		2.72	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5;
4866	14746	24525	4.32	2.0E-20	Q28983	SWISSPROT	ZONADIESIN PRECURSOR
4866	14746	24526	4.32	2.0E-20	Q28983	SWISSPROT	ZONADIESIN PRECURSOR
5090	14960		11.35	2.0E-20	5174538	NT	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
7301	17177	27378	2.95	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
7301	17177	27379	2.95	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
8993	18797	28089	1.95	2.0E-20	AA766765.1	EST_HUMAN	oa55b08.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1306935 3' similar to contains MER4.b2 MER4 repetitive element;

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8993	18797	28090	1.95	2.0E-20	AA766755.1	EST_HUMAN	ca35b08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306935 3' similar to contains MER4.b2
9574	19482	25129	1.5	2.0E-20	H65371.1	EST_HUMAN	MER4 repetitive element;
1967	12648	21751	5.25	1.0E-20	AA281961.1	EST_HUMAN	CHR2203:10 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
4338	14235	24018	1	1.0E-20	BF115158.1	EST_HUMAN	z11406.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
7285	17161	27359	2.42	1.0E-20	11418497	NT	MER19 repetitive element;
8839	18652	28940	2.81	1.0E-20	AF223391.1	NT	hr84b05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element;
9321	19011		1.84	1.0E-20	AA420453.1	EST_HUMAN	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
2883	12810		1.08	9.0E-21	AJ003514.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9045	18830		2.35	9.0E-21	AW895189.1	EST_HUMAN	nc80g08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.13 L1 repetitive element;
7115	16992		1.74	8.0E-21	AW674891.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library/Homo sapiens cDNA clone MP1212-8J21
8825	18638	28922	3.42	8.0E-21	AA809411.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
9207	18938		4.02	8.0E-21	O21330	SWISSPROT	bb30a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2984714 5' similar to SW.NIAM_HUMAN
2023	11914	21803	2.07	7.0E-21	P15800	SWISSPROT	O95169 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR;
2023	11914	21804	2.07	7.0E-21	P15800	SWISSPROT	cb71f06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
4161	14061		4.96	7.0E-21	AA046502.1	EST_HUMAN	ATP SYNTHASE A CHAIN (PROTEIN 6)
6887	16766	26962	1.43	7.0E-21	AJ277557.1	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
7036	16913	27102	6.84	7.0E-21	D14718.1	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
8080	17971	28220	2.94	7.0E-21	AA723404.1	EST_HUMAN	z67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
8590	18458	28727	2.37	7.0E-21	7706668	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5
4014	13920	23696	0.94	6.0E-21	BE408611.1	EST_HUMAN	Human chromosomal protein HMG1 related gene
907	10831	20578	1.6	5.0E-21	5902031	NT	zg73d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:368981 3' similar to gb:IM14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains THR.t3 OFR repetitive element;
2234	12119	22021	1.08	5.0E-21	AA928194.1	EST_HUMAN	Homo sapiens PTD013 protein (PTD013), mRNA
4266	14165	23942	2.65	5.0E-21	BE968839.1	EST_HUMAN	607304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
4696	14582	24375	5.98	5.0E-21	4885474	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
							Homo sapiens PRO-POL-DUTPASE POLYPYRROLINE; om23g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541908 3' similar to TR:002711
							O02711 PRO-POL-DUTPASE POLYPYRROLINE; 601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
							Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5109	14977		0.95	5.0E-21	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1701	11602	21473	1.24	4.0E-21	AA970713.1	EST_HUMAN	cc86e08.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16630 PMS3 MRNA ;contains ORF.t1 ORF repetitive element ;
6106	16000	26138	3.06	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
2228	12113	22015	1.06	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3041	12988	22762	4.04	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5749	15657		1.72	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5'
6206	15956	26100	4.79	3.0E-21	BF361093.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
7889	17440	27856	1.55	3.0E-21	AW897760.1	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
9884	10672	24092	1.32	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
140	10114		14.75	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
919	10843	20688	0.85	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
919	10843	20689	0.85	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1196	11106		2.09	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
2599	12468	22361	2.89	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2599	12468	22362	2.89	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5370	15290	25126	1.77	2.0E-21	AI624582.1	EST_HUMAN	ts30f03.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
6870	16749	26944	4.66	2.0E-21	BE141785.1	EST_HUMAN	HYPOTHETICAL 51.1 KD PROTEIN ;
7122	16999	27190	3.43	2.0E-21	AU136779.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
8412	18287		1.98	2.0E-21	BE350127.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
8636	18501	28776	1.92	2.0E-21	BE973826.1	EST_HUMAN	ht09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
8636	18501	28777	1.92	2.0E-21	BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
9425	19072		5.13	2.0E-21	AF176815.1	NT	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1235	11142	20994	1.68	1.0E-21	AA557657.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
1381	11286		2.46	1.0E-21	AI601264.1	EST_HUMAN	ht46d04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element ;
5907	15813		2.43	1.0E-21	AL079752.1	EST_HUMAN	ar88d12.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
6269	16134	26289	4.43	1.0E-21	AI223104.1	EST_HUMAN	DKFZp434i0830.t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434i0830 5'
8021	17871		1.46	1.0E-21	5730038	NT	qq47a05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838335 3' similar to gb:M64241 QM PROTEIN (HUMAN);
4312	14209	23993	2.55	9.0E-22	AI702438.1	EST_HUMAN	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
							tz94a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408
							NEUTRAL PROTEASE LARGE SUBUNIT ;

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7002	16879	27070	1.26	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
7002	16879	27071	1.26	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
8171	18059	28309	3.65	9.0E-22	AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSCCG05 5'
8945	18753	29048	2.92	9.0E-22	AU140358.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE200394 5'
8997	18800		2.39	9.0E-22	9790256	NT	Mus musculus TF-1 cell apoptosis related protein-15 (Tfar15), mRNA
933	10858		4.55	8.0E-22	BE144748.1	EST_HUMAN	CMD1-HT0179-281099-076-H05 HT0179 Homo sapiens cDNA
6609	16489		3.8	8.0E-22	AA046502.1	EST_HUMAN	z67a06.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
649	10585	20401	4.23	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4186	14086	23861	2.32	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
4969	14844	24813	1.18	7.0E-22	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
7044	16921		1.34	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
7127	17004	27196	2.63	7.0E-22	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#36206) Homo sapiens cDNA clone HFBCF07
7538	17389	27599	1.86	7.0E-22	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region
6796	16675		1.82	6.0E-22	AW029123.1	EST_HUMAN	wx05g07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
5927	15832	25955	2.53	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7912	17762	28001	3.97	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
9645	19213		2.03	5.0E-22	BF476511.1	EST_HUMAN	naa27b06.x1 NCI_CGAP_Pyr28 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu repetitive element;
3584	13498		0.85	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
6902	19767		2.7	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8105	17995	28244	2.97	4.0E-22	BF218030.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085434 5'
9803	19315		1.51	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
943	10868		1.2	3.0E-22	A1469679.1	EST_HUMAN	tm14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.L1 L1 repetitive element ;
2523	12397	22288	1.86	3.0E-22	A1859038.1	EST_HUMAN	w166b04.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN
3620	13534		1.49	3.0E-22	D14718.1	NT	Human chromosomal protein HMG1 related gene
4695	14581	24374	2.72	3.0E-22	A1090125.1	EST_HUMAN	qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.t2 MER12 repetitive element ;
6793	16672	26864	2.75	3.0E-22	BE089641.1	EST_HUMAN	RC6-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
1910	11805		2.86	2.0E-22	N24942.1	EST_HUMAN	yz73d05.s1 Soares_melanocyte_2NbHM Homo sapiens cDNA clone IMAGE:267369 3'
2476	12352	22244	1.33	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3373	13292	23091	4.06	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4133	14033	23808	1.26	2.0E-22	AW817794.1	EST_HUMAN	PM1-S10262-261199-001-d12 ST0262 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5570	19447	25561	1.44	2.0E-22	W39456.1	EST_HUMAN	z020f01.r1 Scores_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
5747	15655	25763	3.39	2.0E-22	BF092116.1	EST_HUMAN	RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA
7595	17446	27661	1.49	2.0E-22	AI276522.1	EST_HUMAN	q176h06.x1 Scores_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains MER29.13 MER29 repetitive element;
7840	17490	27710	7.07	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
7640	17490	27711	7.07	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
8974	18779	29071	2.04	2.0E-22	AW418960.1	EST_HUMAN	ha24f04.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2874655 3'
9009	19304	25200	1.85	2.0E-22	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1836	11733	21609	1.78	1.0E-22	AW865517.1	EST_HUMAN	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
2539	12413	22303	2.65	1.0E-22	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
3365	13284	23084	1.74	1.0E-22	D14547.1	NT	Human DNA, SINE repetitive element
6553	16411	26589	1.49	1.0E-22	BE084667.1	EST_HUMAN	MR0-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA
9844	19342		4.71	9.0E-23	AW802801.1	EST_HUMAN	IL2-UM0076-070400-061-F11 UM0076 Homo sapiens cDNA
3523	13439	23236	0.84	8.0E-23	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
5241	15165	24935	1.48	8.0E-23	AI133716.1	EST_HUMAN	HA2340 Human fetal liver cDNA library Homo sapiens cDNA
5241	15165	24936	1.48	8.0E-23	AI133716.1	EST_HUMAN	HA2340 Human fetal liver cDNA library Homo sapiens cDNA
3271	13192		1.45	7.0E-23	AV647246.1	EST_HUMAN	AV647246 GLC Homo sapiens cDNA clone GLCAWC07 3'
4764	14649	24438	1.04	7.0E-23	10092626	NT	Homo sapiens DKFZP564O0463 protein (DKFZP564O0463), mRNA
8398	18274	28526	3.51	7.0E-23	5031952	NT	Homo sapiens Nct56 (D. melanogaster)-like protein (NOT56L) mRNA
3387	13305		1.62	6.0E-23	AF199333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4171	14071	23846	3.12	6.0E-23	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
9146	18899	25338	1.99	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9146	18899	25339	1.99	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9341	19021	25297	2.18	6.0E-23	AI209130.1	EST_HUMAN	qg59c03.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1839480 3' similar to SW:MV10_MOUSE P23249 PROTEIN MOV-10.;
5341	15262	25088	3.51	5.0E-23	U82671.2	NT	Homo sapiens chromosome Xc28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), celltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LIP
5781	19454	25797	3.51	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6397	19454	25797	3.04	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6580	16460	26653	3.56	3.0E-23	AA1307165.1	EST_HUMAN	z55g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.t2 MER29 repetitive element ;
7329	17233	27435	3.61	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
7329	17233	27436	3.61	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
650	10586	20402	4.36	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1126	12644		2.77	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2765	12627	22519	1.06	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2765	12627	22520	1.06	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3325	13245		1.46	2.0E-23	AJ201458.1	EST_HUMAN	qs73H1.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13637 Q13637
3655	13569		3.03	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
3894	13804	23589	2.98	2.0E-23	H59931.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3894	13804	23590	2.98	2.0E-23	H59931.1	EST_HUMAN	yt16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
							yt16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
6595	16475		5.62	2.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
9131	18888		2.69	2.0E-23	M32658.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
9656	19218		2.47	2.0E-23	AF006660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9774	19676		2.02	2.0E-23	AU133931.1	EST_HUMAN	AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
4428	14323	24110	1.6	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4657	14543		4.49	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6034	15937		2.91	1.0E-23	BE378471.1	EST_HUMAN	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608663 5'
6865	16744	26937	4.54	1.0E-23	AA448097.1	EST_HUMAN	zw82c06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.t2 PTR5 repetitive element ;
540	10481		1.88	9.0E-24	AA663213.1	EST_HUMAN	ab75a08.s1 Stratagene fetal retina 637202 Homo sapiens cDNA clone IMAGE:852758 3' similar to TR:E19822 E19822 CA PROTEIN. ;
4549	14442	24225	1.08	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
4549	14442	24226	1.08	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
3796	13708		1.31	7.0E-24	AW937954.1	EST_HUMAN	QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA
690	10623		2.4	6.0E-24	AB001421.1	NT	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
820	10748	20595	10.14	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
3889	13800	23585	7.18	5.0E-24	AJ226043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
5611	15526	25609	3.06	4.0E-24	AA594178.1	EST_HUMAN	nn31h05.s1 NCI CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW:POL_MLVRK P31795 POL POLYPROTEIN ;

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9506	19121	25293	2.12	4.0E-24	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
9748	19309	25203	1.53	4.0E-24	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
6906	16784		3.02	3.0E-24	AW614871.1	EST_HUMAN	h88c08.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967950 3' similar to contains MER29.b2
7449	17258	27463	4.12	3.0E-24	AL163252.2	NT	MER29 repetitive element
9687	19171	25273	5.14	3.0E-24	BF127762.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
2298	12180	22078	2.33	2.0E-24	AA167539.1	EST_HUMAN	601810449F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053396 5'
3729	13641		1.01	2.0E-24	AW898189.1	EST_HUMAN	zp11f09.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
7075	16952	27146	3.14	2.0E-24	AL119198.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
9433	19717		6.55	2.0E-24	M28877.1	NT	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
1670	11572	21438	2.18	1.0E-24	7706340	NT	Human O family dispersed repeat element
2638	12505		1.87	1.0E-24	AW820194.1	EST_HUMAN	Homo sapiens CG1-127 protein (LOC51646), mRNA
2987	12915	22710	0.91	1.0E-24	D86423.1	NT	QV0-ST0294-100400-185-c10 S10294 Homo sapiens cDNA
4173	14073		1.63	1.0E-24	AF143313.1	NT	Mus musculus mRNA for HGT keratin, partial cds
6456	16317	26484	4.07	1.0E-24	AL163303.2	NT	Homo sapiens PTEN (PTEN) gene, exon 2
6633	16513	26703	1.98	1.0E-24	AW901164.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
4926	14805	24575	2.32	7.0E-25	AA489344.1	EST_HUMAN	C10-NN1010-130300-281-c07 NN1010 Homo sapiens cDNA
6785	16664	26855	3.75	7.0E-25	AA468646.1	EST_HUMAN	ne92e10.s1 NCL_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2
8942	18750	29045	7.46	7.0E-25	AA883540.1	EST_HUMAN	MER1 repetitive element
6174	15131		4.32	6.0E-25	W87623.1	EST_HUMAN	ne06a09.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR
6543	16401	26590	11.44	6.0E-25	7305360	NT	repetitive element
5166	15032	24799	0.95	5.0E-25	AW838171.1	EST_HUMAN	mf25h06.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST
8634	18499	28774	3.61	5.0E-25	AW979107.1	EST_HUMAN	P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA. ;
1430	11335	21201	2.08	4.0E-25	T98107.1	EST_HUMAN	zh65h07.r1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'
3356	13275		2.78	4.0E-25	AW887671.1	EST_HUMAN	Mus musculus ctogelin (Otog), mRNA
4221	14119		3.02	4.0E-25	BE170957.1	EST_HUMAN	QV2-LT0051-280300-111-f03 LT0051 Homo sapiens cDNA
3278	13199	22999	2.66	3.0E-25	8923321	NT	EST7391217 IMAGE resequences, MAGP Homo sapiens cDNA
3278	13199	23000	2.66	3.0E-25	8923321	NT	ye55h04.r1 Soares fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
4798	14683	24470	0.85	3.0E-25	P29622	SWISSPROT	PM3-OT0058-280200-001-g07 OT0093 Homo sapiens cDNA
6854	16733	26926	2.47	3.0E-25	AL163210.2	NT	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
							Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
							Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
							KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
							Homo sapiens chromosome 21 segment HS21C010

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8394	18270	28522	2.03	3.0E-25	AA579013.1	EST_HUMAN	nt30h10.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.1 L1
1325	11232	21088	3.37	2.0E-25	5032158	NT	repetitive element ; Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2260	12144	22043	7.11	2.0E-25	BE88016.1	EST_HUMAN	601511530F1 NIH MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2801	12370	22263	4.32	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4096	13996	23773	1.91	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4096	13996	23774	1.91	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
7629	17480	27700	2.25	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Staurides GS) Homo sapiens cDNA
361	10317	20138	1.61	1.0E-25	AL040229.1	EST_HUMAN	DKFZp434H0313_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5'
1228	11135		1.21	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome
2384	12264	22156	2.79	1.0E-25	Q06055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4753	14638	24425	2.71	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-H09 HT0454 Homo sapiens cDNA
6069	19460	26199	2.85	1.0E-25	AA582890.1	EST_HUMAN	nt54h11.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
							zfbg04.s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains
6616	16496	26883	3.15	1.0E-25	AA709079.1	EST_HUMAN	PTR5.13 PTR5 repetitive element ; Homo sapiens
8337	18214	28467	3.5	1.0E-25	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4) and MAGE-B1 (MAGE-B1) genes, complete cds
9143	18897	28796	1.45	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
9143	18897	28797	1.45	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
9914	19389		1.32	1.0E-25	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
2433	12310	22206	1.94	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
9010	19501		1.73	9.0E-26	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5492	15411		1.56	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element.
1559	11464	21321	1.44	7.0E-26	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3898	13808	23594	1.35	7.0E-26	X99211.1	NT	H. sapiens DNA for endogenous retroviral like element
4067	13969	23745	2.03	7.0E-26	AW340153.1	EST_HUMAN	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908366 3'
8923	18731		7.99	7.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5'
9700	19250		1.33	7.0E-26	AW954559.1	EST_HUMAN	similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); EST366629 MAGE resequences, MAGEC Homo sapiens cDNA
2178	12065	21967	2.44	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
3302	13223	23025	1.42	6.0E-26	AA206131.1	EST_HUMAN	zqf2h04.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'
8932	18740	29033	4.98	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1160	11073	20918	3.33	5.0E-26	A1708235.1	EST_HUMAN	as38h08.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371;
1160	11073	20919	3.33	5.0E-26	A1708235.1	EST_HUMAN	as38h08.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371;
9976	19435		1.71	5.0E-26	A1761429.1	EST_HUMAN	wg66d06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2369986 3' similar to contains Alu repetitive element;
1525	11430		1.52	4.0E-26	AA329548.1	EST_HUMAN	EST33446 Embryo, 12 week II Homo sapiens cDNA 5' end
7416	17283		3.77	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
8053	17944	28194	3.74	4.0E-26	BE266187.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
1958	11853	21740	1.5	3.0E-26	AL045855.2	EST_HUMAN	DKFZp4341066.r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp4341066 5'
1987	11880		2.41	3.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3712	13625	23408	1.19	3.0E-26	AA152484.1	EST_HUMAN	z630f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR;
3712	13625	23409	1.19	3.0E-26	AA152484.1	EST_HUMAN	z630f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR;
6131	15978	26114	4.35	3.0E-26	BF245488.1	EST_HUMAN	601864963F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
8108	17998		2.18	3.0E-26	AF036405.1	NT	Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds
8853	18665	28951	1.99	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 P.T0012 Homo sapiens cDNA
8853	18665	28952	1.99	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 P.T0012 Homo sapiens cDNA
8879	18691	28984	10.55	3.0E-26	AA583173.1	EST_HUMAN	m37d05.s1 NCL_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.t1 OFR repetitive element;
666	10600	20418	5.61	2.0E-26	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1825	11722		3.36	2.0E-26	AL038099.2	EST_HUMAN	DKFZp566L171.s1 566 (synonym: hfkid2) Homo sapiens cDNA clone DKFZp566L171 3'
3193	13118	22924	4.26	2.0E-26	X86694.1	NT	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
8135	18023		2.88	2.0E-26	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8549	18420	28650	4.55	2.0E-26	AL001412.1	EST_HUMAN	to89a01.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element; contains element MER20 MER20 repetitive element;
8720	18537		1.82	2.0E-26	AF055066.1	NT	Homo sapiens MHC class 1 region
9252	18962		2.19	2.0E-26	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
132	10106	19927	2.36	1.0E-26	BE170371.1	EST_HUMAN	QV4-HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
2001	11894	21786	1.39	1.0E-26	AL039363.2	EST_HUMAN	DKFZp434H1910.r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H1910 5'
2516	12390	22282	0.84	1.0E-26	BE814966.1	EST_HUMAN	MR2-BN0114-240500-030-g07 BN0114 Homo sapiens cDNA
2564	12521		16.79	1.0E-26	AF261086.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6089	16034		2.75	1.0E-26	BE165980.1	EST_HUMAN	MF3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8266	18146		3.17	1.0E-26	AL038487.1	EST_HUMAN	DKFZp566C2146_r1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZp566C2146 5'
9493	19737		1.84	1.0E-26	H55093.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
7364	17342		3.11	9.0E-27	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
8027	19470	28118	3.48	9.0E-27	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
9013	18812		3.97	9.0E-27	BF445556.1	EST_HUMAN	naa03c07.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.t1
10	9996	19787	3.09	8.0E-27	AI831462.1	EST_HUMAN	wj49c04.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
545	10486		4.13	8.0E-27	AL163227.2	NT	TH-R repetitive element ;
1395	11300	21158	18.87	8.0E-27	AW162737.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1395	11300	21159	18.87	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
2121	12009	21909	0.98	8.0E-27	AW864776.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
3148	13073	22874	3.31	8.0E-27	P12236	SWISSPROT	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
3309	13230	23035	0.91	8.0E-27	AF181897.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
6165	15122		3.12	8.0E-27	BE926560.1	EST_HUMAN	PM2-SN0018-220300-002-a07 SN0018 Homo sapiens cDNA
6196	15956	26088	4	8.0E-27	N84970.1	EST_HUMAN	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
7310	17186	27386	1.68	8.0E-27	AW857579.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
7310	17186	27387	1.68	8.0E-27	AW857579.1	EST_HUMAN	MR4-BT0398-250800-204-d06 BT0398 Homo sapiens cDNA
668	10602		1.22	7.0E-27	Z70684.1	NT	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to
6196	15956	26088	4	8.0E-27	N84970.1	EST_HUMAN	REPETITIVE ELEMENT L1
7310	17186	27386	1.68	8.0E-27	AW857579.1	EST_HUMAN	GM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
7310	17186	27387	1.68	8.0E-27	AW857579.1	EST_HUMAN	GM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
668	10602		1.22	7.0E-27	Z70684.1	NT	Human endogenous retroviral element HC2
5023	14896		2.09	7.0E-27	AW629172.1	EST_HUMAN	h51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:076040
8132	18020		4.22	7.0E-27	AJ271735.1	NT	O76040 ORF2: FUNCTION UNKNOWN ;
9631	19204		2.07	7.0E-27	AV723365.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
8109	17999	28246	6.21	6.0E-27	M26697.1	NT	AV723365 HTB Homo sapiens cDNA clone HTBAHE02 5'
7877	17727	27970	2.92	5.0E-27	BF666814.1	EST_HUMAN	Human nuclear protein (B23) mRNA, complete cds
7877	17727	27971	2.92	5.0E-27	BF666814.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
8046	15949	26080	1.54	4.0E-27	9910569	NT	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
							Mus musculus sperm tail associated protein (Stap) mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6656	16366		1.23	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8880	18692	28985	2.56	4.0E-27	X80211.1	NT	H.sapiens DNA for endogenous retroviral like element
1995	11889	21782	5.42	3.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4174	14074	23849	1.27	3.0E-27	BE071924.1	EST_HUMAN	PMC-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
5278	15200	24976	5.13	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
7365	17343	27549	2.98	3.0E-27	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
36	10023	19820	7.96	2.0E-27	AF064187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1853	11749		18.58	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
3071	12998		10.27	2.0E-27	AW629172.1	EST_HUMAN	h151h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN.;
3187	13112	22916	1.43	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3187	13112	22917	1.43	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3944	13852	23627	1.09	2.0E-27	AF000368.1	NT	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
6712	16592	26790	1.5	2.0E-27	AI866347.1	EST_HUMAN	w128g07.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426268 3'
7338	17206		2.3	2.0E-27	AA551527.1	EST_HUMAN	nh08h05.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.L3 L1 repetitive element;
7768	17618	27847	1.22	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
7768	17618	27848	1.22	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
8324	18201	28450	2.89	2.0E-27	AU121855.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5'
8778	11749		20.82	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
429	10374		1.56	1.0E-27	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
980	10903	20749	1.41	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5943	15848	25972	6.31	1.0E-27	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6105	15909	26136	2.2	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
6105	15909	26137	2.2	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
7005	16882	27075	1.72	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
7104	17071		1.89	1.0E-27	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
7606	17457	27672	2.89	1.0E-27	D87449.1	NT	Human mRNA for KIAA0260 gene, partial cds
8943	18751	29046	3.14	1.0E-27	AF111093.1	NT	Bos taurus latrophilin 3 splice variant bbah mRNA, complete cds

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
136	10109		2.32	9.0E-28	BE348399.1	EST_HUMAN	hw17c11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
308	10270	20089	3.01	9.0E-28	AU126260.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR, [3] TR:Q07280 TR:Q07313 ;
5118	14986	24760	1.21	9.0E-28	AI590115.1	EST_HUMAN	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5' to12b09.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element ;
5118	14986	24761	1.21	9.0E-28	AI590115.1	EST_HUMAN	to12b09.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element ;
9093	18866		3.74	9.0E-28	BF377859.1	EST_HUMAN	CM2-TN0140-070000-372-g01 TN0140 Homo sapiens cDNA
9418	19592		1.97	8.0E-28	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:O60302 O60302 KIAA0655 PROTEIN, ; contains element MER22 repetitive element ;
1164	11077	20922	7.54	7.0E-28	AU142750.1	EST_HUMAN	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5' Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
8523	18395	28660	2.54	7.0E-28	11417866	NT	
9053	18836		1.44	7.0E-28	AV753348.1	EST_HUMAN	AV753348 CB Homo sapiens cDNA clone CBFKA12 5' Homo sapiens mRNA for KIAA0866 protein, complete cds
3987	13894	23670	1.27	6.0E-28	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
3987	13894	23671	1.27	6.0E-28	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
9673	19232		2.73	6.0E-28	AA504562.1	EST_HUMAN	aa60a03.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826340 5' similar to contains Alu repetitive element ; contains element PTR5 repetitive element ;
315	10277		3.08	5.0E-28	AI921003.1	EST_HUMAN	w018c07.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element ;
3927	13836	23616	1.85	5.0E-28	R79762.1	EST_HUMAN	y89f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5' Xn33c09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;
2584	12455	27347	1.42	4.0E-28	AW195066.1	EST_HUMAN	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
3070	12997	22788	3.39	4.0E-28	BE409100.1	EST_HUMAN	q66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
6336	16199	26359	1.59	4.0E-28	AI198941.1	EST_HUMAN	q66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
8239	18119		4.29	4.0E-28	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
8371	18248		53.6	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
8388	16199	26359	2.94	4.0E-28	AI198941.1	EST_HUMAN	q66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
1262	11169		1.89	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
7124	17001	27193	2.19	3.0E-28	BF364030.1	EST_HUMAN	MR3-HT0713-280500-013-09 HT0713 Homo sapiens cDNA
8306	18183	28430	1.84	3.0E-28	U63588.1	NT	Homo sapiens MHC class 1 region

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9489	19106		2.44	3.0E-28	A1831991.1	EST_HUMAN	wj9807.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element ;
83	10067	19884	6.45	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0264-220300-019-c05 BT0254 Homo sapiens cDNA
1149	11062	20905	10	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2427	12304	22200	2.1	2.0E-28	A1349634.1	EST_HUMAN	qo35506.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1 b2 L1 repetitive element ;
5821	15727		4.28	2.0E-28	BF212905.1	EST_HUMAN	601814196F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
7528	17379		5.86	2.0E-28	AW972305.1	EST_HUMAN	EST384394 IMAGE resequences, MAGI Homo sapiens cDNA
8887	18698	28992	2.27	2.0E-28	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1463	11368	21233	2.42	1.0E-28	D36044.1	NT	Human gene for Ah-receptor, exon 7-9
2173	12080	21963	1.55	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
2650	12517	22407	1.03	1.0E-28	AF000395.1	NT	Homo sapiens ubiquitous TPR motif, Y isoform (UTY) mRNA, alternative transcript 2, complete cds
6587	16467		4.48	1.0E-28	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC630391), mRNA
6675	16555		3.02	1.0E-28	8922793	NT	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
7346	17214	27413	2.63	1.0E-28	AA308744.1	EST_HUMAN	EST179615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
7678	17528	27753	5.15	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
7678	17528	27754	5.15	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
9058	18840		3.95	1.0E-28	AA054182.1	EST_HUMAN	zf51c01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
9797	19485		1.43	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9892	19691	24896	2.6	9.0E-29	AW663987.1	EST_HUMAN	hi76g06.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978286 3'
9585	19169		2.92	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1584	11488	21349	0.91	7.0E-29	AW966447.1	EST_HUMAN	EST378521 IMAGE resequences, MAGI Homo sapiens cDNA
9942	19410		5.08	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
580	10518	20325	6.52	6.0E-29	A1936748.1	EST_HUMAN	wp69b01.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
9353	19028		3.88	6.0E-29	BE940436.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
9438	19076		1.86	6.0E-29	BF568097.1	EST_HUMAN	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
4928	14807		0.98	5.0E-29	AL163203.2	NT	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
7088	10945		7.61	5.0E-29	AW887541.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
						EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
3194	13119		1.69	4.0E-29	A1752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH7BC_on15c02 random
5656	15568		6.65	4.0E-29	BE164930.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7079	16656	27149	4.71	4.0E-29	J04988.1	NT	Human 90 kD heat shock protein gene, complete cds
4317	14214	23997	1.45	3.0E-29	AB042297.1	NT	Homo sapiens PIS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
4626	14514	24305	1.31	3.0E-29	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
7070	16947	27138	2.07	3.0E-29	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
7362	17229	27429	1.6	3.0E-29	AW303317.1	EST_HUMAN	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element;
7492	17362		1.64	3.0E-29	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8591	18459	28728	2.22	3.0E-29	AA403053.1	EST_HUMAN	z62b01.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
9248	18959		1.51	3.0E-29	D63882.1	NT	G1335769 GAG-POL POLYPYRROLINE;
484	10427	20240	1.43	2.0E-29	AF084869.1	NT	Human HsLIM15 mRNA for HsLIM15, complete cds
484	10427	20241	1.43	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein R1C-6 (env) gene, complete cds
							Homo sapiens envelope protein R1C-6 (env) gene, complete cds
1516	11421	21278	6.12	2.0E-29	A1963604.1	EST_HUMAN	wr65d10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546
1516	11421	21279	6.12	2.0E-29	A1963604.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN;
4182	14082	23855	2.03	2.0E-29	AL163268.2	NT	wr65d10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546
5750	15658	25765	1.43	2.0E-29	A1806418.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN;
6461	15658	25765	1.43	2.0E-29	A1806418.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C068
7474	17334	27539	2.95	2.0E-29	AL163248.2	NT	wr27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element;
7474	17334	27540	2.95	2.0E-29	AL163248.2	NT	wr27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element;
7879	17729	27973	3.39	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7879	17729	27974	3.39	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8804	18618		1.96	2.0E-29	AW880701.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
9004	18807		1.73	2.0E-29	AL163227.2	NT	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
7105	16982	27174	5.41	1.0E-29	AW983880.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
5966	15871	25995	3.04	9.0E-30	AA761215.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
9132	18889		1.5	9.0E-30	11422745	NT	nz20c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1
5815	15721		8.81	8.0E-30	F08688.1	EST_HUMAN	MER4 repetitive element;
5812	16691	26880	3.37	8.0E-30	AA383873.1	EST_HUMAN	Homo sapiens zinc/iron regulated transporter-like (ZIRT), mRNA
7039	18916	27105	3.53	8.0E-30	A1557072.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
							EST197317 Thymus I Homo sapiens cDNA 5' end similar to EST containing O family repeat
							PT2.1_f3_B11.r tumor2 Homo sapiens cDNA 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1499	11403		1.16	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1549	11454		0.95	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
1736	11637	21505	1.26	6.0E-30	D26303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3153	13078	22878	2.41	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
9915	11454		3.15	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3931	13840	23620	31.23	5.0E-30	A1989992.1	EST_HUMAN	tg92g03.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;
5205	19522		7.35	5.0E-30	U87931.1	NT	Human aconitate hydratase (ACO2) gene, exon 7
8261	18141		3.55	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
8495	18388	28632	6.88	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8495	18388	28633	6.68	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2096	11985	21880	1.64	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
2096	11985	21881	1.64	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
7162	17039	27231	1.49	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA
1134	11048		1.71	3.0E-30	A1338551.1	EST_HUMAN	qq63c05.x1 Soares_talaj_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29 b2 MER29 repetitive element;
3697	13611	23395	0.91	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
8538	18410	28675	2.36	3.0E-30	P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
659	10593	20411	1.18	2.0E-30	AW857315.1	EST_HUMAN	CMO-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA
1068	10984		2.32	2.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
1484	11389	21234	5.91	2.0E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2683	12543	22438	10.97	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2899	12816	22609	6.38	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3721	13633	23419	2.11	2.0E-30	AW206581.1	EST_HUMAN	UHLB11-af0-c-12-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4668	14554	24346	1.72	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4668	14554	24347	1.72	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
6966	16844	27036	3.46	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujiiwara) Homo sapiens cDNA clone GEN-570C01 5'
7019	16896	27085	1.55	2.0E-30	BE570617.1	EST_HUMAN	7e37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR;
7019	16896	27086	1.55	2.0E-30	BE570617.1	EST_HUMAN	7e37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR;
7743	17593	27814	3.3	2.0E-30	AW971588.1	EST_HUMAN	EST338657 IMAGE resequences, MAGL Homo sapiens cDNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7802	17652	27899	4.47	2.0E-30	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
284	10249	20059	10.22	1.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFU1wara) Homo sapiens cDNA clone GEN-570C01 5'
527	10469	20281	1.6	1.0E-30	AW468997.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.3 MER1 MER1 repetitive element ;
699	10632	20457	2.92	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2165	12052	21953	3.24	1.0E-30	AA664377.1	EST_HUMAN	ac77b08.s1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:968599 3'
2413	12290	22187	2.57	1.0E-30	BF347728.1	EST_HUMAN	602022560F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157991 5'
2973	12900	22699	1.03	1.0E-30	5803091	NT	Homo sapiens methionine aminopeptidase; eIF-2-associated p67 (MNPEP), mRNA
3015	12943	22736	0.93	1.0E-30	AA315045.1	EST_HUMAN	EST189668 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
6545	16403	26592	2.32	1.0E-30	BF183230.1	EST_HUMAN	601809932F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
9733	19615		5.1	1.0E-30	H55593.1	EST_HUMAN	CHR220332 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
7013	16830		2.04	9.0E-31	Z38293.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
1060	10977	20820	1.64	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2362	12242		5.14	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
694	10927		1.72	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2833	12500	22392	1.7	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2633	12500	22393	1.7	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
9583	19168	25272	2.56	7.0E-31	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3925	13539		2.79	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6739	16618		3.68	6.0E-31	AF05096.1	NT	Homo sapiens MHC class 1 region
8120	18008	28255	2.11	6.0E-31	AU119105.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
9191	18926	25351	1.88	6.0E-31	AW372868.1	EST_HUMAN	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
9319	19541		1.78	6.0E-31	BE894488.1	EST_HUMAN	601493087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
185	10157	19973	2.85	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
185	10157	19974	2.85	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
6915	16793		1.21	5.0E-31	BF056540.1	EST_HUMAN	7k06f04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT ; contains L1.1 L1 repetitive element ;
581	10519		3.78	4.0E-31	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
							POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAc-T1)
1594	11498	21357	1.04	4.0E-31	Q10473	SWISSPROT	
1775	11674		2.59	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit: Accession No.	Top Hit Database Source	Top Hit Descriptor
2759	12621		1.38	4.0E-31	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
9604	19186		1.52	4.0E-31	11430273	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
9718	19259		1.38	4.0E-31	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
2550	12423	22314	1.42	3.0E-31	6005871	NT	Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA
6341	16204	26366	9.03	3.0E-31	4826853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 ('19KD, ASH1) (NDUFB8) mRNA
6425	16286	26448	1.38	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
6745	16824		1.95	3.0E-31	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7525	17376	27585	2.86	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
8028	17920	28167	2.01	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
8493	18366		6.36	3.0E-31	BF035327.1	EST_HUMAN	601456531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1975	11771	21647	1.83	2.0E-31	AW838171.1	EST_HUMAN	QV2_L70051-260300-111-403 LT0051 Homo sapiens cDNA
2167	12054	21955	1.31	2.0E-31	A1993388.1	EST_HUMAN	tg44405.x1 Sceres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:21111672 3'
2292	12174	22074	2.18	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
2391	12269	22164	4.4	2.0E-31	AA458824.1	EST_HUMAN	aa88f11.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.12 THR repetitive element ;
5502	15421	25483	3.6	2.0E-31	BE350127.1	EST_HUMAN	h019g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
7246	17123		1.8	2.0E-31	AA877764.1	EST_HUMAN	m0604.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7309	17185	27385	3.99	2.0E-31	7661535	NT	Homo sapiens B9 protein (B9), mRNA
7700	17550	27774	1.27	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
7700	17550	27775	1.27	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
7797	17647	27883	2.17	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3683310 5'
7797	17647	27884	2.17	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3683310 5'
9292	18993		2	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
9431	19759		1.81	2.0E-31	A114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
16	10002	19794	8.34	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1640	11544	21403	2	1.0E-31	O95371	SWISSPROT	OLFATORY RECEPTOR 2C1
1640	11544	21404	2	1.0E-31	O95371	SWISSPROT	OLFATORY RECEPTOR 2C1
1640	11544	21405	2	1.0E-31	O95371	SWISSPROT	OLFATORY RECEPTOR 2C1
4535	14428	24209	1.01	1.0E-31	AL134376.1	EST_HUMAN	DKFZp647B235_r1 547 (synonym: hifar1) Homo sapiens cDNA clone DKFZp647B235 5'

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4635	14428	24210	1.01	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547B235 5'
5235	15159	24927	3.15	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-151299-028-a08_1 ST0220 Homo sapiens cDNA
5728	15635	25738	1.87	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite ceb1 repeat region
8288	18167	28411	2.72	1.0E-31	AI086434.1	EST_HUMAN	q121h03.x1 NCL_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16895
2835	12763		0.99	9.0E-32	U05071.1	NT	Q16895 FRAXIN.
6000	15805	26029	2.34	9.0E-32	AV723976.1	EST_HUMAN	Human familial Alzheimer's disease (STM2) gene, complete cds
2032	11923	21815	3.32	8.0E-32	AI055770.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAA01 5'
4754	14639	24426	1.17	7.0E-32	P52591	SWISSPROT	oz15a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675394 3'
9268	18972		2.77	7.0E-32	X17283.1	NT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
2702	12566	22456	0.9	6.0E-32	AI478104.1	EST_HUMAN	Human chromosome 22 immunoglobulin V(K) gene, part with 5' breakpoint between orphon and neighbouring non-amplified region
6359	16222	20779	1.5	6.0E-32	BE888016.1	EST_HUMAN	tm34a10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159894 3' similar to contains MER29.13
1018	10936		29.57	5.0E-32	AF116627.1	NT	MER29 repetitive element;
915	10839		1.74	4.0E-32	AL163246.2	NT	6011511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
6484	16342	26510	2.82	4.0E-32	11432574	NT	Homo sapiens PRO1181 mRNA, complete cds
6484	16342	26511	2.82	4.0E-32	11432574	NT	Homo sapiens chromosome 21 segment HS21C046
448	10392	20213	3.4	3.0E-32	Y17293.1	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
1438	11343	21210	7.67	3.0E-32	AV731500.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7404	17271	27477	6.73	3.0E-32	AV758634.1	EST_HUMAN	Homo sapiens FLI-1 gene, partial
7404	17271	27478	6.73	3.0E-32	AV758634.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK07 5'
8297	18176	28421	8.08	3.0E-32	AA777621.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
9294	18995		3.04	3.0E-32	BE279086.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
9655	15090	24882	2.43	3.0E-32	5174574	NT	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
9655	15090	24883	2.43	3.0E-32	5174574	NT	z195a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.13 THR repetitive element;
9802	19314	24927	4.94	3.0E-32	BE279086.1	EST_HUMAN	601150285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
4783	14667	24454	0.91	2.0E-32	BE296613.1	EST_HUMAN	601150285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
5900	15806	25929	19.01	2.0E-32	Z38133.1	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
5900	15806	25930	19.01	2.0E-32	Z38133.1	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6815	16894	26884	3.41	2.0E-32	AA114294.1	EST_HUMAN	z066c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
6815	16894	26885	3.41	2.0E-32	AA114294.1	EST_HUMAN	z066c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
9908	19385	25175	1.61	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFB/A08 5'
9908	19385	25176	1.61	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFB/A08 5'
3055	12982		1.06	1.0E-32	BE743299.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
6198	15958	26090	7.04	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
6997	16874	27065	5.18	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
3435	13352		4.98	9.0E-33	BE327112.1	EST_HUMAN	hw07d05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 W/W DOMAIN BINDING PROTEIN 11.;
5867	15773		4.19	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
7103	16980	27172	1.99	9.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
8177	18065		5.89	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
54	10041	19850	2.06	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
54	10041	19851	2.06	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2115	12004	21902	2.71	7.0E-33	A1590115.1	EST_HUMAN	to12b09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR repetitive element;
2612	12490		8.4	7.0E-33	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
2800	11573	21439	1.78	7.0E-33	AV730015.1	EST_HUMAN	AV730015 HTF Homo sapiens cDNA clone HTFANF08 5'
3204	13128		12.85	7.0E-33	AW971307.1	EST_HUMAN	EST383396 IMAGE resequences, MAGL Homo sapiens cDNA
8203	18097	28338	3.9	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
8573	18441	28709	2.15	7.0E-33	AW971568.1	EST_HUMAN	EST383657 IMAGE resequences, MAGL Homo sapiens cDNA
9274	18978	25322	3.43	7.0E-33	AA601416.1	EST_HUMAN	nc16h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.t1 L1 repetitive element;
3676	13590		0.85	6.0E-33	AL183285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6988	16865	27059	13.52	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
7049	16926	27117	2.57	6.0E-33	11429198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
7750	17600	27822	1.24	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
7750	17600	27823	1.24	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1739	11640		1.78	5.0E-33	BF373515.1	EST_HUMAN	QV1-FT0169-100700-271-a02 FT0169 Homo sapiens cDNA
1838	11735		1.18	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC6A7), mRNA
1856	11752	21626	1.37	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1856	11752	21627	1.37	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2226	12111		1.3	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
9082	18558		1.62	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1112	11027		3.28	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2078	11968	21861	1.77	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2370	12250		7.39	4.0E-33	AA628621.1	EST_HUMAN	ab51b11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element;
2498	12373	22265	3.77	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4382	14278	24057	1.63	4.0E-33	AW293349.1	EST_HUMAN	U1-HB12-ant-c-03-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5318	15239	25043	20.94	4.0E-33	AA053053.1	EST_HUMAN	z17a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
9007	18810	29102	1.72	4.0E-33	11425635	NT	Homo sapiens killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 (KIR3DL1), mRNA
1073	10989		4.46	3.0E-33	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
1074	10989		3.4	3.0E-33	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
2400	12721		1.48	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLCBFC09 3'
99	10003		2.33	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element;
4322	14219		4.27	2.0E-33	BE159039.1	EST_HUMAN	MRO-HT0405-160300-202-d08 HIT0405 Homo sapiens cDNA
4911	14790	24565	5.1	2.0E-33	AA628683.1	EST_HUMAN	ab51g11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5026	14899	24668	1.73	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5026	14899	24669	1.73	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5869	15775	25894	1.61	2.0E-33	AI277492.1	EST_HUMAN	ql6ed01.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
7261	17138		1.8	2.0E-33	AI052256.1	EST_HUMAN	oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gb:M29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
8	9994		1.44	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
8637	18502	28778	2.02	1.0E-33	AW199818.1	EST_HUMAN	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA
8921	18729	29024	5.33	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
9553	19151		1.92	1.0E-33	AI927191.1	EST_HUMAN	w088c06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462410 3'

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9723	9994		3.04	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
9754	19278	25229	1.34	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCNC12 5'
9927	19399		2.09	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1427	11332	21198	1.98	7.0E-34	T70845.1	EST_HUMAN	ydf15c05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
9340	19020		3.08	7.0E-34	H12866.1	EST_HUMAN	yj14c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
463	10406	20225	1.46	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
463	10406	20226	1.46	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
9153	18903	26340	1.44	6.0E-34	U03886.1	NT	Mus musculus DAB/2J hair-specific (hacl-1) gene
1837	11734		2.23	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
4993	14999	24631	4	5.0E-34	U30983.1	NT	Human splicing factor SRp55-1 (SRp-55) mRNA, complete cds
7144	17021	27215	1.18	5.0E-34	AJ078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8046	17937	28186	2.12	5.0E-34	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
8578	18446		2.01	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1953	11848	21795	2.11	4.0E-34	A1804667.1	EST_HUMAN	tt94c06.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2249194 3'
2687	12552	22441	0.98	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10989 (FLJ10989), mRNA
8492	18365		4.81	3.0E-34	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1488	11393	21254	8.56	1.0E-34	P12236	SWISSPROT	ADP.ATP CARRIER PROTEIN. LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3621	13635	23320	1.46	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3979	13886	23661	0.78	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
3979	13886	23662	0.78	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4381	14277		4.02	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-h08 BT0506 Homo sapiens cDNA
4920	14799		0.86	1.0E-34	AW845706.1	EST_HUMAN	MRO-CT0068-280999-002-d11 CT0068 Homo sapiens cDNA
5731	15639	25743	1.99	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
5731	15639	25744	1.99	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
7155	17032	27226	3.87	1.0E-34	AW368451.1	EST_HUMAN	CM4-HT0193-061099-022-g06 HT0193 Homo sapiens cDNA
7591	17442	27658	8.89	1.0E-34	AL036395.1	EST_HUMAN	DKFZp564A1563_r1 564 (synonym: hfb2) Homo sapiens cDNA clone DKFZp564A1563 5'
9746	19307		2.92	1.0E-34	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3594	13508	23296	1.26	9.0E-35	AW663302.1	EST_HUMAN	hh77b06.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
219	10189		24.25	8.0E-35	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
1703	11604	21475	3.3	8.0E-35	BF599937.1	EST_HUMAN	ne633a08.x1 NCL_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912 O75912 DIACYLGLYCEROL KINASE IOTA.;

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1703	11604	21476	3.3	8.0E-35	BF599937.1	EST_HUMAN	naa33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4761	14646	24435	3.09	8.0E-35	BF183195.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA.;
8075	17966	28217	3	8.0E-35	BE378480.1	EST_HUMAN	601809598F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
9265	18969		3.49	8.0E-35	BF569282.1	EST_HUMAN	601236468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
5905	15811	25937	1.52	7.0E-35	11425417	NT	602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300660 3'
1391	11296	21154	1.28	6.0E-35	AA757115.1	EST_HUMAN	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
1925	11820	21699	1.78	6.0E-35	6005975	NT	ah53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'
6610	16490	26676	3.6	6.0E-35	6005921	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
7698	17548	21771	2.7	6.0E-35	AB037786.1	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
1681	11583	21454	2.29	5.0E-35	X63392.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
							H.sapiens immunoglobulin kappa light chain variable region L14
4311	14208	23992	2.2	5.0E-35	AF023268.1	NT	Homo sapiens cdk2 kinase (CLK2), propin1, coter1, glucocerebrosidase (GBA), and melanin genes, complete cds; melanin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
6761	16840		3.14	5.0E-35	BE890992.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
6779	16658	26848	2.18	5.0E-35	A1208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249 HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.;
6779	16658	26849	2.18	5.0E-35	A1208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249 HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.;
8517	18389		3.42	5.0E-35	AA001786.1	EST_HUMAN	zh8412.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1415	11321	21186	14.91	4.0E-35	BE257907.1	EST_HUMAN	601103719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
							y198a07.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element.;
1776	11675	21552	5.1	4.0E-35	H91193.1	EST_HUMAN	601300705F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5'
5042	14914		1.29	4.0E-35	BE409102.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29 t3
6280	16144		1.82	4.0E-35	BE350127.1	EST_HUMAN	MER29 repetitive element.;
6957	16835	27030	6.84	4.0E-35	AL046596.1	EST_HUMAN	DKFZp434L148_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'
1561	11466	21324	9.63	3.0E-35	BE268182.1	EST_HUMAN	601125280F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2283	12167		2.42	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
4793	14678	24465	1.06	3.0E-35	BF376402.1	EST_HUMAN	MR1-TN0045-130900-010-e01 TN0045 Homo sapiens cDNA
5275	15197	24971	22.73	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
							Q9QZH7 F-BOX PROTEIN FBL2.;
5275	15197	24972	22.73	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
							Q9QZH7 F-BOX PROTEIN FBL2.;

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7465	17325		1.81	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
103	12659	19902	1.74	2.0E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
1171	11063	20928	1.25	2.0E-35	T11909.1	EST_HUMAN	REPETITIVE ELEMENT
2171	12058	21961	5.2	2.0E-35	AB018413.1	NT	A971F Heart Homo sapiens cDNA clone A971
3272	13193	22991	0.97	2.0E-35	6912459	NT	Homo sapiens mRNA for Gab2, complete cds
3272	13193	22992	0.97	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3511	13427		0.88	2.0E-35	AB020702.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
							Homo sapiens mRNA for KIAA0895 protein, partial cds
3635	13747	23539	1.09	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3635	13747	23540	1.09	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4570	14462		2.55	2.0E-35	H49239.1	EST_HUMAN	Yq19a12.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:274079 5'
5426	15347	25401	1.66	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-199-b04 BT0701 Homo sapiens cDNA
8175	18063	26312	3.72	2.0E-35	X59417.1	NT	H. sapiens PROS-27 mRNA
9028	13193	22991	1.36	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
9028	13193	22992	1.36	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
9205	18936	25354	1.51	2.0E-35	BE904978.1	EST_HUMAN	G01496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
9205	18936	25355	1.51	2.0E-35	BE904978.1	EST_HUMAN	G01496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
9725	19264		3.97	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
							K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
9832	12659	19902	4.17	2.0E-35	N88965.1	EST_HUMAN	REPETITIVE ELEMENT
40	10028	19828	4.38	1.0E-35	AA631949.1	EST_HUMAN	frnfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
40	10028	19829	4.38	1.0E-35	AA631949.1	EST_HUMAN	frnfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
735	10667	20500	44.43	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
735	10667	20501	44.43	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
							Yd83a01.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:115752 5' similar to
891	10817		1.16	1.0E-35	T87947.1	EST_HUMAN	SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
2495	12369	22262	2.31	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
							h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
2740	12602	22496	1.11	1.0E-35	BE350127.1	EST_HUMAN	MER29 repetitive element ;
							h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
2740	12602	22497	1.11	1.0E-35	BE350127.1	EST_HUMAN	MER29 repetitive element ;

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3104	13030	22826	1.07	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA
3126	13051	22848	2.2	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCOEF06 3'
3126	13051	22849	2.2	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCOEF06 3'
4325	14222	24003	4.7	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4325	14222	24004	4.7	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
5382	15301	25154	1.43	1.0E-35	11526236	NT	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7501	19489	27578	2	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
7501	19489	27579	2	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
8977	18782		4.16	1.0E-35	AI525119.1	EST_HUMAN	promrna-7.D01.r bvtumor Homo sapiens cDNA 5'
9186	12369	22262	1.69	1.0E-35	7705984	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
9267	18971		1.37	1.0E-35	11418110	NT	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
9620	19198		2.26	1.0E-35	BE792832.1	EST_HUMAN	601584833F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3938985 5'
2900	12827	22622	0.94	7.0E-36	AW657579.1	EST_HUMAN	GM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
3080	13007		4.03	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
6512	16371	26548	6.04	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
6512	16371	26549	6.04	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
9423	19071	25279	5.23	7.0E-36	AF052051.1	NT	Homo sapiens glutathione transferase A4 gene, exon 1
1959	11854	21741	1.88	6.0E-36		NT	Homo sapiens ninjurin 2 (NINJ2), mRNA
2367	12247		6.17	6.0E-36	AB035346.1	NT	Homo sapiens TCL6 gene, exon 12
3587	13501	23290	0.91	6.0E-36	BF515101.1	EST_HUMAN	UI-H-BW1-anv-c-12-d-UI.st NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5268	15190	24965	19.79	6.0E-36	AI435169.1	EST_HUMAN	tf93b06.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
6221	16087	26237	3.34	6.0E-36	AW780143.1	EST_HUMAN	h006h02.x1 NCI CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN
7027	16904	27096	2.21	6.0E-36	AF208161.1	NT	P52282 IMPORTIN ALPHA-2 SUBUNIT ;
						NT	Homo sapiens syncytin precursor, mRNA, complete cds
8833	18646	28931	2.74	6.0E-36	AB30499.1	EST_HUMAN	tf95c09.x1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2
9821	19580	25071	1.69	6.0E-36	BE737154.1	EST_HUMAN	MER9 repetitive element ;
133	10107	19928	6.89	5.0E-36	AJ271735.1	NT	601305084F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3639782 5'
2722	12584	22478	7.71	5.0E-36	BE389436.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
3581	13475	23264	1.96	5.0E-36	AL163209.2	NT	601285567F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3607289 5'
4678	14564	24358	1.42	5.0E-36		NT	Homo sapiens chromosome 21 segment HS21C009
4678	14564	24359	1.42	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
9026	10107	19928	2.64	5.0E-36	AJ271735.1	NT	Homo sapiens API5-like 1 (API5L1), mRNA
						NT	Homo sapiens Xq pseudautosomal region; segment 1/2

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9318	19010	25337	2.36	5.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1205	11115	20961	1.43	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1424	11329	21196	1.54	4.0E-36	P10286	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
1626	11530	21389	1.58	4.0E-36	BE382574.1	EST_HUMAN	ENDONUCLEASE]
2175	12062		1.63	4.0E-36	AW247772.1	EST_HUMAN	601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
3310	13231	23036	3.21	4.0E-36	BE389299.1	EST_HUMAN	2820020:Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3310	13231	23037	3.21	4.0E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5693	15602	25704	2.21	4.0E-36	11497041	NT	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
6511	16370	26547	1.74	4.0E-36	M33320.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
6979	16856	27050	1.41	4.0E-36	D87675.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
6979	16856	27051	1.41	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8356	18233	28481	2.19	4.0E-36	AA400370.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
9334	19015		1.31	4.0E-36	11420516	NT	zu69c10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
9380	19545		2.85	4.0E-36	AV753629.1	EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
681	10614	20437	2.73	3.0E-36	AF099810.1	NT	AV753629 TP Homo sapiens cDNA clone TP.GABH01 5'
2252	12136	22033	0.89	3.0E-36	7662401	NT	Homo sapiens neuroligin III-alpha gene, partial cds
4402	14297	24081	5.15	3.0E-36	10181139	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
8452	18325	28584	1.78	3.0E-36	BF035327.1	EST_HUMAN	Mus musculus junctophilin 1 (Jp1-pending), mRNA
3132	13057	22857	2.7	2.0E-36	BE259267.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
4877	14757	24534	4.62	2.0E-36	AW880376.1	EST_HUMAN	601106943F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
5371	15291	25127	2.16	2.0E-36	AF267747.1	NT	QV0-O T0030-240300-174-r04 O T0030 Homo sapiens cDNA
5587	15483	25556	3.99	2.0E-36	T08756.1	EST_HUMAN	Mus musculus p47-phox gene, complete cds
5962	15867	25989	11.82	2.0E-36	T69629.1	EST_HUMAN	EST08648 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBJ28 5' and
867	10793	20643	1.9	1.0E-36	BE409310.1	EST_HUMAN	yc44a07.r1 Stralagene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
2098	11987	21884	0.86	1.0E-36	BE148523.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2098	11987	21885	0.86	1.0E-36	BE148523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2155	12043	21942	1.31	1.0E-36	BF673761.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
5752	15660		5.94	1.0E-36	AI867714.1	EST_HUMAN	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
6640	16520	26711	2.03	1.0E-36	AA148034.1	EST_HUMAN	wb37c12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu
6640	16520	26712	2.03	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stralagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
7220	17097	27287	2.84	1.0E-36	AW103658.1	EST_HUMAN	zo51a12.r1 Stralagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
7824	17674	27917	4.06	1.0E-36	BF364169.1	EST_HUMAN	xe82b07.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614957 3'
							QV3-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8317	18194	28444	3.43	1.0E-36	AW897636.1	EST_HUMAN	CM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
8686	18574	28857	3.91	1.0E-36	AW504143.1	EST_HUMAN	UI-HF-BNO-ale-c-03-0-UI_r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
9203	18934		3.74	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9374	19040	25305	1.29	1.0E-36	11418121	NT	Homo sapiens chromosome 22 open reading frame 2 (C22ORF2), mRNA
9647	19214		3.07	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
9890	19371		2.89	1.0E-36	AF202723.1	NT	Homo sapiens Sac1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6368	16231	26390	1.96	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
6368	16231	26391	1.96	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
9462	19093		2.79	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
5143	15010	24781	1.38	8.0E-37	AB020684.1	NT	Homo sapiens mRNA for KIAA0877 protein, partial cds
5213	15136		1.7	8.0E-37	BE698077.1	EST_HUMAN	CM0-UT0003-050800-503-c09 UT0003 Homo sapiens cDNA
5559	15475	25547	4.1	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5559	15475	25548	4.1	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5584	15499	25576	5.63	8.0E-37	AW840840.1	EST_HUMAN	MER29 repetitive element ;
6602	16482	26670	6.25	8.0E-37	X87344.1	NT	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
1263	11170		2.51	7.0E-37	AL042800.1	EST_HUMAN	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING6, 9, 13 and 14 genes
8140	18028	28274	6.77	7.0E-37	AB177700.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: htes3) Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.2
8268	18148	28388	4.16	7.0E-37	AF36702.1	EST_HUMAN	wk25b11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.2
9775	19292		2.48	6.0E-37	AF202723.1	NT	PTR5 repetitive element ;
5707	15615	25716	3.37	5.0E-37	AA307123.1	EST_HUMAN	h087g03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1
5707	15615	25717	3.37	5.0E-37	AA307123.1	EST_HUMAN	repetitive element ;
8292	18171		4.17	5.0E-37	7657117	NT	Homo sapiens Sac1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
9198	18931		3.57	5.0E-37	AF149773.1	NT	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2374	12254	22145	2.23	4.0E-37	AA702794.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
5150	15027		1.11	4.0E-37	AF202723.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
1970	11863	21755	2.85	3.0E-37	AL048986.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
1970	11863	21756	2.85	3.0E-37	AL048986.1	EST_HUMAN	z09b04.s1 Soares_fetal_liver_spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
2465	12341		1.7	3.0E-37	AW961150.1	EST_HUMAN	EST52g10 WATM1 Homo sapiens cDNA clone 52g10 similar to human S1S G04101
2936	12863		3.02	3.0E-37	AW961150.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
							DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
							EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
							EST373222 IMAGE resequences, MAGF Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1064	10980	20824	1.94	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1064	10980	20825	1.94	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1921	11816	21695	1.47	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3818	13730	23519	5.05	2.0E-37		NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
6007	15912	26039	3.36	2.0E-37	AA346720.1	EST_HUMAN	EST52931 Fetal heart II Homo sapiens cDNA 5' end
6685	16665	26759	3.23	2.0E-37	BF204032.1	EST_HUMAN	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'
8845	18657	28945	16.4	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
9933	19403		3.15	2.0E-37	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
2041	11932	21828	3.61	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3878	13769	23577	22.51	1.0E-37	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4072	13974	23763	0.96	1.0E-37	BE872365.1	EST_HUMAN	601448619F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3852652 5'
4857	14737	24517	2.13	1.0E-37	BF371719.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
7072	16949	27141	2.85	1.0E-37	AA171406.1	EST_HUMAN	zp21b02.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1, L2 L1 repetitive element;
8082	17973	28222	20.59	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
9508	19122		2.46	1.0E-37	BE771814.1	EST_HUMAN	CM3-FT0096-140700-243-d07 FT0096 Homo sapiens cDNA
5530	15447	25514	3.05	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA
1203	11113	20959	1.95	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2449	12326	22225	1.44	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153992 5'
9568	11113	20959	1.36	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2135	12023	21920	1.38	7.0E-38	AW972625.1	EST_HUMAN	EST384920 IMAGE resequences, MAGI Homo sapiens cDNA
3005	12933	22726	1.76	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:38559348 5'
5432	15352	25407	1.69	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5432	15352	25408	1.69	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
9060	18842		4.46	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
9542	19143	25266	6.66	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
710	10642	20468	1.15	5.0E-38	AW971819.1	EST_HUMAN	EST383908 IMAGE resequences, MAGI Homo sapiens cDNA
2404	12281	22178	1.79	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIIR gene (partial), exon 8
6191	16076	26225	2.42	5.0E-38	BE871610.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5'
113	10062	19909	2.56	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
113	10062	19910	2.56	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete ODS
1141	11055	20897	0.82	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2053	11943		4.39	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3638	13552		1.11	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnaj-like) (HIRIP4), mRNA
3781	13693	23480	1.65	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3781	13693	23481	1.65	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4513	14406		0.85	3.0E-38	BE279301.1	EST_HUMAN	601157633F1 NIH_MGC. 21 Homo sapiens cDNA clone IMAGE:3504272 5'
6050	19459	26083	7.17	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
6478	16337	26504	7.64	3.0E-38	BF373684.1	EST_HUMAN	CM3-FT0181-140700-241-f07 FT0181 Homo sapiens cDNA
7025	16902	27094	1.78	3.0E-38	H85494.1	EST_HUMAN	yw88b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'
7025	16902	27095	1.78	3.0E-38	H85494.1	EST_HUMAN	yw88b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'
7727	17577		1.58	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
44	10032	19835	1.41	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1358	11264	21120	2.6	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1627	11531	21390	1.66	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1627	11531	21391	1.66	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
6941	16819		4.7	2.0E-38	BE165990.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
7316	17192		1.47	2.0E-38	BE222256.1	EST_HUMAN	hu09g02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:O02710 O02710 GAG POLYPEPTIDE ;
7970	17820	28063	1.66	2.0E-38	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
8781	18596	28885	5.24	2.0E-38	BE172790.1	EST_HUMAN	QV2-HT0698-080800-293-a05 HT0698 Homo sapiens cDNA
8907	18715	29008	3.59	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
8907	18715	29009	3.59	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
9112	18876		4.05	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCAXH07 5'
9115	18878		2	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
9412	19064	25313	3.86	2.0E-38	H55641.1	EST_HUMAN	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
9472	19099		2.26	2.0E-38	S74906.1	NT	E1 beta-pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
9924	19396		2.56	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1077	10993		2.29	1.0E-38	AA401570.1	EST_HUMAN	zu62b02.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element MER19 repetitive element ;
1954	11849	21736	0.94	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
1973	11866	21758	1	1.0E-38	7681969	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2445	12322	22221	1.58	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4063	13665	23743	1.41	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4223	14121	23896	0.83	1.0E-38	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4229	14127	23902	1.31	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4229	14127	23903	1.31	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4493	14387	24173	1.21	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
5673	15582	25682	3.61	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
5673	15582	25683	3.61	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
6378	16240	26400	2.78	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
7414	17281	27489	6.23	1.0E-38	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
9264	19481		2.33	1.0E-38	AL163284.2	NT	MER29 repetitive element;
48	10036	19842	5.14	8.0E-39	4502312	NT	Homo sapiens chromosome 21 segment HS21C084
1372	11278	21134	1.51	8.0E-39	4758229	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1788	11686		1.06	8.0E-39	AB23404.1	EST_HUMAN	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
2047	11938	21832	5.54	7.0E-39	AL163227.2	NT	wh58f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
8184	18070	28319	2.12	6.0E-39	BF331829.1	EST_HUMAN	POL PROTEIN ;
9838	19337		2.23	6.0E-39	BE670394.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
991	10912	20757	1.3	5.0E-39	AF003528.1	NT	QV1-BT0631-040900-357-402 BT0631 Homo sapiens cDNA
							7e34c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP-R151.6
							OE00828 ;
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2957	12884	22682	5.13	5.0E-39	AI750154.1	EST_HUMAN	at36b04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
9556	19154		1.54	5.0E-39	11420289	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.1 LTR7 repetitive element ;
538	10479	20291	10.53	4.0E-39	AB015610.1	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA
3525	13441	23238	0.96	4.0E-39	AL163210.2	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
							Homo sapiens chromosome 21 segment HS21C010
6707	16587	26775	1.49	4.0E-39	AA682949.1	EST_HUMAN	ae29g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
9575	19164		3.08	4.0E-39	11418177	NT	OFB.b1 OFR repetitive element ;
9657	19240		2.03	4.0E-39	BE836462.1	EST_HUMAN	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
41	10029	19830	11.27	3.0E-39	AA631949.1	EST_HUMAN	QV0-FN0063-260600-278-c08 FN0063 Homo sapiens cDNA
41	10029	19831	11.27	3.0E-39	AA631949.1	EST_HUMAN	fmfr16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
							fmfr16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
41	10029	19832	11.27	3.0E-39	AA631949.1	EST_HUMAN	fmf16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
9104	18871	28781	5.51	3.0E-39	AID84557.1	EST_HUMAN	ox63a10.s1 Soares_NIHMPfu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;
9104	18871	28782	5.51	3.0E-39	AID84557.1	EST_HUMAN	ox63a10.s1 Soares_NIHMPfu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
9147	18900		4.42	3.0E-39	H37903.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;
879	10805		4.03	2.0E-39	BE409203.1	EST_HUMAN	yp51c06.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190954 3'
894	10820		17.44	2.0E-39	AI625119.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
1075	10933		3.61	2.0E-39	AF000573.1	NT	promna-7 D01 r bflumor Homo sapiens cDNA 5'
1513	11418		10.15	2.0E-39	AW372318.1	EST_HUMAN	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
						EST_HUMAN	PMo-BT0340-211299-003-d02 BT0340 Homo sapiens cDNA
1930	11825	21707	10.03	2.0E-39	AA720574.1	EST_HUMAN	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241139 3' similar to contains THR.13 THR repetitive element;
2587	12438	22349	1.75	2.0E-39	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4303	14201	23985	1.36	2.0E-39	BE370207.1	EST_HUMAN	RC4-FN0037-290700-011-e10 FN0037 Homo sapiens cDNA
5375	15295	25142	3.4	2.0E-39	AA508880.1	EST_HUMAN	ng86f03.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:941693
6360	16223	26384	2.17	2.0E-39	AA080867.1	EST_HUMAN	zn06f02.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'
8731	18587	28874	2.33	2.0E-39	D86964.1	NT	Human mRNA for KIAA0209 gene, partial cds
9922	19394		2.31	2.0E-39	11425464	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
1497	11401	21261	1.78	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQ11 gene
1497	11401	21262	1.78	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQ11 gene
1514	11419	21275	4.95	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4561	14453	24239	5.49	1.0E-39	AW951995.1	EST_HUMAN	EST T364065 IMAGE resequences, MAGB Homo sapiens cDNA
4561	14453	24240	5.49	1.0E-39	AW951995.1	EST_HUMAN	EST T364065 IMAGE resequences, MAGB Homo sapiens cDNA
4604	14492	24279	8.58	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
						EST_HUMAN	yd26g06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains Alu repetitive element;contains LTR1 repetitive element;
5459	15379	25439	1.54	1.0E-39	T80876.1	EST_HUMAN	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5475	15395	25460	4.36	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5475	15395	25461	4.36	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
6083	16028		1.66	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6357	16220	26382	1.75	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
543	10484	20294	1.67	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1215	11123	20671	10.19	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1215	11123	20672	10.19	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1433	11338	21205	5.04	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3892	15069	23586	3.58	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4250	14149	23923	0.82	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
4398	14149	23923	1.12	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3004	12932	22725	0.95	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
3847	13758		2.41	8.0E-40	BE366541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'
6541	16399	26578	1.56	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
6541	16399	26579	1.56	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
8270	18150	28391	2.83	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2696	12560	22449	3.88	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2696	12560	22450	3.88	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
5616	15531		2.07	6.0E-40	BE504766.1	EST_HUMAN	hz40g01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3210480 3'
6141	15989	26124	3.08	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
6141	15989	26125	3.08	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7731	17581	27804	6.82	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLC0GF04 3'
7731	17581	27805	6.82	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLC0GF04 3'
2561	12433	22326	1.89	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1834	11731	21607	1.38	4.0E-40	AI686005.1	EST_HUMAN	tt91b01.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN.;
2061	11951		2.67	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4291	14189	23973	7.85	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
6662	16542	26738	3.76	4.0E-40	AA742809.1	EST_HUMAN	nv34e10.r1 NCI_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
7237	17114	27308	4.87	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
7237	17114	27309	4.87	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
8099	17989	28238	4.07	4.0E-40	AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-c04 CN0017 Homo sapiens cDNA
4040	13943	23721	0.98	3.0E-40	AI925949.1	EST_HUMAN	wh1207.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
8001	15906	28030	6.25	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6882	16761	26959	4.28	3.0E-40	5454187	NT	Homo sapiens HBV associated factor (XAP4) mRNA
7186	17063	27253	1.49	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
7312	17188	27389	1.52	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8387	18294	28515	1.93	3.0E-40	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
8588	18456	28725	11.23	3.0E-40	6005813	NT	MER29 repetitive element ; Homo sapiens serine threonine protein kinase (NDR), mRNA
8855	18667	28954	1.96	3.0E-40	AW118799.1	EST_HUMAN	xd96h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TR:Q15804
322	10283		12.09	2.0E-40	AL223036.1	EST_HUMAN	Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERVS ; qg52h03.x1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
777	10707		2.72	2.0E-40	AW303868.1	EST_HUMAN	xr24e10.x1 NCL_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2781098 3' similar to SW:RS5_MOUSE
1783	11681		1.4	2.0E-40	AV731601.1	EST_HUMAN	P97451 40S RIBOSOMAL PROTEIN S5 ; AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1892	11787	21664	2.19	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1892	11787	21665	2.19	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2026	11917	21807	1.08	2.0E-40	AI668562.1	EST_HUMAN	wf90a11.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929
2123	12011	21910	2.61	2.0E-40	5453502	NT	ZINC FINGER PROTEIN ; Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
2333	12214	22112	2.35	2.0E-40	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
2688	12525		1.08	2.0E-40	BE275932.1	EST_HUMAN	601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
3087	13014	22806	3.59	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
4807	14691	24478	1.49	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4807	14691	24479	1.49	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
865	10791		1.65	1.0E-40	AA225989.1	EST_HUMAN	nc09a09.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2580	12451	22343	1.91	1.0E-40	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
2653	12520		1.92	1.0E-40	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
2707	12570	22460	0.92	1.0E-40	BF541030.1	EST_HUMAN	SYNTAXIN 17 ; 602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
2707	12570	22461	0.92	1.0E-40	BF541030.1	EST_HUMAN	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
3258	13181		1.81	1.0E-40	4507142	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
4505	14398	24184	6.28	1.0E-40	4508012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
4892	14772	24550	0.88	1.0E-40	7705778	NT	Homo sapiens CGI-65 protein (LOC51103), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6215	16081	26230	2.03	1.0E-40	AA573201.1	EST_HUMAN	nj42f04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
6215	16081	26231	2.03	1.0E-40	AA573201.1	EST_HUMAN	nj42f04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
8289	18168	28412	5.72	1.0E-40	AU149345.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
8355	18232	28480	53.3	1.0E-40	AI239572.1	EST_HUMAN	qh31h10.x1 Soares_NFL_T_GEC_S1 Homo sapiens cDNA clone IMAGE:1846339 3'
9521	19622		3.93	1.0E-40	BF334112.1	EST_HUMAN	MR2-CT0222-211099-002-e10 CT0222 Homo sapiens cDNA
6621	16501	26689	1.73	8.0E-41	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
811	12678	20585	2.36	7.0E-41	AI934364.1	EST_HUMAN	wp04h04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
811	12678	20586	2.36	7.0E-41	AI934364.1	EST_HUMAN	wp04h04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5655	15567	25663	3.27	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
9931	19618		4.82	7.0E-41	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
279	10244	20064	1.72	6.0E-41	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
2094	11954	21851	2.19	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
4394	14260	24044	0.94	6.0E-41	BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
1761	11660	21532	1.31	5.0E-41	T62628.1	EST_HUMAN	yc03e10.s1 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:79626 3'
4018	13922		0.98	5.0E-41	4885636	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
5945	15850		2.55	5.0E-41	BE067042.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
395	10332		1.91	4.0E-41	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1082	10998	20839	1.28	4.0E-41	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1388	11283	21149	9.42	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE.; contains LTR5.b1 LTR5 repetitive element;
1388	11283	21150	9.42	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE.; contains LTR5.b1 LTR5 repetitive element;
1404	11309	21170	2.12	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1618	11522	21380	8.5	4.0E-41	AI500406.1	EST_HUMAN	tm96c04.x1 NCL_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element;
2859	12787	22578	3.03	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2859	12787	22579	3.03	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4032	13954	23730	1.89	4.0E-41	X92685.1	NT	H. sapiens DNase I hypersensitive site (HSS-3) enhancer element
5920	15825		1.39	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC06 5'
7590	17441	27657	6.01	4.0E-41	BF304683.1	EST_HUMAN	601880908F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
8925	18733		7.62	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CuAACCC07 5'
9699	19510		2.31	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
932	10857	20704	1.64	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4240	14139	23914	3.08	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5047	14919		0.85	3.0E-41	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
5376	15296	25143	7.36	3.0E-41	X87689.1	NT	H. sapiens mRNA for putative p64 CLCP protein
5949	15755	25873	1.49	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
1782	11445	21305	7.3	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1915	11810	21688	2.3	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end
2172	12059	21962	1.03	2.0E-41	D96962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2221	12106	22010	4.07	2.0E-41	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2798	11445	21305	5.31	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
4521	14414	24199	1.06	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4521	14414	24200	1.06	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
6522	16381	26559	6.59	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
6702	16582	26772	1.33	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
6702	16582	26773	1.33	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
6716	16596	26786	1.39	2.0E-41	AA328265.1	EST_HUMAN	EST31723 Embryo, 12 week I Homo sapiens cDNA 5' end
7188	17065	27255	1.7	2.0E-41	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
8777	18594	28882	3.46	2.0E-41	AA372637.1	EST_HUMAN	EST84565 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
4465	14359	24149	4.64	1.0E-41	6678468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
7420	17287	27494	1.8	1.0E-41	AI217698.1	EST_HUMAN	q775c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'
9197	18930		2.63	1.0E-41	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
6958	16836		1.33	9.0E-42	BE179191.1	EST_HUMAN	RC0-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA
7292	17168	27367	2.63	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
7292	17168	27368	2.63	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
455	10399	20216	5.37	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2062	11952	21849	1.32	8.0E-42	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9238	19625		32.6	8.0E-42	AA493896.1	EST_HUMAN	rh07d02.s1 NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304
916	10840		1.83	7.0E-42	AL163285.2	NT	367BP EXPRESSED SEQUENCE TAG mRNA :
1812	11709	21586	3.25	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
1812	11709	21587	3.25	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2244	12128		3.51	6.0E-42	AW238656.1	EST_HUMAN	xp29108.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.11 L1 repetitive element;
4936	14814		1.04	6.0E-42	AI294770.1	EST_HUMAN	qu24h09.x1 NCI_CGAP_Br12 Homo sapiens cDNA clone IMAGE:1965761 similar to contains Alu repetitive element;
5355	15275	25105	1.81	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5504	15275	25105	1.72	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
131	10105		5.44	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
431	10376	20197	1.17	5.0E-42	BE217913.1	EST_HUMAN	h31e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
478	10422		2.94	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
479	10423		1.27	5.0E-42	5730038	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6016	15920	26050	1.76	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6016	15920	26051	1.76	5.0E-42	11433063	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
6072	16055	26203	2.75	5.0E-42	11417957	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
6274	16138	26294	1.57	5.0E-42	AF071569.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
7098	16975	27168	2.76	5.0E-42	AB037715.1	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
8366	18243	28494	2.15	5.0E-42	8923162	NT	Homo sapiens MHC class 1 region
736	10668	20502	8.89	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
736	10668	20503	8.89	4.0E-42	AF055066.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
1050	10967	20809	2.67	4.0E-42	AF189011.1	NT	H. sapiens PROS-27 mRNA
4100	14000	23779	1.61	4.0E-42	X99417.1	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4156	14056	23830	4.52	4.0E-42	4506496	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
4480	14374	24162	10.26	4.0E-42	4508008	NT	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
8041	17932	28179	2.07	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
8041	17932	28180	2.07	4.0E-42	AW818630.1	EST_HUMAN	60145853.1F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
8714	18531	28815	3.22	4.0E-42	BF035327.1	EST_HUMAN	ab14e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR.12 THR repetitive element;
98	10084		0.78	3.0E-42	AA486105.1	EST_HUMAN	RCO-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
1467	11372	21239	3.63	2.0E-42	BF376834.1	EST_HUMAN	RC3-NN0070-270400-011-h10 TN0070 Homo sapiens cDNA
2361	12241		3.86	2.0E-42	AW898344.1	EST_HUMAN	2819293.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'
2375	12255	22146	2.15	2.0E-42	AW250059.1	EST_HUMAN	EST367438 MAGE resequences, MAGC Homo sapiens cDNA
5519	15437	25500	10.2	2.0E-42	AW955388.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripter
5519	15437	25501	10.2	2.0E-42	AW955368.1	EST_HUMAN	EST1367438 MAGE resequences, MAGC Homo sapiens cDNA
7663	17513	27739	1.27	2.0E-42	BE538919.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
717	10648	20478	1.06	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1026	10944	20789	0.96	1.0E-42	AW295809.1	EST_HUMAN	U1-HB11-afn-e-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1085	11001	20842	1.11	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1085	11001	20843	1.11	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1222	12688	20983	12.78	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1222	12688	20984	12.78	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1673	11575	21443	1.46	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
1986	11879	21772	0.91	1.0E-42	AF110296.1	NT	Homo sapiens PDNP1 gene, exon 17
2497	12372	22264	1.98	1.0E-42	5174456	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2935	12862	22662	8.93	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3647	13561	23347	2.15	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3849	13780	23553	1.02	1.0E-42	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4153	14053	23827	1.72	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4489	14383	24170	0.86	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161099-012-a03 ST0197 Homo sapiens cDNA
4640	14528	24316	2.85	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4640	14528	24317	2.85	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4669	14555	24348	5.35	1.0E-42	4506756	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4769	14654	24442	1.2	1.0E-42	AB033114.1	NT	Homo sapiens mRNA for KIAA1288 protein, partial cds
5048	14920	24693	0.98	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
5048	14920	24694	0.98	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
7805	17655	27893	3.89	9.0E-43	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
8397	18273	28525	2.84	9.0E-43	AA435719.1	EST_HUMAN	z79a07 s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728532 3'
636	10573	20386	12.13	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
636	10573	20387	12.13	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
685	10618	20441	4.33	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
685	10618	20442	4.33	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
685	10618	20443	4.33	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
3589	13503	23292	6.05	7.0E-43	AW246442.1	EST_HUMAN	2822251.5ptm NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'

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7092	16969		1.76	7.0E-43	AB936748.1	EST_HUMAN	wp69b01.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
1320	11227		10.17	6.0E-43	AA491890.1	EST_HUMAN	ne72db06.e1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909803 similar to gb:L05095 60S
2547	12421		4.15	6.0E-43	AV708201.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN); AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
5811	15716	25829	2.02	6.0E-43	9955973	NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
6128	15975	26111	2.02	6.0E-43	AW468897.1	EST_HUMAN	hd30b04.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.t3 MER1 MER1 repetitive element ;
7668	17518	27745	1.83	6.0E-43	AA195154.1	EST_HUMAN	zr35e06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665410 5' similar to TR:G529641 G529641 DB1, COMPLETE CDS, ;contains element PTR7 repetitive element ;
8449	18322		6.54	6.0E-43	AL119158.1	EST_HUMAN	DKFZp761L1712.r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
137	10111		1.98	5.0E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
494	10437	20249	3.01	5.0E-43	AA382780.1	EST_HUMAN	EST96033 Testis1 Homo sapiens cDNA 5' end
2816	12745	22539	1.36	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC06 5'
7390	17308	27514	4.47	5.0E-43	AA465288.1	EST_HUMAN	aa33d08.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
7945	17795	28035	2.2	5.0E-43	AI733244.1	EST_HUMAN	o652c10.x5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P60591 P60591 PV14 GENE ;
7964	17814	28055	1.41	5.0E-43	AL049110.1	EST_HUMAN	DKFZp434D0119.r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D0119
8145	18033	28280	5.46	5.0E-43	AW863007.1	EST_HUMAN	MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA
8338	18215	28468	2.67	5.0E-43	W29011.1	EST_HUMAN	55a4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8753	17902	28146	2.6	5.0E-43	X15904.1	NT	Human mRNA for alpha-actinin
957	12643	20728	4.85	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6231	16097		1.72	4.0E-43	11416793	NT	Homo sapiens protocadherin beta 6 (PCDH6), mRNA
6757	16636	26824	4.46	4.0E-43	AI244941.1	EST_HUMAN	q176a02.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ;
6757	16636	26825	4.49	4.0E-43	AI244341.1	EST_HUMAN	q176a02.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ;
8624	18489	28761	1.8	4.0E-43	T77380.1	EST_HUMAN	y072h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113827 5'
9174	18915		1.89	4.0E-43	R20650.1	EST_HUMAN	y06b05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element ;
1195	11105		2.84	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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1669	11571	21437	1.48	3.0E-43	X97869.1	NT	H.sapiens gene encoding La autoantigen
3524	13440	23237					AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4193	14093	23872	0.95	3.0E-43	S69002.1	NT	
5837	15743	25855	1.71	3.0E-43	AA548154.1	EST_HUMAN	nk55d06.s1 NCI_CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419
5837	15743	25856	1.71	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6037	15940	26072	3.78	3.0E-43	U65487.1	NT	Mus musculus otogelin (Otog), mRNA
6746	16625		6.68	3.0E-43	AA458824.1	EST_HUMAN	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
7120	16997	27188	1.18	3.0E-43	7661721	NT	aa88f11.s1 Stralagene fetal retina 997202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.t2 THR repetitive element;
8962	18769	29061	2.02	3.0E-43	5730038	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
177	10148		4.27	2.0E-43	AI190764.1	EST_HUMAN	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6312	16175	26332	1.36	2.0E-43	AW207390.1	EST_HUMAN	qd61c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733988 3' similar to contains PTR7.t3 PTR7 PTR7 repetitive element;
6836	16715		7.53	2.0E-43	U43701.1	NT	UIH-B11-af1-e-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
8532	18404		3.38	2.0E-43	T03007.1	EST_HUMAN	Human ribosomal protein L23a mRNA, complete cds
1630	11534	21394	2.92	1.0E-43	AF154836.1	NT	FB1G5 Fetal brain, Stralagene Homo sapiens cDNA clone FB1G5 3' end similar to LINE-1
1630	11534	21395	2.92	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1678	11590	21450	3.36	1.0E-43	AL163284.2	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
2692	12557	22444	4.95	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5987	15892	26014	12.07	1.0E-43	4507168	NT	60202313F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157686 5'
5987	15892	26015	12.07	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6159	15117	24860	1.63	1.0E-43	R19751.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4) mRNA
6700	16590		1.63	1.0E-43	AF198490.1	NT	yg40e01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34732 5' similar to SP:BD38_MOUSE_P28656 BRAIN PROTEIN DN38 ;
7129	17008	27199	25.23	1.0E-43	AW963676.1	EST_HUMAN	Homo sapiens 8q22.1 region and MTO8 (CBFA2T1) gene, partial cds
8331	18208	28458	6.75	1.0E-43	AI694961.1	EST_HUMAN	EST375749 MAGE sequences, MAGH Homo sapiens cDNA
8672	18560	28844	3.2	1.0E-43	11424378	NT	wr87h01.x1 NCI_CGAP_K1c11 Homo sapiens cDNA clone IMAGE:2494705 3'
9117	18880		3.66	1.0E-43	AL137964.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
9405	19058	25311	1.89	1.0E-43	AI675416.1	EST_HUMAN	DKFZp761D1015_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761D1015 5'
9618	19196	26255	2.52	9.0E-44	11418322	NT	wb99h04.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2313775 3'
872	10798	20648	5.98	8.0E-44	AI222985.1	EST_HUMAN	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
872	10798	20649	5.98	8.0E-44	AI222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845562 3'
6968	16845	27037	3.87	8.0E-44	X94354.1	NT	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845562 3'
							H.sapiens DNA for Cone cGMP-PDE gene

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8504	18377	28643	3.39	8.0E-44	Y10498.2	NT	Homo sapiens mRNA for thymidine kinase, partial
8935	18743	29038	5.06	8.0E-44	L29139.1	NT	Homo sapiens myosin mRNA, partial cds
9359	19031	28304	2.59	8.0E-44	11527399	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
9400	19369	25191	1.99	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
9742	19532	25059	1.75	8.0E-44	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
9885	19369	25191	1.84	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2:22), mRNA
643	10580		0.95	7.0E-44	R08035.1	EST_HUMAN	ye89e01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124920 5'
2187	12074	21978	1.2	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2937	12864	22663	2.2	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2937	12864	22664	2.2	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3786	13698	23485	2.28	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4148	14048	23821	1.17	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4148	14048	23822	1.17	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
6762	16641	26828	2.05	7.0E-44	AU159839	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000496 3'
8986	18791	29080	2.51	6.0E-44	AW954050.1	EST_HUMAN	EST368120 MAGC reassessments, MAGC Homo sapiens cDNA
300	10284		2.52	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZ1FL1 gene
329	10288		2.04	5.0E-44	AJ298880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZ1FL1 gene
6605	16485	26672	3.79	5.0E-44	AI688523.1	EST_HUMAN	tr40d02.x1 NCJ_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.t1
7399	17317		2.59	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element ;
3368	13287	23086	2.9	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
8584	18433	28702	13.3	4.0E-44	U90878.1	NT	Homo sapiens chromosome 21 segment HS21C103
1746	11646		1.07	3.0E-44	6912477	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
2485	12360	22254	1.54	3.0E-44	BE880626.1	EST_HUMAN	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA
3059	12986	22777	5.08	3.0E-44	AA169851.1	EST_HUMAN	6014915239F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893839 5'
1033	10951	20793	2.75	2.0E-44	4826686	NT	zp18b05.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'
1033	10951	20794	2.75	2.0E-44	4826686	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1189	11099	20945	4.63	2.0E-44	5803200	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1189	11099	20946	4.63	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1290	11197	21052	2.79	2.0E-44	AF135588.1	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1346	11252	21108	1.43	2.0E-44	BE465325.1	EST_HUMAN	Homo sapiens RAB36 (RAB36) mRNA, complete cds
2105	11994	21894	2.03	2.0E-44	AF070651.1	NT	hw14g06.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182938 3' similar to SW-620X_HUMAN
2529	12403	22294	1.1	2.0E-44	D25303.1	NT	P22059 OXYSTEROL-BINDING PROTEIN ;
						NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
						NT	Human mRNA for integrin alpha subunit, complete cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2567	12438		3.32	2.0E-44	5901933	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
3425	13342	23147	1.36	2.0E-44	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4468	14362	24152	1.76	2.0E-44	AW864379.1	EST_HUMAN	PM4-SN0016-120500-003-a04 SN0016 Homo sapiens cDNA
5709	15617	25719	1.39	2.0E-44	11449901	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
6097	15107	24870	1.46	2.0E-44	AF039968.1	NT	Homo sapiens general transcription factor 2-I (GTF2I) mRNA, alternatively spliced product, complete cds
6383	16245	26406	3.86	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
6383	16245	26407	3.86	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
7009	16896	27078	1.88	2.0E-44	BE388058.1	EST_HUMAN	301286914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613586 5'
9022	18816		2.22	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795
9710	19735	24910	2.72	2.0E-44	AB002374.1	NT	Human mRNA for KIAA0376 gene, partial cds
9906	19383		1.38	2.0E-44	11526283	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
46	10034	19839	3.64	1.0E-44	7657334	NT	Homo sapiens Missshapen/NIK-related kinase (MINK), mRNA
46	10034	19840	3.64	1.0E-44	7657334	NT	Homo sapiens Missshapen/NIK-related kinase (MINK), mRNA
566	10505	20312	1.85	1.0E-44	AW853132.1	EST_HUMAN	RC1-CT0249-030300-026-h12 CT0249 Homo sapiens cDNA
1179	11090		1.52	1.0E-44	AW994803.1	EST_HUMAN	RC1-BN0039-110300-012-b01 BN0039 Homo sapiens cDNA
1555	11460		5.54	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2177	12064	21965	3.53	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.I3 THR repetitive element;
2177	12064	21966	3.53	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.I3 THR repetitive element;
2237	12716	22024	1.05	1.0E-44	AA398099.1	EST_HUMAN	z188g11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729476 5'
2732	12594	22489	1.39	1.0E-44	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
3664	13578		5.08	1.0E-44	AA455869.1	EST_HUMAN	aa01c09.s1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
5061	14931	24702	0.81	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5061	14931	24703	0.81	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8378	18255		10.75	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DOB Homo sapiens cDNA clone DCBBYE03 5'
8816	18629	28918	4.18	1.0E-44	10092664	NT	Homo sapiens Sush1 domain (SCR repeat) containing (BK35A8.2), mRNA
8869	18681	28970	3.43	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
8869	18681	28971	3.43	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4476	14370	24159	1.74	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4476	14370	24160	1.74	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
2477	12353	22245	3.9	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TRK) mRNA
5015	14889	24656	7.49	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TRK) mRNA
3886	13806		5.25	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
9707	19718		1.46	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
874	10800		1.11	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1957	11852	21739	5.01	5.0E-45	BF333627.1	EST_HUMAN	CM4-CN0044-180200-515-01 CN0044 Homo sapiens cDNA
3173	13098	22904	2.01	5.0E-45	AI523766.1	EST_HUMAN	tg94f07.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116483 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1 ;
5384	15303	25155	8.83	5.0E-45	AA397781.1	EST_HUMAN	z172d03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element ;
7226	17103	27292	1.67	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
8940	18748	29043	2.87	5.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1127	11041	20883	8.96	4.0E-45	X95926.1	NT	H.sapiens ART4 gene
2246	12130	22027	1.98	4.0E-45	BE265622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
9613	19192		1.62	4.0E-45	BF676077.1	EST_HUMAN	602084052F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248253 5'
3997	13210		1.17	3.0E-45	T71490.1	EST_HUMAN	y935f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
6920	16798		1.51	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
7104	16981	27173	3.44	3.0E-45	4758451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
7907	17757	27996	8.37	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7907	17757	27997	8.37	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9814	19690		1.33	3.0E-45	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2454	12331		2.17	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
2996	12924	22716	0.93	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5929	15834	25957	4.82	2.0E-45	L01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
6489	16347	26516	1.75	2.0E-45	BE782184.1	EST_HUMAN	601467793F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 5'
8179	19471	28315	27.64	2.0E-45	BE934350.1	EST_HUMAN	MR0-HT0923-190800-201-a02 HT0923 Homo sapiens cDNA
8516	18388	28652	3.96	2.0E-45	AA459770.1	EST_HUMAN	aa87f12.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to TR:G1144569 G1144569 R-SLY1 ;
8794	18608	28898	2.13	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCL CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
8794	18608	28899	2.13	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCL CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
9853	19346		2.76	2.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA

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Table 4

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Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
118	10349		2.22	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608183 5'
403	10349		2.7	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608183 5'
464	10407	20227	1.5	1.0E-45	4506412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1157	11070	20915	1.7	1.0E-45	7657290	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3065	12992	22784	6.76	1.0E-45	U32169.1	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3447	13364	23171	1.04	1.0E-45	8659558	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3626	13442	23239	0.81	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1561 protein, partial cds
4378	14274	24055	4.08	1.0E-45	BE369633.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619903 5'
4884	14765	24541	1.05	1.0E-45	11545796	NT	Homo sapiens niban protein (NIBAN), mRNA
7274	17151	27347	5.22	1.0E-45	BE887843.1	EST_HUMAN	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
7485	17355	27559	1.25	1.0E-45	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
9231	18950	25358	4.3	1.0E-45	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
9415	19067		5.38	1.0E-45	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
9421	19070		2.56	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9820	19324	25207	3.17	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
6790	16669	26861	2.28	9.0E-46	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
7018	16895		6.71	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7986	17836	28077	7.89	9.0E-46	AW246964.1	EST_HUMAN	2822449.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2392	12270	22165	8.79	8.0E-46	AI433261.1	EST_HUMAN	t32108.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_ma2
2392	12270	22166	8.79	8.0E-46	AI433261.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
6992	16572		3.97	8.0E-46	BE167244.1	EST_HUMAN	RC5-HT0506-280200-012-C12 HT0506 Homo sapiens cDNA
4478	14372		6.54	7.0E-46	BE386165.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4701	14587		1.01	7.0E-46	BE064396.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
5883	15592	25693	4.01	7.0E-46	8922708	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
5912	15818	25943	1.35	7.0E-46	BF105845.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042735 5'
9543	19144		1.35	7.0E-46	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2726	12588	22483	5.53	6.0E-46	AI884381.1	EST_HUMAN	wm31f08.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
2726	12588	22484	5.53	6.0E-46	AI884381.1	EST_HUMAN	MER19 repetitive element;
5727	15634	25737	8.85	6.0E-46	AI635448.1	EST_HUMAN	ts58f10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363 SA GENE.;

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8684	17878		3.03	6.0E-46	BE784971.1	EST_HUMAN	601478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880995 5'
197	10169		6.41	5.0E-46	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3484	13400	23205	1.12	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
3484	13400	23206	1.12	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6039	15942	28074	1.79	5.0E-46	BF590442.1	EST_HUMAN	naa38107.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258757 3' similar to TR:O75202
6144	16017	26155	3.52	5.0E-46	BF347229.1	EST_HUMAN	O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC ;
625	10562		1.51	4.0E-46	AA601143.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
1676	11578	21446	3.57	4.0E-46	AW770544.1	EST_HUMAN	nc54e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X63741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1676	11578	21447	3.57	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
1676	11578	21447	3.57	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
2710	12573	22464	3.55	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
4320	14217	23999	1.07	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
4320	14217	24000	1.07	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
5338	15258	25082	1.84	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
5338	15258	25083	1.84	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
9660	19221	25237	1.91	4.0E-46	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4294	14192	23976	0.8	3.0E-46	4508376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4666	14552	24343	1.13	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.1.1.2) germline; Ig-Light-Lambda; VLambda
4666	14552	24344	1.13	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.1.1.2) germline; Ig-Light-Lambda; VLambda
7081	16968	27151	8.3	3.0E-46	A1831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
8856	18668	28955	2.63	3.0E-46	D31765.1	NT	Human mRNA for KIAA0061 gene, partial cds
819	10747	20594	5.91	2.0E-46	AA468646.1	EST_HUMAN	ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element ;
1542	11447		1.32	2.0E-46	AA678246.1	EST_HUMAN	z127a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3'
1623	11527	21385	2.43	2.0E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
4899	14779	24555	1.15	2.0E-46	AA399286.1	EST_HUMAN	z59e02.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN. ;
6418	16280	26442	6.78	2.0E-46	9910569	NT	Mus musculus sperm tail associated protein (Slap), mRNA
6703	16583		1.17	2.0E-46	BE869151.1	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849287 5'
8571	18439		1.87	2.0E-46	7657233	NT	Homo sapiens small acidic protein (IMAGE745052), mRNA
9157	19629		1.75	2.0E-46	BF028854.1	EST_HUMAN	601765225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3997326 5'
9409	19525		1.44	2.0E-46	H48391.1	EST_HUMAN	y32d01.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:206977 5'
9728	19515	25136	3.81	2.0E-46	AW27214.1	EST_HUMAN	xq78h03.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
1213	11121	20970	5.19	1.0E-46	4502894	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2236	12121	22023	4.6	1.0E-46	AW978516.1	EST_HUMAN	EST390625 MAGC resequences, MAGP Homo sapiens cDNA
2351	12231	22128	2.59	1.0E-46	H97330.1	EST_HUMAN	EST748b095 WATM1 Homo sapiens cDNA clone 48b095
3211	13135	22936	2.81	1.0E-46	AA631912.1	EST_HUMAN	np78b02.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens MT-1l mRNA. (HUMAN);
4772	14656		2.84	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIA0980 protein, partial cds
5495	15414	25477	4.18	1.0E-46	BF194707.1	EST_HUMAN	7c92b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
5636	19449	25639	5.66	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
5636	19449	25640	5.66	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
8236	15414	25477	4.26	1.0E-46	BF194707.1	EST_HUMAN	7c92b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
9188	18923	25348	1.43	1.0E-46	BF531102.1	EST_HUMAN	602072264F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215398 5'
9188	18923	25349	1.43	1.0E-46	BF531102.1	EST_HUMAN	602072264F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215398 5'
9925	19397		1.53	1.0E-46	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAE03 5'
749	10679		4.51	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
4848	14729	24512	2.61	9.0E-47	AW770928.1	EST_HUMAN	h93e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009594 3' similar to TR:O75703 O75703 HYPOTHETICAL 12.4 KD PROTEIN. ;
9682	19617	25001	1.84	9.0E-47	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1766	11665	21539	14.02	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
1766	11665	21540	14.02	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2684	12549	22439	1.74	8.0E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
2959	12917	22712	1.72	8.0E-47	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 3/3
2501	12376	22266	3.05	6.0E-47	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7344	17212	27411	6.27	6.0E-47	AI695189.1	EST_HUMAN	tz98h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296659 3'
5963	15868	25990	5.27	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
8174	18062		3.91	5.0E-47	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stralagene (cat#936206) Homo sapiens cDNA clone HFBCF07

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1379	11284	21140	3.41	4.0E-47	4557566	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
6938	16816	27008	2.06	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
6938	16816	27009	2.06	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8905	18713		4.84	4.0E-47	AW515509.1	EST_HUMAN	xx66b07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848697 3' similar to SW:INT6_MOUSE
532	10474	20287	1.75	3.0E-47	BE907634.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 [1];
532	10474	20288	1.75	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
801	10730	20571	5.17	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
930	10855	20703	8.9	3.0E-47	AL163284.2	NT	y54b04.s1 Scarses_multiple_sclerosis_2Nbl-HMSP Homo sapiens cDNA clone IMAGE:277327 3'
1984	11877	21770	1.5	3.0E-47	AB007899.1	NT	Homo sapiens chromosome 21 segment HS21C084
3885	13796		4.99	3.0E-47	U93181.1	NT	Homo sapiens KIAA0439 mRNA, partial cds
4265	14164	23941	0.97	3.0E-47	M12959.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
5659	15571	25666	4.26	3.0E-47	AW408800.1	EST_HUMAN	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
5659	15571	25667	4.26	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-act-d-07-0-U1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
5953	15858		1.89	3.0E-47	AI222413.1	EST_HUMAN	UI-HF-BM0-act-d-07-0-U1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
142	10116	19936	4.27	2.0E-47	4505318	NT	qh04e07.x1 Scarses_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
952	10876	20722	2.18	2.0E-47	AL163209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
952	10876	20723	2.18	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1548	11453		1.18	2.0E-47	A1969279.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
1575	11479	21338	1.22	2.0E-47	7662109	NT	wq96b02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2479851 3'
1654	11557	21420	4.44	2.0E-47	AA524514.1	EST_HUMAN	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
2185	12072	21974	2.3	2.0E-47	AF060568.1	NT	ng43h12.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:937607 3'
4251	14150	23924	1.66	2.0E-47	4504866	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
4287	14186	23967	1.75	2.0E-47	AA569592.1	EST_HUMAN	Homo sapiens ring finger protein (C3HC4 type) 8 (RNFB), mRNA
4287	14186	23968	1.75	2.0E-47	AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652
4406	14300	24084	2.06	2.0E-47	AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652
4707	14593	24384	1.1	2.0E-47	AW905166.1	EST_HUMAN	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
5635	15549	25637	1.6	2.0E-47	BE778475.1	EST_HUMAN	EST1377238 MAGE resequences, MAGE1 Homo sapiens cDNA
5635	15549	25638	1.6	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6532	19464		1.33	2.0E-47	L097931.1	NT	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6643	18523	26716	2.1	2.0E-47	D87675.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
6643	18523	26717	2.1	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
7060	18937	27127	1.77	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9070	10116	19936	5.77	2.0E-47	4505318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9219	19658	24988	1.98	2.0E-47	R42423.1	EST_HUMAN	y92a08.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:29966 3' similar to contains OFR
9257	19659		1.32	2.0E-47	AL163209.2	NT	repetitive element ;
1383	11288	21142	4.5	1.0E-47	AB333429.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
3749	13662	23443	0.79	1.0E-47	BE280477.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
3749	13662	23444	0.79	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3138893 5'
5008	14882	24648	2.59	1.0E-47	AW813906.1	EST_HUMAN	601155321F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3138893 5'
6194	15954	28086	7.68	1.0E-47	AB80886.1	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA
7928	17778	28017	1.75	1.0E-47	L30115.1	NT	at19a06.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995
1595	11499	21358	2.34	9.0E-48	AF223391.1	NT	RAS-RELATED PROTEIN RAP-1A (HUMAN);
3509	13425	23228	0.83	9.0E-48	BF359947.1	EST_HUMAN	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
8460	18333	28595	3.22	9.0E-48	BE39813.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1230	11138		1.32	8.0E-48	4501900	NT	CNM2-MT0100-310700-290-105 MT0100 Homo sapiens cDNA
1231	11138		1.51	8.0E-48	4501900	NT	601310479F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3632083 5'
3096	13023	22818	3.62	8.0E-48	AW768477.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
3096	13023	22819	3.62	8.0E-48	AW768477.1	EST_HUMAN	hk61b03.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
482	10426		1.37	7.0E-48	AB033035.1	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
483	10426		13.37	7.0E-48	AB033035.1	NT	hk61b03.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
1482	11387	21250	1.12	7.0E-48	6912719	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
1620	11524	21382	3.49	7.0E-48	5730038	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
5947	15852	25975	22.88	7.0E-48	11416831	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
7275	17152	27348	1.52	6.0E-48	AF026816.1	NT	Homo sapiens tousel-like kinase 1 (TLK1), mRNA
7500	17370	27577	1.9	6.0E-48	11427428	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
7587	17438	27654	3.38	6.0E-48	AA185080.1	EST_HUMAN	Homo sapiens histidyl-tRNA synthetase (HARS), mRNA
3269	15067	22989	1.39	5.0E-48	4826891	NT	Homo sapiens putative oncogene protein mRNA, partial cds
8325	18202	28451	3.55	4.0E-48	AB20420.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
1363	11289	21124	0.92	3.0E-48	AV690964.1	EST_HUMAN	tu47a02.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2254154 3'
1933	11828	21710	18.97	3.0E-48	4885170	NT	AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5'
1933	11828	21711	18.97	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3579	13493	23284	0.88	3.0E-48	AW664531.1	EST_HUMAN	h14b12.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN
5592	15507	25582	2.35	3.0E-48	BE084571.1	EST_HUMAN	P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
6889	16768		2.86	3.0E-48	AA659930.1	EST_HUMAN	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
8248	18128	28376	7.08	3.0E-48	BF514170.1	EST_HUMAN	nv03105.s1 NCL_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1
39	10027	19827	1.18	2.0E-48	AA631940.1	EST_HUMAN	PTR5 repetitive element ;
4431	14326	24114	1.35	2.0E-48	BE246065.1	EST_HUMAN	UIH-BW1-anti-a-10-0-UI.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'
5553	15469	25539	72.29	2.0E-48	AA613171.1	EST_HUMAN	fmc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26
5553	15469	25540	72.29	2.0E-48	AA613171.1	EST_HUMAN	TCBAPrD3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
6440	16301	26464	4.29	2.0E-48	AB040934.1	NT	no18g01.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
6440	16301	26465	4.29	2.0E-48	AB040934.1	NT	no18g01.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
6447	16308	26473	2.9	2.0E-48	11496238	NT	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
6864	16743	26936	2.39	2.0E-48	AV743451	EST_HUMAN	AV743451 CB Homo sapiens cDNA clone CBCCGG10 5'
9184	15082	24828	2.45	2.0E-48	AA465007.1	EST_HUMAN	zx80c03.r1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:810082 5'
9511	19579	25070	1.63	2.0E-48	BE731764.1	EST_HUMAN	G01305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
50	10037	19844	0.95	1.0E-48	7706534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
855	10782	20632	6.93	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-1, Alzheimer disease) (APP), mRNA
1274	11182	21032	3.28	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 8 (RBM8) mRNA
1876	11772	21648	44.65	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3443	13360	23167	1.23	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5082	14982	24728	1.1	1.0E-48	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6303	16167	26325	2.21	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
7337	17205	27404	5.72	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
7626	17377	27586	4.48	1.0E-48	BF304683.1	EST_HUMAN	G01883098F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
7934	17784	28023	5.06	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
7934	17784	28024	5.06	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
8999	18802	29094	1.73	1.0E-48	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
8999	18802	29095	1.73	1.0E-48	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
9145	19606		1.56	1.0E-48	W26785.1	EST_HUMAN	15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
5692	15601	25702	2.95	8.0E-48	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5682	15601	25703	2.95	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6827	16706	26900	3.19	8.0E-49	U23850.1	NT	Human inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
134	10335	20157	1.47	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
134	10335	20158	1.47	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
388	10335	20157	1.74	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
388	10335	20158	1.74	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
389	10335	20157	1.99	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
389	10335	20158	1.99	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1202	11112	20958	4.05	7.0E-49	AL163284.2	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
4560	14443	24227	0.95	7.0E-49	O60811	SWISSPROT	Homo sapiens chromosome 21 segment HS21C084
							HYPOTHETICAL PROTEIN DJ845024.3
5351	15271	25100	1.93	7.0E-49	A1807191.1	EST_HUMAN	wf25h04.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
5357	15277	25107	1.34	7.0E-49	AL120937.1	EST_HUMAN	O54923 RSEC15. ; DKFZp762C033_s1.762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762C033 3'
							bat5g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element; complete (MOUSE);
190	10162	19979	11.77	6.0E-49	AW731740.1	EST_HUMAN	UH-BI3-alc-a-05-0-U1.s1 NC1 CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
8600	18467	28738	2.92	6.0E-49	AW452218.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
8920	18728	29022	2.69	6.0E-49	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
8920	18728	29023	2.69	6.0E-49	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
9507	19498		3.43	6.0E-49	AA707567.1	EST_HUMAN	z29c08.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451694 3'
695	10628	20452	3.37	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
695	10628	20453	3.37	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
							zp29c07.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610960 5' similar to TR:G233226 G233226 RTVL-H PROTEIN ; contains LTR7.13 LTR7 LTR7 repetitive element ;
1753	11653	21524	1.94	5.0E-49	AA172121.1	EST_HUMAN	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
2721	12583	22477	5.18	5.0E-49	U17714.1	NT	
3235	13159	22957	5.13	5.0E-49	11493655	NT	Homo sapiens similar to ribosomal protein S27 (metalloproteinase 1) (H. sapiens) (LOC63362), mRNA
514	10456	20266	37.46	4.0E-49	AW189533.1	EST_HUMAN	x08b01.x1 NC1 CGAP_U14 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP:B0350.2B CE06703 ;
9376	19710		2.43	4.0E-49	AA210798.1	EST_HUMAN	z90f05.r1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:982977 5'
9459	19090		3.3	4.0E-49	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
548	10489	20298	0.93	3.0E-49	X08968.1	NT	H.sapiens mRNA for acetyl-CoA carboxylase

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2611	12479		2.01	3.0E-49	AA016131.1	EST_HUMAN	ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.t3 L1
4909	14788	24564	2.08	3.0E-49	U46999.1	NT	repetitive element ; Human type IV collagen (COL4A6) gene, exon 40
6386	16248	28409	9.6	3.0E-49	H39479.1	EST_HUMAN	EST25e12 WATM1 Homo sapiens cDNA clone 25e12
8621	18487	28759	2.3	3.0E-49	AA337561.1	EST_HUMAN	EST42572 Endometrial tumor Homo sapiens cDNA 5' end
645	10582		2.66	2.0E-49	BE165980.1	EST_HUMAN	MR3-HT0487-150200-173-g01 HT0487 Homo sapiens cDNA
3185	13110	22914	1.4	2.0E-49	N26446.1	EST_HUMAN	yx23d06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262571 5'
3521	13437	23235	0.93	2.0E-49	AF026564.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
							oz88d02.x1 Soares senescent fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:1692403 3' similar to gb:M31470 RAS-LIKE PROTEIN TC10 (HUMAN);contains Alu repetitive element;contains element MER22 repetitive element ;
4693	14579	24373	1.12	2.0E-49	AH167357.1	EST_HUMAN	
4704	14590	24381	1.25	2.0E-49	BF511846.1	EST_HUMAN	UJH-BI4-aps-d-02-0-UJ.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3088538 3'
6040	15943	26075	1.47	2.0E-49	AV717938.1	EST_HUMAN	AV717938 DCB Homo sapiens cDNA clone DGBALB01 5'
6717	16597		1.97	2.0E-49	M86033.1	EST_HUMAN	EST02558 Fetal brain, Striatogene (cat#936206) Homo sapiens cDNA clone HFBCY50
9487	19599		1.53	2.0E-49	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
881	10807		3.95	1.0E-49	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1760	11659	21531	2.58	1.0E-49	BE255216.1	EST_HUMAN	601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33556273 5'
5289	15210	25011	4.97	1.0E-49	BF131007.1	EST_HUMAN	601820053F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5'
6287	16151	26307	2.93	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
6287	16151	26308	2.93	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
							yw79g12.s1 Soares placenta_8t69weeks_2NbHP8t69W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
6322	16185	26346	2.17	1.0E-49	N25894.1	EST_HUMAN	yw79g12.s1 Soares placenta_8t69weeks_2NbHP8t69W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
6322	16185	26347	2.17	1.0E-49	N25894.1	EST_HUMAN	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
6709	16589	26777	1.29	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
6709	16589	26778	1.29	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
7200	17077	27262	1.22	1.0E-49	BE408340.1	EST_HUMAN	601300992F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
7830	17680	27924	1.21	1.0E-49	AL043129.2	EST_HUMAN	DKFZp434D2423_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2423 5'
8630	18495	28789	3.88	1.0E-49	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
9018	18813		1.73	1.0E-49	BE159343.1	EST_HUMAN	MR0-HT0407-010200-006-f02 HT0407 Homo sapiens cDNA
9367	19035		2	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
4923	14802		1.06	9.0E-50	AF101475.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
163	10136	19951	2.59	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
702	10635	20460	1.89	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
702	10635	20461	1.89	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1016	10934		1.21	8.0E-50	AF000573.1	NT	Homo sapiens homotetrasate 1,2-dioxygenase gene, complete cds
1727	11628	21497	2.51	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2432	12309	22204	1.36	8.0E-50	7708394	NT	Homo sapiens p47 (LOC51674), mRNA
2432	12309	22205	1.36	8.0E-50	7708394	NT	Homo sapiens p47 (LOC51674), mRNA
2666	12531	22421	1.69	8.0E-50	4828658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
8711	18528	28811	2.1	8.0E-50	AA633467.1	EST_HUMAN	np62d06.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130891 3' similar to gb:J05459
603	10539	20349	0.96	7.0E-50	BE089591.1	EST_HUMAN	GLUTATHIONE S-TRANSFERASE TESTIS/BRAIN (HUMAN);
8139	18027	28273	9.52	7.0E-50	AB72137.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
6781	16660		4.47	6.0E-50	BE044076.1	EST_HUMAN	wm55g11.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
8190	18076	28326	3.17	6.0E-50	AA312079.1	EST_HUMAN	h03dh04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29 b3
8190	18076	28327	3.17	6.0E-50	AA312079.1	EST_HUMAN	MER29 repetitive element;
1752	11652	21522	0.85	5.0E-50	BF332938.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1752	11652	21523	0.85	5.0E-50	BF332938.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
7255	17132		5.64	5.0E-50	AA557683.1	EST_HUMAN	CMD-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
8991	18795	29086	1.85	5.0E-50	AA403053.1	EST_HUMAN	CMD-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
899	10824		1.29	4.0E-50	AA601143.1	EST_HUMAN	nl45h10.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1049683 similar to contains PTR5.b3 PTR5
1896	11791		2.45	3.0E-50	MT18048.1	NT	repetitive element;
3259	13182	22981	1.14	3.0E-50	AA746142.1	EST_HUMAN	z162b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
3692	13606	23392	4.6	3.0E-50	AW755254.1	EST_HUMAN	G1335769 GAG-POL POLYPROTEIN.;
6056	16039	26180	1.55	3.0E-50	11421514	NT	no54e09.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X63741_rna1
6505	16364	26540	4.01	3.0E-50	AF233436.2	NT	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
6505	16364	26541	4.01	3.0E-50	AF233436.2	NT	Human endogenous retrovirus RTVL-H2
7649	17499	27721	1.17	3.0E-50	AB046818.1	NT	ob03f06.s1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'
8760	17909	28153	5.94	3.0E-50	AJ245621.1	NT	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
							Cardiomyopathy associated gene 5
							Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
							Homo sapiens mRNA for KIAA1598 protein, partial cds
							Homo sapiens CTL2 gene

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
761	10691		4.91	2.0E-50	AF055086.1	NT	Homo sapiens MHC class 1 region
1063	10979	20823	4.6	2.0E-50	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
1425	11330	21197	18.02	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
6924	16802	26995	6.27	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
6924	16802	26996	6.27	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
7686	17536	27761	1.53	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 8g (Krt2-8g), mRNA
7686	17536	27762	1.53	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 8g (Krt2-8g), mRNA
235	10204	20018	1	1.0E-50	BE007080.1	EST_HUMAN	PM3-BN0137-290300-002-g11 BN0137 Homo sapiens cDNA
235	10204	20019	1	1.0E-50	BE007080.1	EST_HUMAN	PM3-BN0137-290300-002-g11 BN0137 Homo sapiens cDNA
454	10398	20215	2.1	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2314	12195		8.96	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7375	17244	27450	1.22	9.0E-51	AA043738.1	EST_HUMAN	zklc09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486352 5'
4467	14361	24151	4.89	8.0E-51	AA610842.1	EST_HUMAN	np86a09.s1 NC1_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_ma1
6510	16369	26546	2.34	8.0E-51	11439587	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7448	17257		1.28	8.0E-51	AL138590.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
3245	13166	22967	1.36	7.0E-51	AW869219.1	EST_HUMAN	AI138590 PLACE1 Homo sapiens cDNA clone PLACE1008887 5'
3317	13238	23042	0.83	7.0E-51	AW274720.1	EST_HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
4076	13978	23757	1.26	7.0E-51	AL079628.1	EST_HUMAN	xn34a03.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340
4076	13978	23758	1.26	7.0E-51	AL079628.1	EST_HUMAN	Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
4254	14153	23927	2.38	7.0E-51	AW265603.1	EST_HUMAN	DKFZp43B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp43B2229 5'
1936	11831	21714	5.3	6.0E-51	7657266	NT	DKFZp43B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp43B2229 5'
3428	13345	23150	12.92	6.0E-51	7657266	NT	UIH-BW0-alp-b-05-0-U1.s1 NC1_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729817 3'
4212	14110	23887	0.78	6.0E-51	9910553	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4212	14110	23888	0.78	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
5645	15558	25651	2.26	6.0E-51	X01768.1	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
5650	15562	25656	6.68	6.0E-51	AF070083.1	NT	Human haptoglobin related (Hpr) gene exon 3
5650	15562	25657	6.68	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6158	15116	24859	2.16	6.0E-51	11429685	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
7583	17434	27649	2.26	6.0E-51	7661535	NT	Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA
8550	18448	28716	1.72	6.0E-51	11526289	NT	Homo sapiens B9 protein (B9), mRNA
							Homo sapiens interleukin 17 receptor (IL17R), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
774	10704	20543	10.92	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
766	10715	20557	1.47	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
975	12692	20745	1.37	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1550	11494	21354	0.84	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2548	12422	22311	11.48	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 155
3863	13774	23566	1.08	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3863	13774	23567	1.08	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5004	14879	24643	2.34	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8601	18468	28739	3.72	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3) mRNA
130	10104	19926	0.92	3.0E-51	AI597348.1	EST_HUMAN	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326
1159	11072	20917	4.16	3.0E-51	AI587348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4232	14130	23906	2.13	3.0E-51	AL159142.1	NT	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326
6474	16333	26500	1.73	3.0E-51	R15914.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
7131	17008		5.87	3.0E-51	M29063.1	NT	Novel human gene mapping to chromosome 22
9675	19233		1.58	3.0E-51	AF003528.1	NT	ye47c08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4
362	10318	20139	1.91	2.0E-51	4507798	NT	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);contains LTR5 repetitive element ;
673	10607	20424	1.08	2.0E-51	BE391063.1	EST_HUMAN	Human hnRNP C2 protein mRNA
673	10607	20425	1.08	2.0E-51	BE391063.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1662	11564	21431	2.24	2.0E-51	AA233352.1	EST_HUMAN	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
3672	13586	23373	2.21	2.0E-51	A1492415.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
4392	14288	24071	1.02	2.0E-51	AW137826.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
5662	15573	25670	2.96	2.0E-51	BE782015.1	EST_HUMAN	zr30a05.1r1 Stralagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233226 G233226 RTVL-H PROTEIN ;contains LTR7.13 LTR7 repetitive element ;
7047	16924	27114	1.61	2.0E-51	BE901994.1	EST_HUMAN	tr27g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
7047	16924	27115	1.61	2.0E-51	BE901994.1	EST_HUMAN	U1-H-B1-adj-d-02-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
7478	17348	27552	1.68	2.0E-51	A1917078.1	EST_HUMAN	601470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
7539	17390	27600	5.25	2.0E-51	BE165980.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
							601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
							ts74d07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN
							Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
							MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7962	17812	28054	1.71	2.0E-51	AV682474.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
8640	15259	25084	8.63	2.0E-51	AI732851.1	EST_HUMAN	0634f09.x8 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
8640	15259	25085	8.63	2.0E-51	AI732851.1	EST_HUMAN	0634f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
9668	19227	25240	1.33	2.0E-51	11419159	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLL.T4), mRNA
109	10090	19905	4.4	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF-4A1) mRNA
1478	11383		22.7	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBC12 5'
4309	14206	23989	0.96	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
4309	14206	23990	0.96	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
5310	15231	25036	3.12	1.0E-51	T18862.1	EST_HUMAN	b12056t Testis 1 Homo sapiens cDNA clone b12056
8959	19771		3.57	1.0E-51	AV760590.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSCBB02 5'
9454	19086		3.28	9.0E-52	AA777621.1	EST_HUMAN	z95a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.t3 THR repetitive element ;
146	10120	19939	7.31	8.0E-52	AA720574.1	EST_HUMAN	nw21g02.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element ;
1481	11386	21249	1.33	8.0E-52	X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
1633	11537	21397	2.05	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1633	11537	21398	2.05	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3913	11537	21397	6.44	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3913	11537	21398	6.44	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7211	17088	27278	1.48	7.0E-52	W56471.1	EST_HUMAN	zc59a06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element;
1170	11082		0.86	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271299-049-d07 BT0537 Homo sapiens cDNA
1688	11570	21436	2.25	6.0E-52	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
8540	18412	28678	2.23	6.0E-52	BE048172.1	EST_HUMAN	tz46f04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGRM_MOUSE_Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR ;

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4340	14237	24021	2.07	5.0E-52	Z78698.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18H7
1639	11543	21402	0.93	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1748	11648	21516	8.58	4.0E-52	4758843	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
3850	13761	23554	0.82	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
6686	16566	26760	1.24	4.0E-52	BE622032.1	EST_HUMAN	601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916836 5'
6965	16843	27035	7.25	4.0E-52	11417036	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4) mRNA
9291	18992		4.25	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1) mRNA
9778	19293		5.09	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4002	13908		9.98	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10875 (FLJ10875) mRNA
550	10491	20299	1.39	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
550	10491	20300	1.39	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2450	12327	22226	1.75	2.0E-52	BE207575.1	EST_HUMAN	bb68507.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);
2706	12569		20.53	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
4902	14782	24557	2.74	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5497	15416	25479	2.74	2.0E-52	AW64804.1	EST_HUMAN	IL3-CT0214-231299-053-E12 CT0214 Homo sapiens cDNA
5841	15747	25860	1.49	2.0E-52	11141868	NT	Homo sapiens interleukin 21 receptor (IL21R) mRNA
7028	16905		8.39	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
7458	17267		1.98	2.0E-52	4758789	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
7825	17675	27918	4.53	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
7825	17675	27919	4.53	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
8536	18408	28671	5.33	2.0E-52	AB831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
8536	18408	28672	5.33	2.0E-52	AB831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
8547	18419	28689	3.09	2.0E-52	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
8659	18548		2.08	2.0E-52	W770260.1	EST_HUMAN	zd49gt12.t1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344038 5'
8891	18701		3.22	2.0E-52	11417960	NT	Homo sapiens LIM domain kinase 2 (LIMK2) mRNA
9101	19755	24894	8.86	2.0E-52	AW236297.1	EST_HUMAN	xnt72e07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element; contains element LTR2 repetitive element;
9496	19112		4.28	2.0E-52	AB080985.1	EST_HUMAN	wf67d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TR:Q16859 Q16859 CARBOXYLESTERASE;
522	10464	20276	1.37	1.0E-52	AA634445.1	EST_HUMAN	zu75ht12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1349	11255	21111	8.25	1.0E-52	4504026	NT	Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL) mRNA
2499	12364		1.2	1.0E-52	4502238	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
3021	12949	22741	1.41	1.0E-52	S61070.1	NT	pol=reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 680 nt]
5270	15192	24967	3.59	1.0E-52	M29426.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
5851	15757	25875	2.11	1.0E-52	U38964.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
6394	16256	26417	3.19	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
6932	16810		1.64	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8023	17873		1.61	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8147	18035	28283	1.84	1.0E-52	U48296.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
8210	18094		2.04	1.0E-52	1142632.1	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA
3723	13635	23420	1.03	9.0E-53	4506064	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4293	14191	23975	1.01	9.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
4966	14841	24611	0.93	9.0E-53	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
9338	19018		2.06	7.0E-53	BF238465.1	EST_HUMAN	Homo sapiens predicted osteoblast protein (GS3786), mRNA
9752	19632		2.98	7.0E-53	A1421782.1	EST_HUMAN	tf4407.x1 NCL_OGAP_Bn23 Homo sapiens cDNA clone IMAGE:4132793 5'
4009	13915	23690	2.2	5.0E-53	4758543	NT	THR repetitive element :
9389	19048		1.72	5.0E-53	AW813563.1	EST_HUMAN	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
43	10031	19834	1.92	4.0E-53	AL163285.2	NT	RC3-ST0197-151099-011-g10 ST0197 Homo sapiens cDNA
43	10031	19835	1.92	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4715	14601	24387	1.09	4.0E-53	7705414	NT	Homo sapiens chromosome 21 segment HS21C085
8545	18417	28665	3.33	4.0E-53	BF128701.1	EST_HUMAN	Homo sapiens hook1 protein (HOOK1), mRNA
8545	18417	28686	3.33	4.0E-53	BF128701.1	EST_HUMAN	Homo sapiens hook1 protein (HOOK1), mRNA
2625	12493	22384	2.59	3.0E-53	AB026898.1	NT	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
3670	13584	23371	1.29	3.0E-53	AW50836.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
4486	14380	24167	1.18	3.0E-53	AW803563.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4833	14715	24498	0.85	3.0E-53	BE069344.1	EST_HUMAN	wz22c07.x1 Soares_Dieckgraefe_colon_NHOD Homo sapiens cDNA clone IMAGE:2558796 3'
6833	16712	26905	9.88	3.0E-53	S72043.1	NT	IL2_U00081-240300-055-D03 UNM0081 Homo sapiens cDNA
7238	17115		8.59	3.0E-53	5901953	NT	QV3-BT0381-270100-073-006 BT0381 Homo sapiens cDNA
450	10394		4.25	2.0E-53	AA366556.1	EST_HUMAN	GIF-growth inhibitory factor [human, brain, Genomic, 2015 nt]
2279	12163	22060	2.98	2.0E-53	U78027.1	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
							EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2490	12365		10.54	2.0E-53	4502316	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP9E), mRNA
2694	12559	22446	6.93	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2, translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2694	12559	22447	6.93	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2, translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3207	13131	22933	1.18	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
3970	13877	23653	2.06	2.0E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
4390	14286	24068	1.07	2.0E-53	4509982	NT	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA
5091	14961	24735	1.12	2.0E-53	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5091	14961	24736	1.12	2.0E-53	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5331	15251	25056	3.11	2.0E-53	BF334740.1	EST_HUMAN	PM1-C10396-170800-001-g03 CT0396 Homo sapiens cDNA
5331	15251	25057	3.11	2.0E-53	BF334740.1	EST_HUMAN	PM1-C10396-170800-001-g03 CT0396 Homo sapiens cDNA
7413	17280		5.6	2.0E-53	AW245676.1	EST_HUMAN	2822665:5prime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2822665 5'
1429	11334	21200	0.9	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3364	13283	23083	1	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6021	15925	26056	1.42	1.0E-53	BF364201.1	EST_HUMAN	CM4-NN1029-150800-543-e02 NN1029 Homo sapiens cDNA
7262	17129	27322	5.14	1.0E-53	X79536.1	NT	H. sapiens mRNA for hnRNPcore protein A1
5152	15019	24787	0.8	9.0E-54	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5152	15019	24788	0.8	9.0E-54	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5244	19439	24939	4.71	9.0E-54	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
200	10172	19988	3.09	8.0E-54	BE386785.1	EST_HUMAN	601272863F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3814031 5'
1794	11692	21568	1.33	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
4629	14517	24307	1.25	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
4629	14517	24308	1.25	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5030	14517	24307	1.08	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5030	14517	24308	1.08	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5614	15529	25612	20.81	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
379	10363	20186	1.26	7.0E-54	AA812537.1	EST_HUMAN	ai79c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element;
1789	11687	21563	1.54	7.0E-54	Y16845.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2
2158	12045	21945	4.61	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_86cweeks_2NbHP86cW Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7 b3 LTR7 repetitive element;

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7831	17681	27925	2.23	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
8611	18478		6.24	7.0E-54	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element;
22	10009	19802	1.54	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MIOB, exon 4, 5 and partial cds
1833	11730	21605	0.87	6.0E-54	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
1833	11730	21606	0.87	6.0E-54	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3246	13169	22968	0.84	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3923	13832	23612	2.4	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4359	14255	24040	1.24	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAAC10 5'
4774	14658		1.71	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p86 isoform
4930	14658		1.3	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p86 isoform
8750	17899	28143	1.77	6.0E-54	AW813567.1	EST_HUMAN	RC3-ST0197-151099-011-f08 ST0197 Homo sapiens cDNA
2104	11993	21893	2.25	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
176	10147		106.86	4.0E-54	AF110103.1	NT	Tupaiia belangeri beta-actin mRNA, partial cds
940	10865	20712	41.94	4.0E-54	AA308764.1	EST_HUMAN	EST177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1764	11663	21536	3.24	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1764	11663	21537	3.24	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3168	13093		1.17	4.0E-54	AI935086.1	EST_HUMAN	wd28d11.x1 Soares_NFL_T_GBC_ST1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711
88	10072	19888	5.11	3.0E-54	AA313487.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
2522	12396	22287	0.92	3.0E-54	AL110383.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2593	12454		0.88	3.0E-54	AI908757.1	EST_HUMAN	DKFZp434E0731_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0731 5'
5598	15512	25590	1.48	3.0E-54	4502434	NT	IL-BT189-190399-007 BT189 Homo sapiens cDNA
6373	16235	26394	1.68	3.0E-54	AA844061.1	EST_HUMAN	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
6373	16235	26395	1.68	3.0E-54	AA844061.1	EST_HUMAN	ai92c08.st1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
8435	18309	28565	4.17	3.0E-54	BF345600.1	EST_HUMAN	ai92c08.st1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
							602019408F1 NCI_OGAP_Brm67 Homo sapiens cDNA clone IMAGE:4155121 5'
8675	18563	28847	3.34	3.0E-54	AA393362.1	EST_HUMAN	z170f12.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G191315
9199	18932	26353	2.86	3.0E-54	AW954559.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
9242	19714		7	3.0E-54	AW748965.1	EST_HUMAN	EST366629 MAGC rescuees, MAGC Homo sapiens cDNA
626	10563	20374	6.29	2.0E-54	5031900	NT	RC1-BT0313-131199-011-b09 BT0313 Homo sapiens cDNA
1342	11248	21105	1.94	2.0E-54	4507184	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
							Homo sapiens nuclear antigen Sp100 (SP100) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1529	11434	21290	1.6	2.0E-54	AA655008.1	EST_HUMAN	nt78a09.s1 NCL_CGAP_P1r3 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element;
2493	12387	22261	1.3	2.0E-54	AW163175.1	EST_HUMAN	au92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to
2556	12428	22321	1.92	2.0E-54	AL163210.2	NT	SW:CUL1_HUMAN Q13616 CULLIN HOMOLOG 1 ; Homo sapiens chromosome 21 segment HS21C010 .
2865	12793	22587	1.65	2.0E-54	AW057524.1	EST_HUMAN	wy60b12.x1 Soares NSF_F8_9W_OT_PA_P_31 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
3501	13418		4.06	2.0E-54	AA532925.1	EST_HUMAN	nt45g08.s1 NCL_CGAP_P1r9 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);
4110	14010		2.03	2.0E-54	4502642	NT	Homo sapiens chaperonin containing 1-complex subunit 6 (CCT6) mRNA
4343	14240		1.13	2.0E-54	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4780	14684	24450	1.45	2.0E-54	7706448	NT	Homo sapiens peptidylarginine deiminase type III (LOC51702), mRNA
5156	15023	24790	0.84	2.0E-54	AF083823.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 7
5363	15283	25116	3.75	2.0E-54	4759098	NT	Homo sapiens small inducible cytokine subfamily A (Oye-Cys), member 14 (SCYA14) mRNA
5440	15380	25417	1.34	2.0E-54	BE047864.1	EST_HUMAN	tz43c11.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291348 5'
5521	15439	25503	3.59	2.0E-54	11426657	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
5573	15488	25564	18.19	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
5573	15488	25565	18.19	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6227	16083	26243	8.14	2.0E-54	11426544	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
7552	17403	27617	3.62	2.0E-54	AB001025.1	NT	Homo sapiens mRNA for brain nyanodine receptor, complete cds
7749	17599	27821	1.26	2.0E-54	11429127	NT	Homo sapiens Janus Kinase 2 (a protein tyrosine Kinase) (JAK2), mRNA
8963	18770		2.57	2.0E-54	7657454	NT	Homo sapiens pscadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
9693	19244	25216	1.46	2.0E-54	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
4363	14259		1.07	1.0E-54	BF315418.1	EST_HUMAN	601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
9852	19345		2.26	1.0E-54	AL077341.1	EST_HUMAN	AL077341 Sugeno cDNA library Homo sapiens cDNA clone Zv6C880 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5 end
1294	11201		14.56	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1297	11204		2.32	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
8530	18402		2.76	8.0E-55	AW409714.1	EST_HUMAN	fn02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960907 5'
1065	10981	20826	1.19	7.0E-55	R09346.1	EST_HUMAN	yf28e04.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:127998 5' similar to
7297	17173	27373	1.26	7.0E-55	AA889581.1	EST_HUMAN	SP:C581_BOVIN P10897 CYTOCHROME ;
7315	17191	27393	1.59	7.0E-55	AU139909.1	EST_HUMAN	ak28at11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407280 3'
							AU139909 PLACE1 Homo sapiens cDNA clone PLACE1011576 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8541	18413	28679	12.75	7.0E-55	AF610566.1	EST_HUMAN	tq29f09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
8541	18413	28680	12.75	7.0E-55	AF610566.1	EST_HUMAN	tq29f09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
9823	19648		4.3	7.0E-55	H23396.1	EST_HUMAN	ym57g07.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52444 5'
8803	18617	28908	1.98	6.0E-55	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
1732	11633	21500	1.12	5.0E-55	AA704971.1	EST_HUMAN	z95b09.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
1732	11633	21501	1.12	5.0E-55	AA704971.1	EST_HUMAN	z95b09.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
5941	15846	28969	1.82	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
5941	15846	28970	1.82	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
7229	17106	27296	2.06	5.0E-55	4508302	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
7770	17620	27851	1.86	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
7770	17620	27852	1.86	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
7869	17719	27965	1.19	5.0E-55	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
9283	18985		2.13	5.0E-55	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
49	12656	19643	1.36	4.0E-55	AW957994.1	EST_HUMAN	EST370064 MAGe resequences, MAGe Homo sapiens cDNA
666	10591	20409	33.95	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1422	11328	21193	1.89	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1422	11328	21194	1.89	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1498	11402		1.26	4.0E-55	BF061411.1	EST_HUMAN	7j52b10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1 L3 L4 repetitive element
1979	11872	21763	1.53	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
1979	11872	21764	1.53	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2039	11930	21824	7.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2039	11930	21825	7.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2262	12146	22046	1.25	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
2545	12419		1.04	4.0E-55	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
3242	13165	22964	1.38	4.0E-55	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
6857	16736		6.44	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8559	18429		4.46	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
9200	18933		2.38	4.0E-55	BF303941.1	EST_HUMAN	601886575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
9138	18894		2.76	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
9866	19356		1.65	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
373	10327	20150	2.3	2.0E-55	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
539	10490		0.89	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
633	10570	20383	3.08	2.0E-55	4507296	NT	Homo sapiens syntaxin-binding protein 1 (STXB1) mRNA, and translated products

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2928	12855	22656	0.79	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4665	14551	24342	2.97	2.0E-55	BE719986.1	EST_HUMAN	CM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA
7284	17160		4.3	2.0E-55	AI002836.1	EST_HUMAN	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;
8319	18195	28446	2.2	2.0E-55	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA100583 5'
91	10075	19891	1.6	1.0E-55	4505060	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
182	10154	19869	11.9	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
1132	11046	20888	3.55	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1907	11802	21680	0.86	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
1907	11802	21681	0.86	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
2277	12161		2.3	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2290	12651	22071	1.03	1.0E-55	AF000990.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2470	12346	22238	33.19	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2507	12381	22271	4.71	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2507	12381	22272	4.71	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2588	12439	22331	1.35	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
3363	13282	23082	1.15	1.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
3907	13817	23597	3.47	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4197	14097	23678	1.04	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4721	14607	24392	0.98	1.0E-55	AB037163.1	NT	Homo sapiens DSCR55 mRNA, complete cds
4721	14607	24393	0.98	1.0E-55	AB037163.1	NT	Homo sapiens DSCR55 mRNA, complete cds
5081	14951	24727	1.19	1.0E-55	8923125	NT	Homo sapiens DSCR5b mRNA, complete cds
5794	15700	25809	5.75	1.0E-55	11433046	NT	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA
5794	15700	25810	5.75	1.0E-55	11433046	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
8284	18163	28405	4.74	1.0E-55	AL163210.2	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
8284	18163	28406	4.74	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8745	17894	28138	2.58	1.0E-55	U60950.1	NT	Homo sapiens chromosome 21 segment HS21C010
8859	18671	28959	2.04	1.0E-55	10567821	NT	Human infant brain unknown product mRNA, complete cds
6358	16221	26383	1.81	9.0E-56	BE379074.1	EST_HUMAN	Homo sapiens DNA-binding protein (LOC56242), mRNA
							601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609552 5'
							yn62g03.r1 Soares adult brain N255HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element;
2703	12567	22457	5.18	7.0E-56	H19934.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
6504	16363	26638	1.84	7.0E-56	AW361213.1	EST_HUMAN	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6504	16363	25539	1.84	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
1666	11568	21434	2.26	5.0E-56	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
7940	17790		1.31	5.0E-56	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
9375	19701	24902	2.68	5.0E-56	H55099.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
25	10012	19805	6.15	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
25	10012	19806	6.15	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2676	12541	22431	4.11	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2676	12541	22432	4.11	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2781	10457	20268	3.05	4.0E-56	AF003523.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5788	15694	25802	6.29	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
5788	15694	25803	6.29	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
7959	17849	28090	1.23	4.0E-56	AF043349.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
8295	18174	28417	8.75	4.0E-56	AI498066.1	EST_HUMAN	tm85g12.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163046 3'
8295	18174	28418	8.75	4.0E-56	AI498066.1	EST_HUMAN	tm85g12.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163046 3'
1318	11225	21081	9.85	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
2103	11992	21892	2.7	3.0E-56	6912697	NT	Homo sapiens oncogene TC21 (TC21), mRNA
3086	13013	22804	1.58	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3086	13013	22805	1.58	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3761	13674		1.39	3.0E-56	AF055086.1	NT	Homo sapiens MHC class 1 region
4327	14224	24006	4.05	3.0E-56	AL183288.2	NT	Homo sapiens chromosome 21 segment HS21C068
4470	14364	24154	2.14	3.0E-56	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
5486	15405	25467	1.57	3.0E-56	4759163	NT	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5486	15405	25468	1.57	3.0E-56	4759163	NT	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
6109	16003	26141	6.34	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
7117	16994	27185	5.74	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
7687	17837	28078	1.52	3.0E-56	11434956	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
8124	18012	28259	10.72	3.0E-56	AB042556.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
8632	18497	28771	3.89	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
8632	18497	28772	3.89	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
9240	18955	25315	2.3	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
9240	18955	25316	2.3	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
513	10455		2.94	2.0E-56	AA199818.1	EST_HUMAN	zq62a08.s1 Stragene neuroepithellum (#937231) Homo sapiens cDNA clone IMAGE:645206 3'
716	12675	20476	1.19	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
716	12675	20477	1.19	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2334	12215	22113	1.02	2.0E-56	M26031.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
2334	12215	22114	1.02	2.0E-56	M26031.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
2959	12886	22684	0.93	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3489	13405	23210	1.08	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
954	10887		1.44	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3622	13536	23321	1.79	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2946452 3'
3622	13536	23322	1.79	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2946452 3'
4963	14838	24606	1.52	1.0E-56	AI905162.1	EST_HUMAN	QV-BT077-130199-079 BT077 Homo sapiens cDNA
7780	17630	27863	1.86	1.0E-56	AW845987.1	EST_HUMAN	RC2-CT0163-220999-001-E02 CT0163 Homo sapiens cDNA
609	10545		1.97	9.0E-57	AW880885.1	EST_HUMAN	QV0-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA
4109	14009	23786	1.17	9.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4109	14009	23787	1.17	9.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
13	9999	19790	1.55	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
294	10258	20079	2.91	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
866	10792	20642	5.79	8.0E-57	AW264599.1	EST_HUMAN	xr05d10.x1 NCL_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875
1774	11673	21551	1.63	8.0E-57	AA498109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
3335	13255	23060	1.02	8.0E-57	4758279	NT	zvf1b12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'
3335	13255	23061	1.02	8.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
5107	14975	24750	0.96	8.0E-57	AA971001.1	EST_HUMAN	Homo sapiens EphA4 (EPHA4) mRNA
5207	19624	25004	6.35	8.0E-57	11418185	NT	op67h02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1581939 3'
5888	15794	25915	11.76	8.0E-57	AB023177.1	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
5888	15794	25916	11.76	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
6557	16415	26594	67.76	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
6557	16415	26595	67.76	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
8771	9999	19790	3.32	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
9468	19097		1.27	8.0E-57	7019528	NT	Homo sapiens monocarboxylate transporter 3 (SLC16A8), mRNA
9607	19188	25251	2.02	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
9622	19188	25251	1.39	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
2592	12462	22353	2.02	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2592	12462	22354	2.02	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3212	13136	22937	0.92	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3212	13136	22938	0.92	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3233	13157	22956	6.49	7.0E-57	6005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3801	13713	23500	2.17	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
3801	13713	23501	2.17	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
9834	19656		2.99	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
3694	13608	23393	1.23	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4935	14813	24581	0.96	4.0E-57	BE783649.1	EST_HUMAN	601471228F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874135 5'
767	10716	20558	0.79	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1309	11215		11.34	3.0E-57	AA230279.1	EST_HUMAN	nc13107.s1 NCI_CGAP_P41 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2342	12222	22119	2.83	3.0E-57	AA348335.1	EST_HUMAN	P46783 40S RIBOSOMAL PROTEIN S10 ;
2670	12535	22425	1.62	3.0E-57	BE676622.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' end
2670	12535	22426	1.62	3.0E-57	BE676622.1	EST_HUMAN	733b10.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2
3514	13430	23230	1.15	3.0E-57	AF232708.1	NT	733b10.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2
3639	13553		115.94	3.0E-57	AW853964.1	EST_HUMAN	Homo sapiens cell-line tsA201a chloride ion current inducer protein [(Cin) gene, complete cds
5723	15630	25733	3.34	3.0E-57	BE796537.1	EST_HUMAN	RC3-CT0254-110300-027-d10 CT0254 Homo sapiens cDNA
6736	16615	26805	3.95	3.0E-57	W28130.1	EST_HUMAN	601589895F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6751	16630	26817	1.95	3.0E-57	11545798	NT	4216 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6751	16630	26818	1.95	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
7142	17019	27212	4.65	3.0E-57	AU117659.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8279	18159	28400	20.31	3.0E-57	AW248374.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
9247	19721	24907	5.2	3.0E-57	W23871.1	EST_HUMAN	2820473.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
9608	19628		2.15	3.0E-57	AW178575.1	EST_HUMAN	zb45d11.r1 Soares fetal lung NbhL19W Homo sapiens cDNA clone IMAGE:306549 5'
2699	12563	22453	1.19	2.0E-57	AA845419.1	EST_HUMAN	RC0-HT0112-080999-001-C06 HT0112 Homo sapiens cDNA
3392	13309		2.91	2.0E-57	AL163204.2	NT	ak02b02.s1 Soares parathyroid tumor NbhPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
3504	13421	23223	0.84	2.0E-57	R07702.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
3504	13421	23224	0.84	2.0E-57	R07702.1	EST_HUMAN	ye08h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
4409	14303	24086	6.88	2.0E-57	AL163283.2	NT	ye08h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5478	15398		1.43	2.0E-57	AA016131.1	EST_HUMAN	z331c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element;
5676	15585		28.14	2.0E-57	BF115266.1	EST_HUMAN	7n80f04.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570966 3' similar to contains TAR1.t1 MER22 repetitive element;
7017	16894	27084	1.29	2.0E-57	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
7665	17515	27742	1.71	2.0E-57	AF057722.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
8592	18460	28729	2.22	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
8592	18460	28730	2.22	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
2184	12071	21973	1.12	1.0E-57	AW503208.1	EST_HUMAN	UI-HF-BND-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
7045	16922		2.08	1.0E-57	BE043031.1	EST_HUMAN	h032a08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039082 3' similar to TR:O00246 O00246 HYPOTHETICAL 9.3 KD PROTEIN;
9401	19055		3.47	1.0E-57	AW470791.1	EST_HUMAN	ha33d06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element;
9663	19223	25238	1.43	9.0E-58	BE395061.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
574	10512		1.41	8.0E-58	BE368715.1	EST_HUMAN	601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
638	10575	20389	2.62	8.0E-58	AI798376.1	EST_HUMAN	tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN;
638	10575	20390	2.62	8.0E-58	AI798376.1	EST_HUMAN	tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN;
1813	11710	21588	2.23	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1813	11710	21589	2.23	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2945	12872		2.83	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
8231	18112		5.61	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B) mRNA
8300	18179	28425	3.25	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BND-ali-g-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
8300	18179	28426	3.25	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BND-ali-g-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
2207	12094	21997	0.9	6.0E-58	BE395061.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2324	12205	22105	2.96	6.0E-58	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001283 5'
2871	12798	22592	1.19	6.0E-58	BE242150.1	EST_HUMAN	TCAAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
2871	12798	22593	1.19	6.0E-58	BE242150.1	EST_HUMAN	TCAAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
7909	17759	28000	1.3	6.0E-58	11434746	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
9492	19109		1.8	6.0E-58	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
297	10261	20081	2.9	5.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
693	10626	20451	5.87	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA
1176	11088	20932	4.47	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1176	11088	20933	4.47	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1177	11088	20932	2.99	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1177	11088	20933	2.99	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3281	13202	23002	3.56	5.0E-58	AA988183.1	EST_HUMAN	cr88e07.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
5458	15378		2.21	5.0E-58	11496282	NT	Homo sapiens placenta-specific 1 (PLAC1), mRNA
5748	15656	25764	5.86	5.0E-58	H23072.1	EST_HUMAN	ym51h07.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52071 5'
5894	15800	25924	1.45	5.0E-58	11421330	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
6647	16527	26721	6.77	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10826 (FLJ10826), mRNA
7829	17679	27923	1.56	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
9215	19650		3.26	5.0E-58	11528293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
9876	19362		2.49	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
369	10325	20147	17.97	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
779	10709	20548	1.58	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1452	11357	21221	1.24	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2631	12405	22297	0.97	4.0E-58	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
2590	12461	22351	2.7	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3283	13204	23004	1.1	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3680	13594	23380	2.11	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
8651	18515	28798	7.54	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA
332	10291		1.17	3.0E-58	R17879.1	EST_HUMAN	yg10e02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
1367	11273	21129	2.34	3.0E-58	4759881	NT	Homo sapiens peptide YY (PYY) mRNA
3141	13066	22864	2.91	3.0E-58	BF569848.1	EST_HUMAN	G02185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3141	13066	22865	2.91	3.0E-58	BF569848.1	EST_HUMAN	G02185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
6002	15907	26031	1.39	3.0E-58	AV712977.1	EST_HUMAN	AV712977 DCA Homo sapiens cDNA clone DCAAZG04 5'
925	10850	20698	8.16	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
							ba08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391.60S
1268	11175		12.06	2.0E-58	BE208532.1	EST_HUMAN	RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
5288	19441	24986	4.42	2.0E-58	BE907186.1	EST_HUMAN	G01489861F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5288	19441	25010	4.42	2.0E-58	BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
							am57e02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP:ZK328.1 CE06066 UBQUITIN CONJUGATING ENZYME1; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
5721	15628	25731	1.74	2.0E-58	AH24874.1	EST_HUMAN	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
6246	16112	26263	2.76	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
6246	16112	26264	2.76	2.0E-58	AF14838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
8123	18011	28258	10.79	2.0E-58	BF307745.1	EST_HUMAN	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
8332	18209	28459	2.26	2.0E-58	AW87264.1	EST_HUMAN	hm25f08.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
705	10638	20463	0.93	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3' end
1052	10969	20811	5.45	1.0E-58		NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1305	11212	21067	2.17	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1305	11212	21068	2.17	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1375	11281	21136	1.07	1.0E-58	AJ238093.1	NT	Homo sapiens partial A1F-4 gene, exons 2 to 7 and Alu repeat elements
1641	11545	21406	2.02	1.0E-58	BE466132.1	EST_HUMAN	hy10f08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3196835 3'
2771	12633	22527	0.96	1.0E-58	4759160	NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA
3493	13409	23215	0.98	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3493	13409	23216	0.98	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3659	13573	23360	0.84	1.0E-58	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA
4627	14515	24306	0.99	1.0E-58	M95983.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 4
4895	14775	24553	4.96	1.0E-58	AI141063.1	EST_HUMAN	oz43h01.x1 Scarses_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678129 3'
7146	17023	27217	6.7	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8985	18790		3.46	1.0E-58	X63392.1	NT	Hi.sapiens immunoglobulin kappa light chain variable region L14
2182	12089	21971	27.47	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
6759	16638	26826	1.2	8.0E-59	AI761963.1	EST_HUMAN	wh50d06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3'
171	12680		1.63	6.0E-59	BF038327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3088	13015	22807	6.21	5.0E-59	AB07484.1	EST_HUMAN	wf48c11.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
4559	14451	24237	5.85	5.0E-59	X83497.1	NT	Hi.sapiens DNA for ZNF80-linked ERV9 long terminal repeat
							au66c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element:
6173	15130	24850	7.46	5.0E-59	AW162304.1	EST_HUMAN	AV762869 MDS Homo sapiens cDNA clone MDSEIC12 5'
7596	17447	27662	1.71	5.0E-59	AV762869.1	EST_HUMAN	Homo sapiens hypothetical protein (LOC57143), mRNA
8278	18158	28399	2.8	5.0E-59	11434908	NT	Human mRNA for KIAA0184 gene, partial cds
776	10706	20546	2.42	4.0E-59	D90006.1	NT	
4685	14571	24368	1.2	4.0E-59	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA

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Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4685	14571	24369	1.2	4.0E-59	4506788	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
9356	19586		2.16	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
9	9995		5.96	3.0E-59	AW965524.1	EST_HUMAN	EST377582 MAGE resequences, MAGI Homo sapiens cDNA
221	10191	20002	4.12	3.0E-59	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1682	11584	21455	9.87	3.0E-59	4506860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1682	11584	21456	9.87	3.0E-59	4506860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2082	11972	21866	7.68	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2082	11972	21867	7.68	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3090	13017	22811	3.71	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3090	13017	22812	3.71	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3753	13686	23449	1.17	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4683	14569	24366	1.07	3.0E-59	4759329	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY) mRNA
4734	14619	24406	1.85	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR1), mRNA
5772	15679	26786	2.03	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
6352	16215	26377	1.82	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
6629	16509	26697	1.23	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
6629	16509	26698	1.23	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
9333	19014		1.64	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity1 (GGTLA1), mRNA
9474	19101		3.9	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity1 (GGTLA1), mRNA
7555	17406		5.01	2.0E-59	AA309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end
8003	17853		2.47	2.0E-59	BF365554.1	EST_HUMAN	RCO-NT00036-100700-032-a07 NT0036 Homo sapiens cDNA
8205	18089	28341	1.84	2.0E-59	AW410698.1	EST_HUMAN	fn07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5'
8205	18089	28342	1.84	2.0E-59	AW410698.1	EST_HUMAN	fn07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5'
9235	18953	26359	5.14	2.0E-59	A631809.1	EST_HUMAN	wa36c12.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542
9756	19611	24997	2.75	2.0E-59	L11645.1	NT	Q86542 RTVL-H PROTEIN; contains LTR7, b1 LTR7 repetitive element;
157	10131		3.58	1.0E-59	BE296411.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
2575	12446		2.46	1.0E-59	AA748468.1	EST_HUMAN	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
6463	16322	26488	1.29	1.0E-59	AJ130894.1	NT	ca56h11.s1 NCL_CGAP_GGB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13537
7400	17318	27524	1.22	1.0E-59	11419630	NT	Q13537 MER37 TRANSDUCIBLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
8229	16322	26488	8.32	1.0E-59	AJ130894.1	NT	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
1455	11360	21224	2.71	8.0E-60	4759159	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2125	12013	21911	2.7	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
2125	12013	21912	2.7	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
5640	15563	25645	1.41	8.0E-60	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6844	16524	26718	2.6	8.0E-60	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
7174	17051	27240	2.26	8.0E-60	11428949	NT	Homo sapiens S-antigen; retina and pineal gland (arrestin) (SAG), mRNA
7451	17260	27465	1.98	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7451	17260	27466	1.98	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8207	18091	28344	5.38	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8207	18091	28345	5.38	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
737	10689	20504	6.89	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
738	10689	20504	32.94	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
798	10727	20567	1.15	7.0E-60	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
2081	11971	21865	1.56	7.0E-60	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4088	13988	23765	2.63	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
7412	17279	27488	3.28	7.0E-60	H88041.1	EST_HUMAN	yr12f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element ;
8671	18589	28843	1.96	7.0E-60	H88041.1	EST_HUMAN	yr12f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element ;
6914	16792		7.13	6.0E-60	H52456.1	EST_HUMAN	wj78h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains OFR repetitive element ;
78	10062	19878	1.94	5.0E-60	AB07917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
78	10062	19879	1.94	5.0E-60	AB07917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2188	12075	21979	0.93	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BNO-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2188	12075	21980	0.93	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BNO-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2942	12869		1.12	4.0E-60	AA299037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
1815	11712	21591	4.85	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1815	11712	21592	4.85	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1826	11723		2.22	3.0E-60	6031190	NT	Homo sapiens prohibitin (PHB), mRNA
4554	14250	24035	2.08	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5463	15383	25443	2.06	3.0E-60	AW836196.1	EST_HUMAN	RC3-L_T0023-200100-012-a01 LT0023 Homo sapiens cDNA
6153	15111	24875	1.31	3.0E-60	A192814.1	EST_HUMAN	ol60h11.y5 NC1_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE P52824 URIDINE PHOSPHORYLASE ;
6896	16775	26968	5.4	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
6896	16775	26969	5.4	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6990	16867	27061	2.59	3.0E-60	AI040235.1	EST_HUMAN	ox56d09.x1 Soares_NIH-MIPu_S1 Homo sapiens cDNA clone IMAGE:1660337 3' similar to SW:FORM_MOUSE_Q05860 FORMIN;
7077	16954	27147	4.7	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
7569	17420	27637	3.84	3.0E-60	BF102612.1	EST_HUMAN	601646227F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3930990 5'
28	10015	19810	1.79	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1405	11310	21171	2.89	2.0E-60	Z11694.1	NT	H.sapiens 41kDa protein kinase related to rat ERK2
1691	11593	21462	1.29	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
3839	13750	23543	0.78	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
5910	15816	25941	1.57	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
6093	15103	24980	2.44	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6093	15103	24881	2.44	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6222	16088	26238	3.22	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to prothymosin, alpha
6222	16088	26239	3.22	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to prothymosin, alpha
7145	17022	27216	3.86	2.0E-60	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
7732	17592	27806	1.99	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
7732	17592	27807	1.89	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
9509	19123		2.86	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
9639	19573		1.31	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
9641	19209		1.46	2.0E-60	11418098	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC63504), mRNA
9658	19220		1.47	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9957	19420	25169	1.4	2.0E-60	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
511	10453	20264	1.56	1.0E-60	BE178586.1	EST_HUMAN	PM3-HT0605-270200-001-e06 HT0605 Homo sapiens cDNA
3827	13739	23531	1.12	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
4874	14754	24533	1.1	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
7086	16963		2.9	1.0E-60	AA244041.1	EST_HUMAN	nc04e12.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.t1 L1 repetitive element;
7101	16978	27170	1.58	1.0E-60	AV754081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'
1083	10999	20840	1.9	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2635	12502	22395	1.39	8.0E-61	AW006478.1	EST_HUMAN	wf05b10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2606555 3'
2635	12502	22396	1.39	8.0E-61	AW006478.1	EST_HUMAN	wf05b10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2606555 3'
2921	12848		1.74	8.0E-61	X57147.1	NT	Human endogenous retrovirus pl-E.1 (ERV9)

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Table 4.
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
122	10098	19918	0.94	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
122	10098	19919	0.94	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	10098	19918	0.96	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	10098	19919	0.86	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
265	10230	20045	2	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
794	10723	20564	1.69	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1299	11206	21060	10.28	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1612	11516	21376	0.95	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1628	11532	21392	2.12	6.0E-61	AA596033.1	EST_HUMAN	nm6809.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
3266	13189	22987	8.19	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
5674	15583	25684	2.92	6.0E-61	S79249.1	NT	Ig-beta/529g-CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
6344	16207	26370	1.93	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
6492	16351	26521	2.03	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2-l (GTF2l) mRNA, complete cds
9417	10723	20564	1.43	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1655	11588	21421	1.78	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3000	12928	22720	1.92	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3114	13039	22835	0.84	5.0E-61	AB020632.1	NT	Homo sapiens mRNA for KIAA0825 protein, partial cds
3161	13086	22890	1.9	5.0E-61	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3899	13809		1.68	5.0E-61	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
9213	18941		2.76	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFARB01 5'
4119	14019	23797	1.13	3.0E-61	BE396279.1	EST_HUMAN	601309785F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631220 5'
490	10433	20246	1.5	2.0E-61	8922828	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1194	11104	20950	1.35	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-c01 HT0513 Homo sapiens cDNA
1194	11104	20951	1.35	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-c01 HT0513 Homo sapiens cDNA
1642	11546	21407	1.31	2.0E-61	N53039.1	EST_HUMAN	yv53d11.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:246453 3' similar to gb:L25444.60S RIBOSOMAL PROTEIN L35A (HUMAN);
2109	11998	21897	1.41	2.0E-61	4758003	NT	Homo sapiens calmagin (CLGN), mRNA
2604	12472		1.16	2.0E-61	N93937.1	EST_HUMAN	yv03f11.r1 Soares melanocyte 2NbtHM Homo sapiens cDNA clone IMAGE:270189 5'
5871	15777	25896	1.7	2.0E-61	11428166	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA
7212	17089	27279	1.33	2.0E-61	AV694317.1	EST_HUMAN	AV694317 GKCC Homo sapiens cDNA clone GKCELG06 5'
7707	17557	27783	1.62	2.0E-61	AW500256.1	EST_HUMAN	UJ-HF-BNO-akd-f-12-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'
7885	17735	27979	3.09	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (RPC39), mRNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8268	18138		7.14	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
428	10373		0.95	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
756	10686	20524	1.32	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1377	11283	21138	1.09	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1731	11632		0.97	1.0E-61	U32657.1	NT	Human polymorphic trinucleotide repeat in X-linked retinitis pigmentosa (RP3) gene region
1814	11711	21590	4.47	1.0E-61	6005983	NT	Homo sapiens zona pellicula glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2150	12038	21935	1.49	1.0E-61	AW927281.1	EST_HUMAN	nm11b09.y1 NCL_CGAP_L15 Homo sapiens cDNA clone IMAGE:2683369 5' similar to contains element
2804	12794	22533	1.97	1.0E-61	BE386363.1	EST_HUMAN	MSR1 repetitive element
3330	13250	23055	0.88	1.0E-61	7662319	NT	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
3671	13565	23372	1.47	1.0E-61	BE174455.1	EST_HUMAN	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
4339	14236	24019	0.95	1.0E-61	4769249	NT	QV2-HT0577-140300-077-g06 HT0577 Homo sapiens cDNA
4339	14236	24020	0.95	1.0E-61	4769249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4751	14636	24422	7.93	1.0E-61	AW298181.1	EST_HUMAN	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4751	14636	24423	7.93	1.0E-61	AW298181.1	EST_HUMAN	UI-H-BW0-aj1-b-08-Q-U1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4878	14758	24535	0.85	1.0E-61	AL163210.2	NT	UI-H-BW0-aj1-b-08-Q-U1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
6124	15971	26107	7.19	1.0E-61	M30135.1	NT	Homo sapiens chromosome 21 segment HS21C010
6268	16133	26287	1.4	1.0E-61	8923130	NT	Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds
6268	16133	26288	1.4	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
6729	16609	26800	3.38	1.0E-61	11034840	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
6838	16717	26910	3.59	1.0E-61	AF224669.1	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
7348	17216		2.79	1.0E-61	AW999726.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
7763	17613	27840	6.28	1.0E-61	11428892	NT	MR0-BN0070-040400-010-H01 BN0070 Homo sapiens cDNA
8031	17923	28169	1.96	1.0E-61	11425578	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
9110	19631		1.28	1.0E-61	AB011399.1	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
9149	19620	25002	2.96	1.0E-61	11430460	NT	Homo sapiens gene for AF-6, complete cds
9149	19620	25003	2.96	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9515	19128	25261	1.8	1.0E-61	M20809.1	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9805	19317	25205	8.25	1.0E-61	11418127	NT	Human kappa-immunoglobulin germline pseudogene (Chr1) variable region (subgroup V kappa I)
4451	14345	24138	0.79	8.0E-62	AA830420.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
9953	19417		1.56	8.0E-62	AA768861.1	EST_HUMAN	oc66h11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1364725 3' similar to SW:POL_MLVRK
1091	11007	20848	1.27	7.0E-62	AV714334.1	EST_HUMAN	P31795 POL_POLYPYRROLINE; nz75g01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1301328 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3462	13378	23184	0.79	7.0E-62	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90)
8657	18546	28829	4	7.0E-62	A1208681.1	EST_HUMAN	qg56a04.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O15103 O15103 HYPOTHETICAL 27.3 KD PROTEIN ;
2969	12896		1.07	6.0E-62	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
3338	13258		3.93	6.0E-62	11418255	NT	Homo sapiens CGI-56 protein (CGI-56), mRNA
6496	16355	26525	3.33	6.0E-62	A1762801.1	EST_HUMAN	wf04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
6496	16355	26526	3.33	6.0E-62	A1762801.1	EST_HUMAN	wf04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
6804	16683	26873	1.4	6.0E-62	11431139	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
7386	17255	27460	2.76	6.0E-62	AW814393.1	EST_HUMAN	MIR3-ST0203-130100-025-a09 ST0203 Homo sapiens cDNA
410	10356	20183	1.49	5.0E-62	A1950528.1	EST_HUMAN	wx51a07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2847204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95, contains element MER22 repetitive element ;
2356	12236	22132	3.26	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2356	12236	22133	3.26	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3372	13291	23090	2.17	5.0E-62	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
4233	14131	23907	1.65	5.0E-62	AA431093.1	EST_HUMAN	zw78a09.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
7482	17352	27656	6.17	5.0E-62	AW410687.1	EST_HUMAN	P47245 NARDILYSIN ;
8687	18455	28723	4.91	5.0E-62	11426574	NT	Homo sapiens muscle specific gene (M9), mRNA
8587	18455	28724	4.91	5.0E-62	11426574	NT	Homo sapiens muscle specific gene (M9), mRNA
822	10750	20597	3.47	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
822	10750	20598	3.47	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
823	10750	20597	4.63	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
823	10750	20598	4.63	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1446	11351		0.89	4.0E-62	AA311281.1	EST_HUMAN	EST182043 Jurkat T-cells V Homo sapiens cDNA 5' end
2409	12286	22163	1.39	4.0E-62	A1827900.1	EST_HUMAN	wf12b08.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57138_maf1 HISTONE H2B.2 (HUMAN);
2409	12286	22184	1.39	4.0E-62	A1827900.1	EST_HUMAN	wf12b08.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57138_maf1 HISTONE H2B.2 (HUMAN);
3353	13273		6.6	4.0E-62	4557887	NT	Homo sapiens keratin 18 (KRT18), mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4947	14824		2.03	4.0E-62	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5609	15524	25606	1.66	4.0E-62	4506978	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
5804	15709	25822	2.42	4.0E-62	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
6254	16120	26273	1.68	4.0E-62	11421041	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
6498	16357	26528	2.21	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
6498	16357	26529	2.21	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
7134	17011	27204	6.3	4.0E-62	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
8377	18254	28505	2.43	4.0E-62	Z78766.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA16D3
8377	18254	28506	2.43	4.0E-62	Z78766.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA16D3
9135	18891	28792	2.95	4.0E-62	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
9355	19578		2.98	4.0E-62	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae) like 1 (NHP2L1), mRNA
9743	19305	25201	1.99	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
9792	19302	25198	4.2	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9792	19302	25199	4.2	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9835	19335	25210	1.51	4.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
68	10053	19868	1.12	3.0E-62	4557794	NT	Homo sapiens neurofibronin 2 (bilateral acoustic neuroma) (NF2) mRNA
3008	12936	22728	0.95	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1475 protein, partial cds
3008	12936	22729	0.95	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1475 protein, partial cds
3640	13554	23340	1.92	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
6969	16846	27038	4.35	3.0E-62	A1632793.1	EST_HUMAN	wa33f04.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2299903 3' similar to contains THR.t2
1211	11120	20969	1.5	2.0E-62	AL163284.2	NT	THR repetitive element ;
7096	16973	27165	4.8	2.0E-62	BF329911.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
7096	16973	27166	4.8	2.0E-62	BF329911.1	EST_HUMAN	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
							RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
7846	17696		3.94	2.0E-62	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8936	18744		8.93	2.0E-62	BF330676.1	EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
1028	10946	20791	1.24	1.0E-62	AF248540.1	NT	Homo sapiens interectin 2 (SH3D1B) mRNA, complete cds
1526	11431	21288	6.83	1.0E-62	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
1758	11657	21528	1.02	1.0E-62	AA625207.1	EST_HUMAN	af70et1.r1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1
2884	12811	22806	1.12	1.0E-62	AL039C44.1	EST_HUMAN	CE03453 ; DKFZp566F104_r1 566 (synonym: hfkid2) Homo sapiens cDNA clone DKFZp566F104 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4426	14321	24108	1.32	1.0E-62	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
6236	16102	26251	2.17	1.0E-62	AA722878.1	EST_HUMAN	2g89f10.s1 Soares_fetal_heart_Nbt-H19W Homo sapiens cDNA clone IMAGE:409771 3'
6236	16102	26252	2.17	1.0E-62	AA722878.1	EST_HUMAN	2g89f10.s1 Soares_fetal_heart_Nbt-H19W Homo sapiens cDNA clone IMAGE:409771 3'
7239	17116	27310	1.53	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
7239	17116	27311	1.53	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
7262	17139	27331	1.81	1.0E-62	X15533.1	NT	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
7262	17139	27332	1.81	1.0E-62	X15533.1	NT	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
7512	17300	27507	2.81	1.0E-62	AA465170.1	EST_HUMAN	aa33408.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'
8673	18861	28845	2.13	1.0E-62	Z78698.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment SCOpA14D8
8623	19199		1.94	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (OELSR1), mRNA
9815	19322	25206	2.3	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
335	10294	20109	2.14	9.0E-63	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-005 ST0234 Homo sapiens cDNA
2297	12179		1.51	9.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (TF-ujiiwara) Homo sapiens cDNA clone GEN-558C10 5'
3955	13963	23638	7.42	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
3955	13963	23639	7.42	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5210	15088	29106	6.51	9.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (AGO2), mRNA
5354	15274	25104	1.31	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for PKB kinase
6262	16127	26281	4.39	9.0E-63	11426885	NT	Homo sapiens nucleoporin 88kD (NUP88), mRNA
6845	16724	26917	1.37	9.0E-63	11421160	NT	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA
2296	12178	22077	1.52	8.0E-63	4557734	NT	Homo sapiens monamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2322	12203	22102	2.17	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3415	13332	23134	3.81	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3415	13332	23135	3.81	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4168	14068	23843	3.37	8.0E-63	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
913	10837		1.78	7.0E-63	AB72137.1	EST_HUMAN	wnt55g11.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
5274	15196		40.61	6.0E-63	AA420803.1	EST_HUMAN	nc63f02.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S
3279	13200	23001	0.98	4.0E-63	AL163278.2	NT	RIBOSOMAL PROTEIN (HUMAN);
5679	15785	25905	2.86	4.0E-63	AW750372.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
5679	15785	25906	2.86	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
8474	18347	28611	2	4.0E-63	AW134709.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
8474	18347	28612	2	4.0E-63	AW134709.1	EST_HUMAN	UI-H-B1-abq-a-02-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1893	11788	21686	1.97	3.0E-63	AB018260.1	NT	UI-H-B1-abq-a-02-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
							Homo sapiens mRNA for KIAA0717 protein, partial cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2753	12615	22506	1.34	3.0E-63	J00310.1	NT	Human Met-IRNA-i gene 1
2791	11127	20978	8.97	3.0E-63	6005963	NT	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
5896	15802	25926	27.69	3.0E-63	11545810	NT	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA
7597	17448	27663	1.82	3.0E-63	BE876158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
7597	17448	27664	1.82	3.0E-63	BE876158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
184	10156	19972	1.11	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
191	10163	19980	1.74	2.0E-63	4865226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
489	10432		1.39	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8KD) (GLCLG) mRNA
809	10738	20583	5.29	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
1547	11452	21312	2.47	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1547	11452	21313	2.47	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
3119	13044	22841	1.68	2.0E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3248	13171	22970	1.78	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3831	13743	23535	1.86	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4760	14645	24434	1.13	2.0E-63	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5587	15502	25578	2.45	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
5587	15502	25579	2.45	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
							Human germ-line T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
6025	15929	26061	1.37	2.0E-63	U66059.1	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
6208	15968	26103	1.41	2.0E-63	9910366	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
6208	15968	26104	1.41	2.0E-63	9910366	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
6964	16842	27034	3.8	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
							zb18b05.s1 Soares_fetal_lung_NbHL19w Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:X17206.40S RIBOSOMAL PROTEIN S4 (HUMAN);
8129	18017	28265	12.54	2.0E-63	N78945.1	EST_HUMAN	Homo sapiens neurexin III-alpha gene, partial cds
8154	18042	28292	3.02	2.0E-63	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
8154	18042	28293	3.02	2.0E-63	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
9243	19523	25058	10.85	2.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
9864	19354	25186	1.39	2.0E-63	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
4246	14145	23918	2.91	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4246	14145	23919	2.91	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd111
5526	15443	25509	1.39	1.0E-63	AW582266.1	EST_HUMAN	QY0-ST0215-060100-083-b09 ST0215 Homo sapiens cDNA
6935	16813		2.3	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9879	19633		3.02	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6591	16471	26661	4.78	9.0E-64	AL478186.1	EST_HUMAN	tm50b07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 3'
1030	10948		7.89	8.0E-64	BE280796.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
5733	15641	25747	3.16	8.0E-64	BE885755.1	EST_HUMAN	601508969F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
9059	18841		2.61	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9111	18875		2.56	8.0E-64	T60651.1	EST_HUMAN	y08b02.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79179 5'
3486	13402		0.99	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4625	14513	24303	2.44	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4625	14513	24304	2.44	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
7766	17616	27844	2.13	7.0E-64	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
1692	11594	21463	1.7	6.0E-64	AI651992.1	EST_HUMAN	w651e07.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1692	11594	21464	1.7	6.0E-64	AI651992.1	EST_HUMAN	w651e07.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3084	13011	22801	3.7	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'
3084	13011	22802	3.7	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'
5454	15375	25433	2.64	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5454	15375	25434	2.64	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5464	15384	25444	4.41	6.0E-64	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
6293	16157	26312	2.58	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
6293	16157	26313	2.58	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7376	17245	27451	7.8	6.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
7472	17332	27538	2.06	6.0E-64	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
7604	17455	27669	2.34	6.0E-64	S76475.1	NT	trkC [human, brain, mRNA, 2715 nt]
8151	18039	28287	7.57	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
8151	18039	28288	7.57	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
9262	18967	25321	4.06	6.0E-64	11526198	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
803	10732	20574	2.44	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
803	10732	20575	2.44	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1402	11307	21167	2.42	5.0E-64	IL40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1402	11307	21168	2.42	5.0E-64	IL40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1683	11585	21457	1.67	5.0E-64	U89356.1	NT	Human I(3)mbt protein homolog mRNA, complete cds
2766	11370	21235	2.66	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2796	11370	21236	2.66	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3876	13787	23575	5.61	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
8188	18074	28324	3.9	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
8188	18074	28325	3.9	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
2151	12039	21936	3.85	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-569E02 5'
3216	13140	22943	0.95	3.0E-64	BE794381.1	EST_HUMAN	601589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
3396	13313	23112	1.51	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3396	13313	23113	1.51	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
5703	15611	25713	1.34	3.0E-64	Z26273.1	NT	H. sapiens isoform 1 gene for L-type calcium channel, exon 28
5911	15817	25942	3.39	3.0E-64	BF70000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6933	16811	27005	1.81	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
6933	16811	27006	1.81	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
6946	16824	27016	1.3	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
6946	16824	27017	1.3	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
7422	17289	27497	1.26	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7422	17289	27498	1.26	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8565	18434	28703	1.76	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8565	18434	28704	1.76	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8938	18746	29040	4.59	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1072	10983	20831	0.94	2.0E-64	AA069940.1	EST_HUMAN	af09cd08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1376	11282	21137	1.32	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA
2478	12354		1.78	2.0E-64	AI927030.1	EST_HUMAN	w087b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element ;
2484	12359	22252	3.03	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2484	12359	22253	3.03	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3101	13027	22823	2.56	2.0E-64	4504068	NT	Homo sapiens glutamic-oxalacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
3719	13631	23416	1.33	2.0E-64	AW958145.1	EST_HUMAN	EST1370215 MAGe resequences, MAGe Homo sapiens cDNA
3719	13631	23417	1.33	2.0E-64	AW958145.1	EST_HUMAN	EST1370215 MAGe resequences, MAGe Homo sapiens cDNA
5653	15565	25662	2.62	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5783	15689	25799	1.3	2.0E-64	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
5906	15812	25938	4.97	2.0E-64	BF668537.1	EST_HUMAN	602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5'
5976	15880	26004	1.31	2.0E-64	AJ078387.1	EST_HUMAN	oz29503.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676717 3'
6024	15928	26060	3.96	2.0E-64	M77185.1	NT	H.sapiens dopamine receptor D5 pseudogene 1, partial cds
8144	18032	28279	2.85	2.0E-64	BF528114.1	EST_HUMAN	602042882F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180556 5'
8406	18282	28534	6.4	2.0E-64	AJ922811.1	EST_HUMAN	wn81b06.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2452211 3'
8406	18282	28535	6.4	2.0E-64	AJ922911.1	EST_HUMAN	wn81b06.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2452211 3'
9182	18921	25347	1.73	2.0E-64	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
9617	19195		2.68	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
258	10224	20039	1.74	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1740	11641	21508	5.88	1.0E-64	AJ929419.1	EST_HUMAN	au60501.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb.L21696_cds1 PROTHYMOSIN ALPHA (HUMAN);contains element MSR1 repetitive element ;
3466	13382	23188	5.61	1.0E-64	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
3536	13452	23248	1.32	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3536	13452	23249	1.32	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
9154	18904		1.62	1.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2230	12115	22017	0.93	9.0E-65	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2230	12115	22018	0.93	9.0E-65	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
8822	18635		15.1	9.0E-65	BF330676.1	EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
8799	18613	28903	10.83	8.0E-65	AJ929244.1	EST_HUMAN	au66h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21. ;
7841	17691	27936	2.05	7.0E-65	BE081653.1	EST_HUMAN	QV2-BT0635-240400-162-e02 BT0635 Homo sapiens cDNA
1040	10958	20801	1.52	6.0E-65	AV721898.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC06 5'
1880	11776		8.32	6.0E-65	AA550929.1	EST_HUMAN	ij86d10.s1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:998379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
7080	18957	27150	2.52	6.0E-65	AW083252.1	EST_HUMAN	xc07b09.x1 NCL_CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q63306 Q63306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF's. ;contains L1.b2 L1 repetitive element ;
7209	17086	27275	4.25	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
7209	17086	27276	4.25	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
8247	18127	28375	6.18	6.0E-65	BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
8787	18602	28692	4.76	6.0E-65	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
615	10551	20362	0.91	5.0E-65	AF064604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1331	11238	21094	1.62	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1331	11238	21095	1.62	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2110	11999	21898	1.02	5.0E-65	AB033768.1	NT	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
3217	13141	22944	1.91	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3217	13141	22945	1.91	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
186	10158	19975	1.09	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108.5
728	10660	20491	1.56	4.0E-65	AI286498.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2NbpP8to9W Homo sapiens cDNA clone IMAGE:1891800.3
728	10660	20492	1.56	4.0E-65	AI286498.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2NbpP8to9W Homo sapiens cDNA clone IMAGE:1891800.3
1062	10978	20822	1.88	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1470	11375	21240	8.28	4.0E-65	4506636	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2288	12171	22068	1.03	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102.3
2288	12171	22069	1.03	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102.3
5138	15005	24775	0.95	4.0E-65	9065269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI), mRNA
5138	15005	24776	0.95	4.0E-65	9065269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI), mRNA
5740	15648	25754	3.93	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
5740	15648	25755	3.93	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6285	16149	26304	2.29	4.0E-65	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
8020	17870		2.17	4.0E-65	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8446	18320	28579	7.47	4.0E-65	AF119946.1	NT	Homo sapiens PRO1474 mRNA, complete cds
9471	10978	20822	1.34	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
9975	19434	25152	1.58	4.0E-65	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
1212	12646		5.37	3.0E-65	X79932.1	NT	H. sapiens HZF9 mRNA for zinc finger protein
1780	11679	21557	1.14	3.0E-65	AI000692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173.3 similar to contains element
3239	13162	22962	1.39	3.0E-65	4504950	NT	MSR1 repetitive element;
3660	13574	23361	0.98	3.0E-65	AI000692.1	EST_HUMAN	Homo sapiens laminin, beta 1 (LAMB1), mRNA
4551	14444	24228	1.41	3.0E-65	6912385	NT	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173.3 similar to contains element
7793	17643	27876	1.43	3.0E-65	BE787366.1	EST_HUMAN	MSR1 repetitive element;
							Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
							601479686F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405.5

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Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8693	17877	28119	9.69	3.0E-65	AA430008.1	EST_HUMAN	zw65a06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
3358	13277	23078	5.27	2.0E-65	BF680294.1	EST_HUMAN	602155062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295966 5'
5938	15843		4.55	2.0E-65	BE263373.1	EST_HUMAN	601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534741 5'
6233	16099	26247	23.12	2.0E-65	BF576922.1	EST_HUMAN	602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5'
7133	17010	27202	1.27	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ000356 protein, partial cds
7133	17010	27203	1.27	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ000356 protein, partial cds
8048	17939	28189	2.85	2.0E-65		NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA
9109	18874		4.15	2.0E-65	AA307904.1	EST_HUMAN	EST T178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to endogenous retrovirus
9580	19504		2.37	2.0E-65	BF246086.1	EST_HUMAN	601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'
85	10069		1.06	1.0E-65	BF125544.1	EST_HUMAN	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
528	10470	20282	1.32	1.0E-65	7657495	NT	Homo sapiens putative Rab5 GTP/GTP exchange factor homologue (RABEX5), mRNA
1994	11898	21781	0.91	1.0E-65	AB040945.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3326	13246	23052	0.89	1.0E-65	BE466681.1	EST_HUMAN	hz24a09.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:3208888 3'
3917	13826	23606	2.13	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
3917	13826	23607	2.13	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
4112	14012	23789	2.37	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4112	14012	23790	2.37	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
6802	16681	26670	1.58	1.0E-65	AW820481.1	EST_HUMAN	QV2-S T0298-140200-042-f12 ST0298 Homo sapiens cDNA
6802	16681	26671	1.58	1.0E-65	AW820481.1	EST_HUMAN	QV2-S T0298-140200-042-f12 ST0298 Homo sapiens cDNA
6842	16721	26614	2.38	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
6842	16721	26615	2.38	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
7132	17009	27201	1.76	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
7215	17092	27282	1.62	1.0E-65	AU129040.1	EST_HUMAN	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
7215	17092	27283	1.62	1.0E-65	AU129040.1	EST_HUMAN	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
7222	17099		2.83	1.0E-65	11431994	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 1 (ITPR1), mRNA
7456	17265	27469	6	1.0E-65	A191716.1	EST_HUMAN	qd56a02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M29581 ZINC FINGER PROTEIN 8 (HUMAN); contains MER19.1 MER19 repetitive element;
7687	17537	27763	1.25	1.0E-65	AU153793.1	EST_HUMAN	AU153793 NT2RP3 Homo sapiens cDNA clone NT2RP3004016 3'
8042	17933	28181	2.23	1.0E-65	M26167.1	NT	Human platelet factor 4 variation 1 (PF4var1) gene, complete cds
8158	18046	28298	12.99	1.0E-65	4506660	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
8473	18346	28610	2.18	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8542	18414	28681	2.35	1.0E-65	AI621017.1	EST_HUMAN	ts76a06.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb:L15533_ma1 PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
9155	18905		2.27	1.0E-65	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
9254	18963	25318	4.85	1.0E-65	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
9665	19225		1.44	1.0E-65	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
65	10051	19864	1.51	9.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
65	10051	19865	1.51	9.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
1332	11239	21096	2.49	9.0E-66	5031990	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1332	11239	21097	2.49	9.0E-66	5031990	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1468	11373		4.18	9.0E-66	M87299.1	NT	Human transposon-like element, partial
3826	13738	23529	0.9	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3826	13738	23530	0.9	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4591	14479	24266	0.88	8.0E-66	AA424304.1	EST_HUMAN	z60c05.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:767048 5'
8654	18543		1.73	7.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
4269	14168	23944	1.22	6.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A OE18595 ;
4269	14168	23945	1.22	6.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A OE18595 ;
4269	14168	23946	1.22	6.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A OE18595 ;
8499	18372	28636	7.07	6.0E-66	X69181.1	NT	H. sapiens mRNA for ribosomal protein L31
1344	11250	21107	2.25	5.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
7357	17225	27424	12.31	5.0E-66	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
773	10703	20542	0.79	4.0E-66	6679816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
2235	12120	22022	1.94	4.0E-66	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2425	12302		3.66	4.0E-66	AJ223364.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4674	14560		5.15	4.0E-66	9635487	NT	Human endogenous retrovirus, complete genome
5407	15326	25376	3.35	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cyclohydrolase (MTHFD2), mRNA
5512	15430	25494	1.78	4.0E-66	AW939119.1	EST_HUMAN	QV1-DT0069-110200-067-g10 DT0069 Homo sapiens cDNA
6056	15106	24869	4.71	4.0E-66	AW965473.1	EST_HUMAN	EST377546 IMAGE resequences, MAGI Homo sapiens cDNA
6232	16098	26246	6.89	4.0E-66	U78168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
6708	16588	26776	6.38	4.0E-66	11421638	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8052	17943	28193	1.96	4.0E-66	BF507493.1	EST_HUMAN	UI-H-BW1-emr-a-10-UJ st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070747 3'
1408	11313	21175	24.62	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1408	11313	21176	24.62	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1939	11834	21717	0.84	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612;
1939	11834	21718	0.84	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612;
1939	11834	21719	0.84	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612;
2675	12540	22430	2.91	3.0E-66	11141880	NT	Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA
3079	13006	22797	5.47	3.0E-66	7662223	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
5528	15445	25511	1.64	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5528	15445	25512	1.64	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
8800	18614	28804	8.3	3.0E-66	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
45	10033	19837	1.02	2.0E-66	7657334	NT	Homo sapiens Missshapen/NIK-related kinase (MINK), mRNA
45	10033	19838	1.02	2.0E-66	7657334	NT	Homo sapiens Missshapen/NIK-related kinase (MINK), mRNA
416	9983	19774	0.93	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
416	9983	19775	0.93	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1784	11692	21560	2.02	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2944	12871	22669	0.95	2.0E-66	X65859.1	NT	H. sapiens pseudogene for the low affinity IL-8 receptor
3975	13862	23657	0.86	2.0E-66	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
4556	14448	24233	12.69	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4556	14448	24234	12.69	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
7135	17012	27205	2.16	2.0E-66	N45480.1	EST_HUMAN	yz59c02.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:277826 5'
9475	19712	27205	2.22	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
2864	12792	22585	1.38	1.0E-66	AV717817	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
2864	12792	22586	1.38	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4288	12792	22585	3.26	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4288	12792	22586	3.26	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5306	15227	25031	5.36	1.0E-66	BF673088.1	EST_HUMAN	602152966F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294151 5'
6143	15991	26126	1.49	1.0E-66	BF328623.1	EST_HUMAN	RC5-BN0193-010900-034-G06 BN0193 Homo sapiens cDNA
6926	16804	26998	1.37	1.0E-66	AA688868.1	EST_HUMAN	aa0604.s1 NCI_OGAP_GCB1 Homo sapiens cDNA clone IMAGE:827262 3'
8312	18189	28438	2.39	1.0E-66	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9260	18965		2.09	9.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
4829	14711		0.84	8.0E-67	M78158.1	EST_HUMAN	EST01750 Subtracted Hippocampus, Striatum (cat. #836205) Homo sapiens cDNA clone HHCPN31 similar to L1 repetitive element
376	10360	20184	6.19	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1360	11266	21122	2.63	7.0E-67	AA383416.1	EST_HUMAN	EST96812 Testis 1 Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK353
1535	11439	21296	1	7.0E-67	W85947.1	EST_HUMAN	zh566005.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1535	11439	21297	1	7.0E-67	W85947.1	EST_HUMAN	zh566005.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1988	11881	21773	1.06	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-trisphosphate 5/6 kinase (ITPK1), mRNA
1988	11881	21774	1.06	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-trisphosphate 5/6 kinase (ITPK1), mRNA
2779	10360	20184	7.07	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
5793	15699	25807	2.04	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
5793	15699	25808	2.04	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
9039	18826	29111	1.56	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9039	18826	29112	1.56	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9501	19116	25292	3.33	7.0E-67	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9868	19357		1.43	7.0E-67	11421527	NT	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA
547	10488	20297	1.32	6.0E-67	X68998.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
778	10708	20547	1.5	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1252	11159	21008	0.93	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3,4,5,6 & 7
3131	13056	22856	1.24	6.0E-67	4506434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3391	13308	23106	1.2	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3391	13308	23107	1.2	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4035	13938	23714	1.28	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4035	13938	23715	1.28	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4607	14495	24283	3.37	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4607	14495	24284	3.37	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5125	14761		2.1	6.0E-67	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3184	13109	22913	2.45	5.0E-67	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8352	18229		2.1	5.0E-67	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1306	11213	21089	1.83	4.0E-67	R90819.1	EST_HUMAN	yr02d11.11 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167263 5'
6883	16762		1.22	4.0E-67	BF357321.1	EST_HUMAN	RC0-HT0934-150900-026-c03 HT0934 Homo sapiens cDNA
8416	18290		2.3	4.0E-67	AA714294.1	EST_HUMAN	hw06a01.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385
2782	10553	20365	0.93	3.0E-67	AA333378.1	EST_HUMAN	PRO-POL-DUTPASE POLYPROTEIN;
3407	13324	23125	1.14	3.0E-67	BE064410.1	EST_HUMAN	EST37903 Embryo, 9 week Homo sapiens cDNA 5' end
4596	14484	24270	3.14	3.0E-67	AW669159.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
6760	16639	26827	1.22	3.0E-67	BF196068.1	EST_HUMAN	MR3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA
8583	18451		19.27	3.0E-67	AA927874.1	EST_HUMAN	h81105.x1 NCL_CGAP Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
180	10152	19987	1.94	2.0E-67	BE346354.1	EST_HUMAN	Q61085 GTP-RHO BINDING PROTEIN 1;
827	10754	20604	6	2.0E-67	AW815405.1	EST_HUMAN	om18b07.s1 Soares_NFL_I_GBG_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
1089	11005		1.74	2.0E-67	AF167480.1	NT	hw16g09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9
1841	11737	21614	1.5	2.0E-67	BE303037.1	EST_HUMAN	CE09617;
1841	11737	21615	1.5	2.0E-67	BE303037.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
2336	12216	22116	0.98	2.0E-67	AF309561.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
2381	12261	22153	1.2	2.0E-67	4758795	NT	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892
3422	13339	23144	3.9	2.0E-67	AA625755.1	EST_HUMAN	KIAA0798 PROTEIN;
3921	13830	23610	2.33	2.0E-67	AL163300.2	NT	Homo sapiens KRAB zinc finger protein ZFOR mRNA, complete cds
5724	15631	25734	4.22	2.0E-67	BF240758.1	EST_HUMAN	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
5803	15708	25820	2.17	2.0E-67	AB051763.1	NT	z191g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
5803	15708	25821	2.17	2.0E-67	AB051763.1	NT	Homo sapiens chromosome 21 segment HS21C100
7202	17079	27264	1.34	2.0E-67	AW602635.1	EST_HUMAN	6018/5351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
7202	17079	27265	1.34	2.0E-67	AW602635.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
8409	19769		3.26	2.0E-67	11436448	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
8558	18428	28698	1.77	2.0E-67	BE295714.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
8751	17900	28144	2.26	2.0E-67	BF377169.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
9388	19577	25069	2.6	2.0E-67	11418189	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
							601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
							PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
							Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
253	10219	20036	4.37	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2129	12017	21915	2.46	8.0E-68	BE870732.1	EST_HUMAN	601448598F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3862254 5'
3794	13706	23492	4.96	8.0E-68	AA209456.1	EST_HUMAN	z682h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC_Q07590 SAV PROTEIN.;
3794	13706	23493	4.96	8.0E-68	AA209456.1	EST_HUMAN	z682h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC_Q07590 SAV PROTEIN.;
1849	11745		2.2	6.0E-68	AW503842.1	EST_HUMAN	U1HF-BN0-alb-c-07-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
7971	17821	28094	2.46	6.0E-68	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
8489	18362	28627	1.93	6.0E-68	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
9676	19234		1.42	6.0E-68	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
9918	19391	25178	1.36	6.0E-68	BF310675.1	EST_HUMAN	601894635F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124144 5'
785	12642	20555	0.87	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
785	12642	20556	0.87	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
802	10731	20572	3.87	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
802	10731	20573	3.87	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3108	13034	22830	2.62	5.0E-68	AB037852.1	NT	Homo sapiens chromosome 21 unknown mRNA
2480	12356	22247	1.01	4.0E-68	11421388	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
2480	12356	22248	1.01	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
4900	14780		17.24	4.0E-68	P04406	SWISSPROT	Homo sapiens transcription factor NRF (NRF), mRNA
6061	16044	26188	5.64	4.0E-68	11055991	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6061	16044	26189	5.64	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7225	17102	27290	5.41	4.0E-68	D63479.2	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7225	17102	27291	5.41	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
7295	17171	27371	2.39	4.0E-68	AB040918.1	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
3611	13525	23312	5.61	3.0E-68	AF236082.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
7441	16454		4.44	3.0E-68	A1342323.1	EST_HUMAN	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
7997	17847	28088	1.45	3.0E-68	F28784.1	EST_HUMAN	q38h02.x1 Sceres_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains THR 42 THR repetitive element;
9872	19502		1.53	3.0E-68	AW939485.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
2832	15076		12.26	2.0E-68	D00822.1	NT	QV1-DT0072-010200-056-h06 DT0072 Homo sapiens cDNA
4583	14473	24261	1.66	2.0E-68	AB008681.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
6110	16004		8	2.0E-68	R45088.1	EST_HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6202	15962	26095	4.79	2.0E-68	BF035316.1	EST_HUMAN	601458514F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862034 5'
9148	19731		1.92	2.0E-68	BE897376.1	EST_HUMAN	601437367F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922192 5'
72	10056	19873	1.31	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
293	10257	20078	9.36	1.0E-68	AW816405.1	EST_HUMAN	QV4-S10234-181169-037-005 ST0234 Homo sapiens cDNA
2205	12092	21994	1.32	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2205	12092	21995	1.32	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2728	12590	22486	1.01	1.0E-68	AW451832.1	EST_HUMAN	U1-H-B13-alk-f-01-Q-U1 s1 NCL_OGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3'
3928	13837	23617	0.95	1.0E-68	BE296032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
4954	14831	24588	0.98	1.0E-68	AA887343.1	EST_HUMAN	al47g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
5261	15183	24959	1.57	1.0E-68	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
8226	18108	28361	2.44	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
8226	18108	28362	2.44	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
8275	18155	28396	2.29	1.0E-68	L76416.1	NT	Homo sapiens MIF2 suppressor (HSMT3) mRNA, complete cds
9659	10056	19873	1.95	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
9862	19669	24991	1.38	1.0E-68	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
19	10006	19797	1.82	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
19	10006	19798	1.82	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1011	10929	20772	1.63	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1011	10929	20773	1.63	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4037	13940	23718	0.78	9.0E-69	4757867	NT	Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
8263	18143		9.27	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000968 5'
3340	13260		1.21	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
5834	15740	25852	6.08	7.0E-69	9966912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
6589	16469	26659	3.61	6.0E-69	AI192764.1	EST_HUMAN	qe62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
6589	16469	26660	3.61	6.0E-69	AI192764.1	EST_HUMAN	qe62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
509	10451		1.88	4.0E-69	AI873630.1	EST_HUMAN	wm28h11.x1 NCL_OGAP_U14 Homo sapiens cDNA clone IMAGE:2437125 3'
5565	15481	25554	4.12	4.0E-69	AI764973.1	EST_HUMAN	wh57b06.x1 NCL_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:O55137 O55137 ACYL-COA THIOESTERASE.;
5995	15900	26024	2.43	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
5995	15900	26025	2.43	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
390	10364	20187	2.81	3.0E-69	BE258012.1	EST_HUMAN	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
596	10532	20340	1.64	3.0E-69	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1536	11440		1.35				yd08a02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24890 5' similar to SP-A48836
2325	12206		0.88	3.0E-69	T80514.1	EST_HUMAN	A48836 SPEGF III=EGF REPEAT-CONTAINING FIBROPELIN-LIKE PROTEIN - SEA URCHIN ;
3990	13897	23674	0.86	3.0E-69	5729910	NT	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
5209	15087	29105	5.94	3.0E-69	A1768988.1	EST_HUMAN	wh68g08.r1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385758 3'
6387	16249	26410	1.37	3.0E-69	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6457	16318	26485	8.43	3.0E-69	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neuregulin (CTNND2) mRNA, partial cds
7091	19968		1.26	3.0E-69	AF268075.1	NT	Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds
7417	17284	27491	1.54	3.0E-69	AA376399.1	EST_HUMAN	EST8807 HSC172 cells II Homo sapiens cDNA 5' end similar to ribosomal protein S18
7493	17363	27568		3.0E-69	X13223.1	NT	H. sapiens mRNA for N-acetylglucosamide-(beta 1-4)-galactosyltransferase
8036	17928	28174	2.24	3.0E-69		NT	H. sapiens mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
8215	18099		3.07	3.0E-69	X06233.1	NT	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
9168	18911		7.12	3.0E-69	11432120	NT	EST8807 HSC172 cells II Homo sapiens cDNA 5' end similar to ribosomal protein S18
124	10344	20170	4.13	3.0E-69	AA976399.1	EST_HUMAN	Homo sapiens HGO6.2 protein (HGO6.2), mRNA
124	10344	20171	1	2.0E-69	11419157	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
398	10344	20170	1	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
398	10344	20171	4.94	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1842	11738	21616	4.94	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
2813	12742		1.2	2.0E-69	BE257857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
1675	15177	21445	2.73	2.0E-69	AA431157.1	EST_HUMAN	zw71g02.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781682 5'
5981	16886	26008	2.35	1.0E-69	AF053768.1	NT	Ratfus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
6080	16063	26211	3.68	1.0E-69	AW393969.1	EST_HUMAN	QV0-TT0010-031199-045-c07 TT0010 Homo sapiens cDNA
6080	16063	26212	1.55	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6088	16033	26173	1.55	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6088	16033	26174	2.93	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7847	17697	27942	2.93	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7847	17697	27943	5.29	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
8246	18126		5.29	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
9105	18872	28785	23.27	1.0E-69	4504918	NT	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
			1.53	1.0E-69	BE125887.1	EST_HUMAN	Homo sapiens keratin 8 (KRT8) mRNA
			1.53	1.0E-69	BE125887.1	EST_HUMAN	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9510	19124		2.32	1.0E-69	AI809994.1	EST_HUMAN	wf64e08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2284	12717	22065	1.52	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
4277	14176	23954	2.16	8.0E-70	L77566.1	NT	Homo sapiens DGS-I mRNA, 3' end
1771	11670	21547	1.93	7.0E-70	AI497807.1	EST_HUMAN	tm89f01.x1 NCL_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1771	11670	21548	1.93	7.0E-70	AI497807.1	EST_HUMAN	tm89f01.x1 NCL_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1888	11784	21660	1.63	7.0E-70	AA282955.1	EST_HUMAN	zt15h04.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
2018	11909		3.57	7.0E-70	5031688	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4132	14032	23807	3.86	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5369	15289	25124	5.28	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5369	15289	25125	6.28	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6138	15985	26120	1.89	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
6910	16788	26980	2.36	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
6910	16788	26981	2.36	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
7063	16940	27131	3.98	7.0E-70	MT4099.1	NT	Human displacement protein (GCAAT) mRNA
7063	16940	27132	3.98	7.0E-70	MT4099.1	NT	Human displacement protein (GCAAT) mRNA
7283	17159	27357	3.72	7.0E-70	X59841.1	NT	Human PBX3 mRNA
7283	17159	27358	3.72	7.0E-70	X59841.1	NT	Human PBX3 mRNA
7428	16441	26627	3.13	7.0E-70	AF163715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
7445	16457	26648	1.56	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
7445	16457	26649	1.56	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
8875	18687	28978	1.78	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
8875	18687	28979	1.78	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
853	10780	20630	1.93	6.0E-70	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2090	11979	21874	1.36	6.0E-70	M50938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2461	12338	22232	0.99	6.0E-70	8923899	NT	Homo sapiens GMP-N-acetylneuraminic acid synthase (LOC55907), mRNA
2505	12723	22268	1.83	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2505	12723	22269	1.83	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
9116	18879		1.73	5.0E-70	BE166034.1	EST_HUMAN	MF3-HT0487-150200-115-a06 HT0487 Homo sapiens cDNA
1571	11475	21332	0.89	3.0E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
1571	11475	21333	0.89	3.0E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5845	15751	25865	3.88	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
5845	15751	25866	3.88	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
674	10608	20426	13.15	2.0E-70	N42161.1	EST_HUMAN	y07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
674	10608	20427	13.15	2.0E-70	N42161.1	EST_HUMAN	y07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
689	10622	20449	2.01	2.0E-70	AI246899.1	EST_HUMAN	qx51h01.x1 NCJ_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1004	10922	20766	1.7	2.0E-70	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1167	11079	20924	1.95	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1167	11079	20925	1.95	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1387	11292	21148	0.97	2.0E-70	BE467311.1	EST_HUMAN	hz64c12.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3212768 3'
1708	11609	21479	2.09	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2272	12156		3.62	2.0E-70	AA054010.1	EST_HUMAN	zf48g04.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
3963	13870	23648	3.95	2.0E-70	M69181.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
5385	15304	25156	8.05	2.0E-70	X72862.1	NT	H.sapiens gene for schwannomin (CS8)
5385	15304	25157	8.05	2.0E-70	X72862.1	NT	H.sapiens gene for schwannomin (CS8)
5766	15673	25780	1.42	2.0E-70	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
5999	15904	26028	1.88	2.0E-70	D12625.1	NT	Human mRNA for NFT protein isoform (neurofibromin isoform), complete cds
6010	15915	26042	9.83	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6010	15915	26043	9.83	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6177	15134	24853	1.69	2.0E-70	11422642	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
6618	16498	26685	7.67	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
7835	17685	27930	1.3	2.0E-70	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
8422	18296	28550	3.19	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
8422	18296	28551	3.19	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
8908	18716	29010	5.82	2.0E-70	4503520	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6) mRNA
9499	19114	25289	2.58	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9499	19114	25290	2.58	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9347	13267		2.97	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
7642	17492		2.57	1.0E-70	AA442292.1	EST_HUMAN	zv54c03.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757444 5'
8305	18182	28429	13.73	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLGB10 5'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5621	15536	25621	6.04	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045 O14045 PHOSPHOTRANSFERASE.;
5621	15536	25622	6.04	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045 O14045 PHOSPHOTRANSFERASE.;
6192	16077	26226	1.88	9.0E-71	AI654903.1	EST_HUMAN	wb52c05.x1 NCI_CGAP_G03 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.;
8811	16077	26226	4.65	9.0E-71	AI654903.1	EST_HUMAN	wb52c05.x1 NCI_CGAP_G03 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.;
7245	17122		1.97	8.0E-71	AA171451.1	EST_HUMAN	zp21df1.1r1 Strategene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL.;
6363	16226	26386	7.91	7.0E-71	AA442230.1	EST_HUMAN	zv60n06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:798075 5' z91a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
7037	16914	27103	1.52	7.0E-71	AA705457.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
8643	18507	28786	4.18	7.0E-71	AL163210.2	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
2163	12050	21951	3.45	5.0E-71	AF056322.1	NT	QV4-ST0234-181199-037-005 ST0234 Homo sapiens cDNA w18h10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425315 3'
4030	13933	23710	1.38	5.0E-71	AW816405.1	EST_HUMAN	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
5144	15011	24782	3.2	5.0E-71	AI829496.1	EST_HUMAN	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
5586	15501	25577	2.14	5.0E-71	4502740	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
6434	16295	26457	1.59	5.0E-71	M38106.1	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
6548	16406	26555	19.78	5.0E-71	AF072810.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
7702	17552		2.26	5.0E-71	X13467.1	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
8348	18225	28477	1.9	5.0E-71	11436514	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC83325), mRNA
8528	18400	28698	2	5.0E-71	11438069	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9067	18848	29116	1.84	5.0E-71	11417862	NT	Homo sapiens RNA binding motif protein 9 (RBM9), mRNA
9411	19063		1.62	5.0E-71	11418039	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
97	10082	19899	1.13	4.0E-71	4507592	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
347	10306	20123	115.63	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
347	10306	20124	115.63	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2850	12778	22566	0.88	4.0E-71	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2850	12778	22567	0.88	4.0E-71	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2857	12785	22575	1.63	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4330	14227	24009	3.35	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4913	14792	24567	4.99	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOUJ), mRNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8077	17968	28218	3.32	3.0E-71	AA557683.1	EST_HUMAN	n145h10.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element;
1210	11119	20968	2.52	2.0E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5259	15181	24957	6.96	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5259	15181	24958	6.96	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
8022	17872	28114	2.56	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
8022	17872	28115	2.56	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
8079	17970	28219	2.3	2.0E-71	BE018477.1	EST_HUMAN	bb81a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048764 5' similar to SW-R23B_HUMAN P54727 UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG B;
9181	18920		6.22	2.0E-71	T95489.1	EST_HUMAN	ye43c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120520 5'
622	10559	20371	2.11	1.0E-71	A1077927.1	EST_HUMAN	oy15e03.s1 Soares senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:166509 16 3' similar to contains LOR1.b2 LOR1 repetitive element;
926	10851	20699	1.93	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1084	11000	20841	4.01	1.0E-71	AF205930.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1317	11224	21080	10.59	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
2036	11927	21821	1.23	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2036	11927	21822	1.23	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2661	12528	22416	4.85	1.0E-71	7657153	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3457	13373	23179	1.17	1.0E-71	AF119665.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3546	13462	23256	4.73	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3546	13462	23257	4.73	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3597	13511	23298	0.94	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3597	13511	23299	0.94	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3681	13595	23381	1.87	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
4370	14266	24050	1.86	1.0E-71	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
6044	15947	26079	1.4	1.0E-71	11428182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
6326	16189	26351	10.62	1.0E-71	U80753.1	NT	Homo sapiens CAGL79 mRNA, partial cds
6750	16629	26816	6.96	1.0E-71	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
6916	16794	26986	4.18	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6916	16794	26987	4.18	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
7748	17598	27820	6.49	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
7792	17642		3.39	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
8164	18052		4.87	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
8256	18136	28383	3.2	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII, A1, polypeptide (F13A1), mRNA
8486	18359	28623	2.33	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
8486	18359	28624	2.33	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
9547	19147		4.48	1.0E-71	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
401	10347	20173	1.15	9.0E-72	AB57635.1	EST_HUMAN	wk5903.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN, ; contains Alu repetitive element;
401	10347	20174	1.15	9.0E-72	AB57635.1	EST_HUMAN	wk5903.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN, ; contains Alu repetitive element;
4023	13926	23700	5.23	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4023	13926	23701	5.23	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4023	13926	23702	5.23	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
6228	16094	26244	2.94	7.0E-72	S41694.1	NT	{pseudogene} PTMAP2=prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
6885	16764		3.72	6.0E-72	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8788	18603	28893	2.22	6.0E-72	BF059578.1	EST_HUMAN	7k63a05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480080 3' similar to SW:KMLC_RABIT
56	10043	19854	0.88	5.0E-72	BF333707.1	EST_HUMAN	P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE ;
56	10043	19855	0.88	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
57	10043	19854	2.95	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
57	10043	19855	2.95	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1122	11037		2.76	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
6150	16023	26163	1.47	5.0E-72	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
7097	16974	27167	3.55	5.0E-72	AW161274.1	EST_HUMAN	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to TR:Q99785 Q99785 HYPOTHETICAL 32.4 KD PROTEIN ; contains element MSR1 repetitive element ;
8569	18437	28706	3.18	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA
8569	18437	28707	3.18	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA
9253	19700		2.43	5.0E-72	BE926645.1	EST_HUMAN	QV1-BT0632-280800-342-e10 BT0632 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4716	14602		1.06	4.0E-72	11034844	NT	Homo sapiens hypothetical protein dJ1057B20.2 (D.J1057B20.2), mRNA
6380	16242	26402	1.4	4.0E-72	5729697	NT	Homo sapiens hec domain and RLD 2 (HERC2), mRNA
7633	17484	27705	1.42	4.0E-72	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
8815	18628	28917	7.32	4.0E-72	H79421.1	EST_HUMAN	yJ28a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5'
8929	18737	29030	2.76	4.0E-72	T81910.1	EST_HUMAN	yJ29d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109649 3'
9603	19185	25249	4.2	4.0E-72	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
885	10811		4.88	3.0E-72	AA723823.1	EST_HUMAN	af63a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1310290 3'
1139	11053	20894	6.06	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1139	11053	20895	6.06	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
3037	12965	22759	10.51	3.0E-72	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3241	13164	22963	2.63	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3750	13663	23445	2.51	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha = T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction) {human, precursor B-cell line REH, mRNA Partial, 211 nt}
4445	14339	24129	3.22	3.0E-72	11416196	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
4835	14717	24500	0.94	3.0E-72	AI654337.1	EST_HUMAN	wb31a08.x1 NCJ_OGAP_GC6 Homo sapiens cDNA clone IMAGE:2307264 3'
5639	15552	25643	2.4	3.0E-72	AF073397.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
5639	15552	25644	2.4	3.0E-72	AF073397.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
5743	15651	25758	4.35	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
5743	15651	25759	4.35	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
5988	15893	26016	3.02	3.0E-72	4826987	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
6475	16334	26501	2.32	3.0E-72	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
6755	16834	26822	1.26	3.0E-72	5031892	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
7960	17810	28051	1.3	3.0E-72	X99289.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
9516	19129	25262	1.85	3.0E-72	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
8122	18010	28257	4.45	2.0E-72	AA789277.1	EST_HUMAN	aj28b09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb:U02067 H sapiens mRNA for 7SL RNA pseudogene (HUMAN);
9600	19182	25246	3.74	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds
2030	11921	21812	2.61	1.0E-72	AA846225.1	EST_HUMAN	af83d02.s1 Soares_parathyroid_tumor_NbHFA Homo sapiens cDNA clone IMAGE:1387395 3'
5524	15441	25506	3.15	1.0E-72	7657676	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
5949	15854	25976	19.78	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5949	15854	25977	19.78	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6501	16360	26533	3.82	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
6501	16360	26534	3.82	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
7532	17383	27594	6.06	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
7532	17383	27595	6.06	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1443	11348	21213	1.23	9.0E-73	AW374968.1	EST_HUMAN	MR0-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA
8320	18197		23.9	9.0E-73	11424099	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1022	10939	20782	1.03	8.0E-73	AW071755.1	EST_HUMAN	ws55c06.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q59050
1399	11304	21163	3.06	8.0E-73	A024877.1	EST_HUMAN	Q59050 HYPOTHETICAL PROTEIN MJ1656. ;
5959	15864	25986	4.6	8.0E-73	11426469	NT	o139h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639743 3'
6716	16595	26785	2	8.0E-73	AF113129.1	NT	Homo sapiens lyszyme homolog (LOC57151), mRNA
							Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
7385	17254	27459	15.88	8.0E-73	BE019900.1	EST_HUMAN	bb62a05.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
7614	17465	27682	2.22	8.0E-73	11528037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
7614	17465	27683	2.22	8.0E-73	11528037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
9446	19081	26282	2.12	8.0E-73	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
9654	19217	25235	2.69	8.0E-73	11418189	NT	Homo sapiens thyrold autoantigen 70kD (Ku antigen) (G22P1), mRNA
1118	11033	20875	0.78	7.0E-73	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3261	13184	22983	1.06	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4863	14743		1.62	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
152	10126		2.37	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
6255	16121	26274	3.36	6.0E-73	BE166574.1	EST_HUMAN	QV0-HT0494-020300-137-d03 HT0494 Homo sapiens cDNA
5215	15138	24832	2.05	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM44A1), mRNA
1818	11715	21595	0.99	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1818	11715	21596	0.99	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
833	10760	20610	1.75	2.0E-73	AF139897.1	NT	Homo sapiens BASST (BASS1) mRNA, partial cds
1902	11798		1.48	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
2251	12135		1.1	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3144	13069	22869	3.48	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3503	13420	23221	0.96	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3503	13420	23222	0.96	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
5902	15908	25933	7.6	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1691 protein, partial cds
6023	15927	26058	1.35	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6023	15927	26059	1.35	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7956	17906	28048	1.34	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
7993	17943	28085	2.45	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
7993	17943	28086	2.45	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
8138	18026	28272	4.14	2.0E-73	11431598	NT	Homo sapiens KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 (KIAA1080), mRNA
8408	18284	28537	3.79	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
8408	18284	28538	3.79	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
8432	18306	28562	1.78	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
9447	11798		1.72	2.0E-73	AW598081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
1743	11644	21512	1.57	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
2434	12311	22207	0.93	1.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2), mRNA, complete cds
7469	17329	27534	1.36	1.0E-73	AI147427.1	EST_HUMAN	qg61b07.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839637 5' similar to contains element
8747	17896	28140	2.67	1.0E-73	BE385477.1	EST_HUMAN	MER22 repetitive element ;
723	10655	20485	1.39	8.0E-74	4557426	NT	601276071F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617105 5'
5606	15521	25602	1.84	8.0E-74	S83194.1	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
5606	15521	25603	1.84	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
1906	11801	21679	3.01	7.0E-74	AJ001699.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
3286	13207	23007	0.99	7.0E-74	AL163246.2	NT	Homo sapiens NKGD2 gene, exon 10
7327	17231	27432	2	7.0E-74	BE967432.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
9653	19216	25234	2.81	7.0E-74	BE266305.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3932997 5'
1106	11022	20865	2.58	6.0E-74	AF109907.1	NT	601649284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3535855 5'
1809	11514	21373	1.03	6.0E-74	AW263177.1	EST_HUMAN	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
2268	12152	22050	9.96	6.0E-74	BE388260.1	EST_HUMAN	xn78g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700636 3'
2268	12152	22051	9.96	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2834	12762	22553	1.39	6.0E-74	AW014039.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2834	12762	22554	1.39	6.0E-74	AW014039.1	EST_HUMAN	UI-H-B10-aah-h-03-0-U1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3652	13566	23352	2.63	6.0E-74	BE048846.1	EST_HUMAN	UI-H-B10-aah-h-03-0-U1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3652	13566	23353	2.63	6.0E-74	BE048846.1	EST_HUMAN	h54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5294	15215	25016	2.49	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
887	10813	20661	2.58	5.0E-74	AW020986.1	EST_HUMAN	d17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2669	12534		5.19	5.0E-74	AW362756.1	EST_HUMAN	PM0-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA
5320	15240	25045	2.15	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5539	15456	25526	10.48	5.0E-74	X89670.1	NT	H. sapiens mRNA for TPCR16 protein
5563	15479	25552	6.74	5.0E-74	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
5602	15516	25594	1.85	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
5602	15516	25595	1.85	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6120	16014	26152	3.73	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6684	16564	26758	2.69	5.0E-74	11345463	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
8117	18006	28252	1.88	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
8117	18006	28253	1.88	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
278	10243	20063	1.89	4.0E-74	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
834	10761	20611	4.95	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1919	11814	21692	2.44	4.0E-74	AB026988.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1919	11814	21693	2.44	4.0E-74	AB026988.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2027	11918	21808	4.34	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2027	11918	21809	4.34	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2085	11975	21870	1.21	4.0E-74	AB032994.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2377	12257	22149	0.99	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3052	12979	22772	4.44	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3483	13399	23204	0.93	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3973	13680	23655	1.31	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4457	14351	24142	1.57	4.0E-74	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4512	14405	24192	0.82	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5006	14880	24644	3.76	4.0E-74	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
5006	14880	24645	3.76	4.0E-74	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
6977	18854		5.03	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37

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Table 4
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7394	17312	27519	2.42	3.0E-74	M78984.1	EST_HUMAN	ES T01132 Subtracted Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCFF91
7921	17771	28010	2.22	3.0E-74	AA001493.1	EST_HUMAN	no17905.s1 NCL_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100984 3'
942	10867	20714	126.24	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
942	10867	20715	126.24	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1158	11071	20916	1.01	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K_T47D
1224	11132	20986	1.16	2.0E-74	AI950528.1	EST_HUMAN	wx51e07.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-96; contains element MER22 repetitive element;
1577	11481	21340	2.94	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1577	11481	21341	2.94	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2558	12430	22323	1.09	2.0E-74	AI557280.1	EST_HUMAN	PT2.1_15_G11.r.tumor2 Homo sapiens cDNA 3'
4937	14815	24582	1.95	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
4937	14815	24583	1.95	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
4942	14820	24588	1.89	2.0E-74	J02963.1	NT	Human platelet glycoprotein IIb mRNA, 3' end
5543	19446	25530	1.84	2.0E-74	BE711134.1	EST_HUMAN	RC6-HT0878-220500-011-C03 HT0878 Homo sapiens cDNA
5594	19448	25584	1.98	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
5594	19448	25585	1.98	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
5629	19448	25584	2.57	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
5629	19448	25585	2.57	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
6219	16085	26235	1.55	2.0E-74	BF030788.1	EST_HUMAN	601557524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'
6631	16511	26700	1.43	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
7398	17316	27523	6.54	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9387	19047		1.46	2.0E-74	AA199181.1	EST_HUMAN	zp96a06.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'
9903	19380	25196	1.26	2.0E-74	BF666588.1	EST_HUMAN	602121428F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278559 5'
47	10035	19841	0.97	1.0E-74	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
334	10293	20108	3.6	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
491	10434	20247	1.19	1.0E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
497	10439	20252	2.7	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
586	10524	20331	1.35	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
983	10906	20751	2.17	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2179	12066	21968	6.19	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM1, complete cds
3100	13026	22822	5.96	1.0E-74	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3887	13798	23584	4.56	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
3974	13881	23656	0.9	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270300-019-06 BT0642 Homo sapiens cDNA
4170	14070	23845	0.9	1.0E-74	BE487769.1	EST_HUMAN	h273h08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:B0511.12
5112	14980	24754	1.19	1.0E-74	D83327.1	NT	CE17351 ;
6894	16574	26765	1.83	1.0E-74	BE549105.1	EST_HUMAN	Homo sapiens DCRR1 mRNA, partial cds
6894	16574	26766	1.83	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
7112	16989	27182	3.92	1.0E-74	AF214562.1	NT	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
7988	17838	28079	1.31	1.0E-74	11420549	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
9024	18818	29108	1.6	1.0E-74	11417856	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA
9106	18873		2.83	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
9249	12066	21968	4.14	1.0E-74	AB020209.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9720	19261		1.36	1.0E-74	AF240786.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
2607	12476		4.07	8.0E-75	AF176228.1	NT	Homo sapiens chromosome 21 segment HS21C002
9406	19059		1.67	8.0E-75	AL163202.2	NT	wk38a08.x1 NCL_CGAP_P122 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4
2273	12157	22055	0.88	6.0E-75	AI817415.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
5128	14995		0.86	6.0E-75	AA789285.1	EST_HUMAN	aj28c06.s1 Soares_testis NHT Homo sapiens cDNA clone 1391626 3' similar to TR:Q15377 Q15377 Y-
5102	14970	24746	1.04	5.0E-75	BE841305.1	EST_HUMAN	CHROMOSOME RNA RECOGNITION MOTIF PROTEIN ;
7395	17313	27520	1.22	5.0E-75	BF690254.1	EST_HUMAN	MRO-SN0040-080600-006-g06 SN0040 Homo sapiens cDNA
							602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'
7876	17726	27969	3.1	5.0E-75	AI638623.1	EST_HUMAN	t31c12.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361
107	10088	19903	1.05	4.0E-75	BE081333.1	EST_HUMAN	HYPOTHETICAL 20.1 KD PROTEIN ;
451	10395		1.23	4.0E-75	N36757.1	EST_HUMAN	QV1-BT0632-210200-079-e02 BT0632 Homo sapiens cDNA
1728	11629	21498	1.5	4.0E-75	AW897230.1	EST_HUMAN	ye00h08.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:269055 5'
2818	12747	22540	4.65	4.0E-75	BE409464.1	EST_HUMAN	GM0-NN0057-150400-335-e11 NN0057 Homo sapiens cDNA
5792	15698	25806	4.29	4.0E-75	5579457	NT	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
6052	15953	25084	1.56	4.0E-75	11417946	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (110KD) (EIF3S8), mRNA
6052	15953	25085	1.56	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
8072	17963	28214	8.72	4.0E-75	7669505	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
986	10909	20754	2.91	3.0E-75	AF157623.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
987	10909	20754	2.25	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1795	11693	21569	1.98	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2065	11955	21852	1.05	3.0E-75	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
2373	12253	22144	3.96	3.0E-75	4759153	NT	Homo sapiens synaptosomal-associated protein, 26kD (SNAP29) mRNA
2988	12916	22711	1.19	3.0E-75	AL183201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3152	13077	22877	1.33	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3306	13227	23030	1.01	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3306	13227	23031	1.01	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4077	13979	23759	1.42	3.0E-75	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4336	14233	24015	0.96	3.0E-75	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
6058	16041	26183	1.53	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6058	16041	26184	1.53	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6234	16100	26248	3.83	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6234	16100	26249	3.83	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6494	16363	26522	2.92	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
6494	16363	26523	2.92	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7193	17070	27259	1.23	3.0E-75	11420804	NT	Homo sapiens snail 1 (drosophila homolog), zinc finger protein (SNAIL), mRNA
5480	15400		1.5	2.0E-75	AV734680.1	EST_HUMAN	AV734680 cDNA Homo sapiens cDNA clone cdABED02 5'
7082	16959	27152	1.73	2.0E-75	AI311783.1	EST_HUMAN	cd91e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915888 3' similar to TR:Q689386 Q689386 POL/ENV GENE ;
2255	12139	22037	5.09	1.0E-75	AW168135.1	EST_HUMAN	xg60d02.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2832707 3' similar to contains PTR7.11
2916	12843	22644	3.17	1.0E-75	X52221.1	EST_HUMAN	PTR7 repetitive element ;
						NT	H.sapiens ERCC2 gene, exons 1 & 2 (partial)
6903	16781		4.13	1.0E-75	AA399270.1	EST_HUMAN	zfs7h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726485 3' similar to gb:U13632 40S
7423	17290	27499	3.73	1.0E-75	BF313645.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN);
7423	17290	27500	3.73	1.0E-75	BF313645.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
8257	18137		3.99	1.0E-75	AA664377.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
						EST_HUMAN	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
8441	18315	28573	2.6	1.0E-75	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9299	15100	24892	1.86	1.0E-75	BE894192.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
38	10026	19825	1.45	9.0E-76	AI652648.1	EST_HUMAN	w630b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
38	10026	19826	1.45	9.0E-76	AI652948.1	EST_HUMAN	wb30b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
2364	12244		1.16	9.0E-76	AA702415.1	EST_HUMAN	285b07.st Soares_fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:447541 3'
7697	17547	27770	23.8	9.0E-76	M12937.1	NT	Human ferritin Heavy subunit mRNA, complete cds
923	10848	20695	1.69	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
923	10848	20696	1.69	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2880	12807	22603	1.06	8.0E-76	7706724	NT	Homo sapiens mediator (Sur2), mRNA
5744	15652	25760	5.38	8.0E-76	11421442	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
6421	16282	26443	1.3	8.0E-76	11435215	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
8057	17948	28198	6.44	8.0E-76	10442821	NT	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA
9636	19207		1.44	8.0E-76	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
							Homo sapiens dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
759	10689	20527	4.12	7.0E-76	5016092	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3254	13177	22975	2.64	7.0E-76	AF066490.1	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3260	13183	22982	7.08	7.0E-76	4505052	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3293	13215	23017	1.1	7.0E-76	4757915	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4275	14174	23951	4.3	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4275	14174	23952	4.3	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1214	11122		19.65	6.0E-76	BE396263.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
8761	17910	28154	2.69	6.0E-76	BE273201.1	EST_HUMAN	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5'
1899	11795	21673	3.69	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1899	11795	21674	3.69	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1899	11795	21675	3.69	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
7759	17609	27834	5.6	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujiwara) Homo sapiens cDNA clone GEN-178G01 5'
7759	17609	27835	5.6	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujiwara) Homo sapiens cDNA clone GEN-178G01 5'
613	10549	20359	1.78	3.0E-76	BF516262.1	EST_HUMAN	UI-H-BW1-anz-b-04-0-UJ.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
613	10549	20360	1.78	3.0E-76	BF516262.1	EST_HUMAN	UI-H-BW1-anz-b-04-0-UJ.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1581	11485	21345	2.78	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1581	11485	21346	2.78	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3382	13300	23099	4.18	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3382	13300	23100	4.18	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
5204	15084	29104	9.13	3.0E-76	Z41314.1	EST_HUMAN	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zq04 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5842	15748	25861	7.85	3.0E-76	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
6737	16616	26806	1.92	3.0E-76	N42671.1	EST_HUMAN	y20g10.r1 Soares melanocyte 2Nbr-IM Homo sapiens cDNA clone IMAGE:271842 5'
7602	17453	27667	3.2	3.0E-76	AW299553.1	EST_HUMAN	xs49h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773009 3'
7615	17466	27684	1.32	3.0E-76	AA442309.1	EST_HUMAN	zv54df11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
7615	17466	27685	1.32	3.0E-76	AA442309.1	EST_HUMAN	zv54df11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
9014	19337	25062	2.13	3.0E-76	AW967984.1	EST_HUMAN	EST380059 MAGE resequenes, MAGJ Homo sapiens cDNA
9120	19745	24895	3.75	3.0E-76	AW96455.1	EST_HUMAN	EST368525 MAGE resequenes, MAGD Homo sapiens cDNA
280	10245	20065	1.22	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
339	10298	20112	3.66	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
339	10298	20113	3.66	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
453	10397		2.17	2.0E-76	4557662	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
575	10513	20320	1.07	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1014	10932	20778	1.03	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1518	11423	21281	1.53	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1518	11423	21282	1.53	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1886	11782	21658	1.43	2.0E-76	AA253954.1	EST_HUMAN	zs60ht11.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
2611	12740	22536	2.83	2.0E-76	P23266	SW/ISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN F5
3257	13180	22979	2.01	2.0E-76	AA445992.1	EST_HUMAN	zv64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;
3257	13180	22980	2.01	2.0E-76	AA445992.1	EST_HUMAN	zv64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
4043	10245	20065	0.94	2.0E-76	D84295.1	NT	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;
4867	14747	24527	6.33	2.0E-76	AW879618.1	EST_HUMAN	Human mRNA for possible protein TPRDII, complete cds
5068	14938	24710	1.25	2.0E-76	5031660	NT	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
5453	15374	25432	4.74	2.0E-76	AB029004.1	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
6518	16377	26554	1.79	2.0E-76	11427410	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7898	17748	27988	3.28	2.0E-76	11437211	NT	Homo sapiens TPCR86 protein (HSTPCR86P), mRNA
8293	18172	28416	2.76	2.0E-76	7549807	NT	Homo sapiens similar to ribosomal protein S26 (H_sapiens) (LOC63150), mRNA
4200	14100	23881	2.18	1.0E-76	D63874.1	NT	Homo sapiens HIRA interacting protein 4 (dnauJ-like) (HIRIP4), mRNA
4200	14100	23882	2.18	1.0E-76	D63874.1	NT	Human mRNA for HMGC-1, complete cds
5345	15266	25093	5.29	1.0E-76	BE796537.1	EST_HUMAN	Human mRNA for HMGC-1, complete cds
6137	15984	26119	3.98	9.0E-77	BE889525.1	EST_HUMAN	601598896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
4421	14315	24101	1.65	8.0E-77	BF205181.1	EST_HUMAN	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
							601866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5347	15268	25095	2.46	8.0E-77	4506230	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7) mRNA
8691	18578	28861	2.12	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
8691	18578	28862	2.12	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
9771	19289	25232	7.25	8.0E-77	R00245.1	EST_HUMAN	ye69104.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element ;
1867	11783	21659	3.28	7.0E-77	AA625755.1	EST_HUMAN	zu191g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2360	12240	22136	2.1	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2360	12240	22137	2.1	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
262	10227	20043	4.29	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1125	11040	20882	0.9	6.0E-77	AW957753.1	EST_HUMAN	EST369823 MAGE resequences, MAGE Homo sapiens cDNA
1524	11429	21287	17.64	6.0E-77	AI204068.1	EST_HUMAN	qe77h12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
1216	11124	20973	1.78	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1337	11243	21101	1.16	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2736	12598	22492	0.97	5.0E-77	4503180	NT	Homo sapiens cullin 1 (CUL1) mRNA
4605	14493	24280	2.02	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
4605	14493	24281	2.02	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
4853	14733	24514	2.05	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G1728 5'
6873	16752	26947	1.39	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyl-Coenzyme A hydrolase (HIBCH), mRNA
6873	16752	26948	1.39	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyl-Coenzyme A hydrolase (HIBCH), mRNA
7519	17338	27543	2.55	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
7519	17338	27544	2.55	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
7990	17840	28080	1.96	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
7990	17840	28081	1.96	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
1929	11824	21705	1.12	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1929	11824	21706	1.12	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
8249	18129	28377	3.31	3.0E-77	BF355917.1	EST_HUMAN	PM3-MT0078-08080-005-g03 MT0078 Homo sapiens cDNA
1330	11237	21093	1.71	2.0E-77	AV764617.1	EST_HUMAN	AV764617 MDS Homo sapiens cDNA clone MDSBT10 5'
1414	11320	21185	1.73	2.0E-77	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
2044	11935	21830	0.84	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2056	11946	21842	2.64	2.0E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2549	12724	22312	2.02	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2549	12724	22313	2.02	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3947	13855	23629	1.33	2.0E-77	BE044316.1	EST_HUMAN	hc43b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4315	14212	23995	0.89	2.0E-77	AI613519.1	EST_HUMAN	tw22g02.x1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245 O65245 F21E10.7 PROTEIN ;
4315	14212	23996	0.89	2.0E-77	AI613519.1	EST_HUMAN	tw22g02.x1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245 O65245 F21E10.7 PROTEIN ;
4492	14386		3.48	2.0E-77	4504088	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4659	14515	24334	3.58	2.0E-77	AA653025.1	EST_HUMAN	ns89g12.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29, [1] ; contains element MSR1 repetitive element ;
5625	15540	25629	1.8	2.0E-77	BE298940.1	EST_HUMAN	601119552F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5'
5745	15653	25761	1.34	2.0E-77	BE787143.1	EST_HUMAN	601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
6257	16123	26276	12.74	2.0E-77	AB33003.1	EST_HUMAN	at74a09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311 Q13311 TAX1-BINDING PROTEIN TXBP151, [1] ;
7489	17359	27564	4.99	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
7489	17359	27565	4.99	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
37	10024	19821	0.97	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
37	10024	19822	0.97	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
271	10237	20054	1.87	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
271	10237	20055	1.87	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
857	12679	20635	4.95	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
857	12679	20636	4.95	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2394	12272	22168	1.22	1.0E-77	AB029024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3007	12935	22727	2.82	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4256	14155	23630	2.99	1.0E-77	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
4423	14317	24103	14.73	1.0E-77	AJ229041.1	NT	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3
4552	14445	24229	1.95	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
5179	15043	24810	2.89	1.0E-77	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5

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Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5610	15525	25607	1.93	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5610	15525	25608	1.93	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5688	15597	25698	1.56	1.0E-77	M25844.1	NT	Human von Willebrand factor gene, exon 20
6197	15957	26089	11.39	1.0E-77	5881412	NT	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
8002	17852	28093	1.22	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
8002	17852	28094	1.22	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
8013	17863	28109	2.53	9.0E-78	AW753302.1	EST_HUMAN	RC3-CT0254-280999-011-b05 CT0254 Homo sapiens cDNA
5880	15786	25907	2.97	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
5880	15786	25908	2.97	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
80	10064	19881	1.83	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
80	10064	19882	1.83	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
5950	15855		2.51	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFR1), mRNA
211	10182	19996	1.1	5.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2515	12389	22281	4.1	5.0E-78	AW673424.1	EST_HUMAN	ba64h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP:Y48B6A.6
3339	13289	23066	3.81	5.0E-78	M55586.1	NT	Human collagenase type IV (CLG4) gene, exon 6
5323	15243	25048	2.39	5.0E-78	AF038536.1	NT	Homo sapiens Best's macular dystrophy related protein mRNA, partial cds
5422	15343	25396	9.35	5.0E-78	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
6244	16110	26262	2.17	5.0E-78	AW953120.1	EST_HUMAN	EST365190 MAGE resequences, MAGB Homo sapiens cDNA
7248	17125	27318	6.5	5.0E-78	U60889.1	NT	Human lysosomal alpha-mannosidase (manB) gene, exon 7
7249	17126	27319	3.75	5.0E-78	BE960836.1	EST_HUMAN	601648061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3331887 5'
1502	11406	21265	1.6	4.0E-78	AL355841.1	NT	Novel human gene mapping to chromosome 22
1629	11533	21393	1.53	4.0E-78	A1985094.1	EST_HUMAN	wf97b12.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2495615 3' similar to SW:WAP_PIG
2270	12154	22053	2.21	4.0E-78	AF17405.1	NT	O46655 WHEY ACIDIC PROTEIN PRECURSOR ;
4227	14125	23899	1.39	4.0E-78	7656876	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4664	14550	24340	1.27	4.0E-78	4505806	NT	Homo sapiens synectin (LOC00816), mRNA
4664	14550	24341	1.27	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase catalytic, alpha polypeptide (PIK4CA) mRNA
7967	17817	28058	1.94	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
7967	17817	28059	1.94	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
8721	18538	28822	1.97	4.0E-78	AF169148.1	NT	Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds
8844	18656	28944	3	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
9664	19224	26239	2.85	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
155	10129	19944	1.6	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
155	10129	19945	1.6	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
3178	13103	22908	0.91	3.0E-78	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
4015	13657	23439	0.93	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
7902	17752		5.56	3.0E-78	BE144758.1	EST_HUMAN	QMO-HT0180-047099-065-c07 HT0180 Homo sapiens cDNA
8349	18226	28478	5.52	3.0E-78	BE156318.1	EST_HUMAN	QVO-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
3083	13010		2.22	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
3932	13841		1.68	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
6412	16274	26435	1.46	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BK0-aaj-g-10-Q-UJ.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
6412	16274	26436	1.46	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BK0-aaj-g-10-Q-UJ.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
6547	16405	26584	3.88	2.0E-78	BF689800.1	EST_HUMAN	602186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298599 5'
6887	16567	26761	2.73	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DC8 Homo sapiens cDNA clone DGBAWF09 5'
6921	16799	26991	1.84	2.0E-78	AI557509.1	EST_HUMAN	P2.1.16 B07.r tumor2 Homo sapiens cDNA 3'
6921	16799	26992	1.84	2.0E-78	AI557509.1	EST_HUMAN	P2.1.16 B07.r tumor2 Homo sapiens cDNA 3'
8429	18303	28559	4.5	2.0E-78	AI197837.1	EST_HUMAN	q150h05.x1 NCI_GGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859961 3' similar to WP.R90.1
8467	18340	28605	3.28	2.0E-78	N69551.1	EST_HUMAN	CE06325 PROTEIN KINASE ;
5247	15170	24943	2.9	1.0E-78	11417304	NT	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
6743	16622		1.68	1.0E-78	U52373.1	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
9189	18924	25350	5.14	1.0E-78	11430460	NT	Human serine/threonine kinase MNB (mnb) mRNA, complete cds
							Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9284	18986	25327	1.26	1.0E-78	11435903	NT	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC63140), mRNA
4600	14488	24274	4.48	9.0E-79	11525891	NT	Homo sapiens peptide YY (PYY), mRNA
4758	14643	24431	2.48	9.0E-79	BE000837.1	EST_HUMAN	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
5335	15255	25078	12.03	9.0E-79	AB028070.1	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
5927	15733	25844	2.18	9.0E-79	5454145	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
7243	17120	27315	4.99	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
7243	17120	27316	4.99	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
7953	17803	28042	1.31	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
7953	17803	28043	1.31	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
8419	18293	28547	1.82	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds
8902	18616	28906	2.82	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
8902	18616	28907	2.82	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
9954	19347	25213	1.49	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3682	13596	23382	1.2	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4391	14287	24069	0.94	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4391	14287	24070	0.94	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
9107	15097	24899	1.4	8.0E-79	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
3214	13138	22941	6.85	7.0E-79	BE619648.1	EST_HUMAN	601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'
9040	18827		1.29	6.0E-79	AA989829.1	EST_HUMAN	z194e04.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
8786	18601	28691	4.15	5.0E-79	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3139	13064		1.12	4.0E-79	8922325	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
4046	14823	24690	1.33	4.0E-79	BF210869.1	EST_HUMAN	601874622F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101245 5'
310	10272	20091	1.4	3.0E-79	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
962	10885	20733	2.88	3.0E-79	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cln) gene, complete cds
3060	12987	22778	1.36	3.0E-79	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5291	15212	25012	4.52	3.0E-79	AF110322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5506	15424	25486	1.71	3.0E-79	AB020099.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5525	15442	25507	3.47	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
5525	15442	25508	3.47	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
6200	15960	26091	3.28	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
6200	15960	26092	3.28	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
618	10555	20367	1.05	2.0E-79	BE379926.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
912	10836	20685	1.14	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1019	10937		1.43	2.0E-79	A1523747.1	EST_HUMAN	th18f07.x1 NCL CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2118685 3'
2101	11990	21888	14.14	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2101	11990	21889	14.14	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2146	12034	21931	0.99	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2265	12149	22049	1.54	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
3838	13749	23542	0.86	2.0E-79	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
4074	13976	23755	1.17	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4590	14478	24265	0.96	2.0E-79	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
6251	16117	26270	1.83	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6251	16117	26271	1.83	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6956	16834	27029	2.6	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
7808	17658	27896	1.44	2.0E-79	S72896.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
7808	17658	27897	1.44	2.0E-79	S72896.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8391	18267	28516	4.22	2.0E-79	BE064366.1	EST_HUMAN	RC4-BT0310-110300-075-f10 BT0310 Homo sapiens cDNA
8391	18267	28517	4.22	2.0E-79	BE064366.1	EST_HUMAN	RC4-BT0310-110300-075-f10 BT0310 Homo sapiens cDNA
9078	15096	24888	2.6	2.0E-79	7682357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
9161	18907	25341	4.23	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
9391	19050	25307	1.96	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
5971	19486		2.78	1.0E-79	BF363071.1	EST_HUMAN	MRO-NN0087-260600-077-b10 NN0087 Homo sapiens cDNA
8694	18704	28998	2.74	1.0E-79	BF087405.1	EST_HUMAN	QV2-HIT0540-120900-358-a05 HT0540 Homo sapiens cDNA
3107	13033	22828	3.79	9.0E-80	AA725848.1	EST_HUMAN	ai23a05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3107	13033	22829	3.79	9.0E-80	AA725848.1	EST_HUMAN	ai23a05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
7751	17601	27824	1.28	9.0E-80	BE798603.1	EST_HUMAN	601581652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936061 5'
8597	18464	28735	11.05	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
8597	18464	28736	11.05	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
3551	13466		0.95	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
6485	16343	26512	2.83	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
6485	16343	26513	2.83	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7409	17276	27482	1.19	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7409	17276	27483	1.19	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
882	10808	20657	2.34	6.0E-80	A1422197.1	EST_HUMAN	tf58d02.x1 NCI_OGAP_Brn23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN
1624	11528	21386	2.05	6.0E-80	U64898.1	NT	Q16795 NADH+UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
4188	14088	23865	1.09	6.0E-80	AB032981.1	NT	Homo sapiens NRD convertase mRNA, complete cds
4188	14088	23866	1.09	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
5545	15461	25532	4.01	6.0E-80	11421462	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
5702	15610	25712	2.56	6.0E-80	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
5776	15683	25791	3.84	6.0E-80	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7123	17000	27191	3.07	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
7123	17000	27192	3.07	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
7214	17091	27281	1.74	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
7672	17522	27748	1.68	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
8311	18188	28437	2.91	6.0E-80	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8555	18425	28694	50.71	6.0E-80	AF226730.1	NT	Homo sapiens Cyt19 mRNA, complete cds
9047	10808	20657	1.98	6.0E-80	AI422197.1	EST_HUMAN	tf65d02.x1 NCI_LGAP_Brn23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16796 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
9172	19592		1.82	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9371	19037		4.55	6.0E-80	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9847	19696		2.25	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium glucose cotransporter (SGLT2 gene)
573	10511	20319	1.11	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
817	10745	20592	1.26	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
817	10745	20593	1.26	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1172	11084		4.77	5.0E-80	X91647.1	NT	H.sapiens nrx1 gene (exon 12)
1440	11345		2.28	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2380	12192	22091	0.92	5.0E-80	U89358.1	NT	Human (3)mbt protein homolog mRNA, complete cds
2764	12626	22518	1.13	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
3953	13861	23636	1.07	5.0E-80	AB019038.1	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
3953	13861	23637	1.07	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4872	14762	24531	1.74	5.0E-80	AL163268.2	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
6866	16745	26938	1.48	5.0E-80	9910293	NT	Homo sapiens chromosome 21 segment HS21C068
7333	17237	27441	7.48	4.0E-80	F25915.1	EST_HUMAN	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
210	10181		4.71	3.0E-80	AL163210.2	NT	HSPD13155 HM3 Homo sapiens cDNA clone s4000045F03
4610	14498	24287	1.43	3.0E-80	BF085009.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
4818	14701		4.97	3.0E-80	BE817465.1	EST_HUMAN	PMO-GN0018-040900-002-E03 GN0018 Homo sapiens cDNA
5554	15470	25541	2.05	3.0E-80	A1091675.1	EST_HUMAN	QV4-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA
1757	11656	21527	6.39	2.0E-80	R35921.1	EST_HUMAN	0023e12.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1567054 3' similar to TR:O35790 O35790 PIG-L ;
1816	11713	21593	1.91	2.0E-80	AI444821.1	EST_HUMAN	TR:O35790 O35790 PIG-L ;
2009	11901	21791	6.6	2.0E-80	AL043116.2	EST_HUMAN	y965a08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:38060 5'
6132	15979	28115	1.58	2.0E-80	11421930	NT	RE14B7 subtracted retina cDNA library/Homo sapiens cDNA clone RET4B7
8243	18123	28373	3.06	2.0E-80	AA393362.1	EST_HUMAN	DKFZp434D1323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1323 5'
337	10296		1.82	1.0E-80	AL163303.2	NT	Homo sapiens Golgi transport complex protein (90 kDa) (GTC90), mRNA
782	10712	20551	1.12	1.0E-80	AF231920.1	NT	z170f12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G191315
						EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN ;
						NT	Homo sapiens chromosome 21 segment HS21C103
						NT	Homo sapiens chromosome 21 unknown mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1911	11806		3.13	1.0E-80	A1732656.1	EST_HUMAN	nm0112.x5 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 OFR repetitive element ;
4358	14254	24039	0.96	1.0E-80	AF077188.1	NT	Homo sapiens culin 4A (CUL4A) mRNA, complete cds
5192	15055	24819	0.97	1.0E-80	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5265	15187		5.63	1.0E-80	BE386615.1	EST_HUMAN	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5'
5633	15547	25635	6.41	1.0E-80	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
5916	15822	25947	1.6	1.0E-80	5174540	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
6470	16329	26496	2.68	1.0E-80	A1948731.1	EST_HUMAN	wq25c05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
6470	16329	26497	2.68	1.0E-80	A1948731.1	EST_HUMAN	wq25c05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
7350	17218	27417	1.23	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
7350	17218	27418	1.23	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
7957	17807	28049	1.19	1.0E-80	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
8044	17935	28183	7.42	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
8044	17935	28184	7.42	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
9443	19079	25281	1.45	1.0E-80	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
9643	19211	25268	1.86	1.0E-80	AB020840.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
9670	19229		1.99	1.0E-80	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
8071	17962	28212	2.33	8.0E-81	A1251752.1	EST_HUMAN	qh90g05.x1 Scarses NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3'
8071	17962	28213	2.33	8.0E-81	A1251752.1	EST_HUMAN	qh90g05.x1 Scarses NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3'
8494	18367	28631	4.95	8.0E-81	BE394825.1	EST_HUMAN	601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
6300	16164	26321	3.06	7.0E-81	A1822115.1	EST_HUMAN	za91c08.x5 Scarses fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299918 3'
4290	14188	23971	4.84	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4290	14188	23972	4.84	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5229	15153	24920	1.93	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5229	15153	24921	1.93	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7325	17201	27401	1.34	6.0E-81	AA360017.1	EST_HUMAN	EST69129 Fetal lung II Homo sapiens cDNA 5' end
9879	19166	25269	1.82	6.0E-81	BF679022.1	EST_HUMAN	602153366F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294801 5'
9879	19166	25270	1.82	6.0E-81	BF679022.1	EST_HUMAN	602153366F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294801 5'
2170	12057	21960	3.14	5.0E-81	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
6901	16780	26974	3.47	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
6901	16780	26975	3.47	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8865	18677	28966	2.51	5.0E-81	9506634	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
214	10185	19998	0.87	4.0E-81	AF252257.1	NT	Homo sapiens CRP2 binding protein mRNA, partial cds

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1779	11678	21556	0.99	4.0E-81	AW779612.1	EST_HUMAN	hm8d02.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW-COPG_BOVIN
3134	13059	22858	3.79	4.0E-81	AB037766.1	NT	P53620 COATOMER GAMMA SUBUNIT ; Homo sapiens mRNA for KIAA1345 protein, partial cds
3576	13490	23280	1.18	4.0E-81	AW004608.1	EST_HUMAN	ws90h03.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR-O43815 O43815
4068	13970	23746	2.14	4.0E-81	AF263306.1	NT	STRIATIN. ; Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4068	13970	23747	2.14	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
6821	16700	26893	2.15	4.0E-81	X06989.1	NT	Human mRNA for amyloid A4(751) protein
6973	16850	27041	3.4	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
6973	16850	27042	3.4	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
7320	17196	27396	5.65	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein Kinase 2, complete cds
7816	17666	27906	1.49	4.0E-81	11425281	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
8522	18394	28658	2.24	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
8522	18394	28659	2.24	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
9069	19627	25007	3.81	4.0E-81	11417862	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
9069	19627	25008	3.81	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9612	19191	25253	2.52	4.0E-81	11417871	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9612	19191	25254	2.52	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
9750	19275	25228	2.57	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
1246	11153	21000	9.36	3.0E-81	Y18000.1	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1246	11153	21001	9.36	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2320	12201	22100	1.7	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2961	12888	22685	5.12	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2961	12888	22686	5.12	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
4933	14811	22530	0.87	3.0E-81	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2802	12732	22530	1.77	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3877121 5'
2802	12732	22531	1.77	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3877121 5'
3707	13620	23404	0.98	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCL_CGAP_Ki111 Homo sapiens cDNA clone IMAGE:2952384 3'
4579	14469	24256	0.85	2.0E-81	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
9888	13620	23404	1.74	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCL_CGAP_Ki111 Homo sapiens cDNA clone IMAGE:2952384 3'
9898	19375	25194	1.35	2.0E-81	8567387	NT	Homo sapiens perid (Drosophila) homolog 3 (PER3), mRNA
1403	11308	21169	3.32	1.0E-81	W26539.1	EST_HUMAN	33f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3602	13516	23304	2	1.0E-81	AW960688.1	EST_HUMAN	EST372729 MAGC resequences, MAGF Homo sapiens cDNA zk45h09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly ;
4414	14308	24091	3.07	1.0E-81	AA040370.1	EST_HUMAN	
4546	14439	24222	7.85	1.0E-81	BE047596.1	EST_HUMAN	tz45c04.y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2291526 5'
5203	15083	29103	9.03	1.0E-81	U87928.1	NT	Human aconitate hydratase (ACO2) gene, exon 3
5284	15206	24982	4.01	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5284	15206	24983	4.01	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5468	15388	25449	3.54	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds
5468	15388	25450	3.54	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds
5737	15645	25750	3.15	1.0E-81	BF67464.1	EST_HUMAN	602137864F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'
5567	16425	26906	6.4	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
7631	17482	27702	2.62	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
7631	17482	27703	2.62	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
7726	17576	27799	4.81	1.0E-81	BE564367.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885483 5'
7819	17669	27909	2.93	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
7819	17669	27910	2.93	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
8000	17850	28091	1.46	1.0E-81	AW897550.1	EST_HUMAN	CM3-NN0059-140400-147-a12 NN0059 Homo sapiens cDNA
8438	18312	28568	1.96	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
8438	18312	28569	1.96	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
8594	13516	23304	2.42	1.0E-81	AW960688.1	EST_HUMAN	EST372729 MAGC resequences, MAGF Homo sapiens cDNA
8810	18624	28915	1.96	1.0E-81	BF204253.1	EST_HUMAN	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
9278	18981	25325	3.62	1.0E-81	11418138	NT	Homo sapiens phorboln (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
12	9998	19789	1.87	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
101	9998	19789	1.26	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
263	10228	20044	1.66	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
797	10726	20566	2.17	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
869	10795	20645	1.11	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1475	11380	21244	1.12	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1636	11540	21400	1.24	8.0E-82	6715601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4150	14050	23825	0.81	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1434	11339	21339	1.27	7.0E-82	BF036327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
2739	12501	22495	1.82	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
4034	13937	23713	0.81	5.0E-82	AA515512.1	EST_HUMAN	rf69e11.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:925196 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1647	11551	21412	6.51	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
8954	18761	28054	6.47	4.0E-82	A1937300.1	EST_HUMAN	wp75e09.x1 NC1_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:O75276
9519	19130		6.19	4.0E-82	AF029701.2	NT	O75276 PKD1 ;
							Homo sapiens presentin-1 gene, exons 1 and 2
276	10242	20061	13.75	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
687	10620	20446	2.19	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-f02 BN0120 Homo sapiens cDNA
770	10700	20539	4.44	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
852	10779	20629	3.22	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1045	10963		13.76	3.0E-82	AA725948.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
1333	11240	21098	5.47	3.0E-82	AW875073.1	EST_HUMAN	RC6-F10001-190100-021-B02 P10001 Homo sapiens cDNA
1450	11355	21219	2.03	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1859	11755	21630	1.82	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
1961	11855	21744	0.9	3.0E-82	4501922	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (plutary) receptor type 1 (ADCYAP1R1) mRNA
3234	13158		2.06	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
4836	14718	24501	0.91	3.0E-82	AA135979.1	EST_HUMAN	zn93b04.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565711 5' similar to
6738	15617	26807	2.84	3.0E-82	11425206	NT	SW:PAGT_BOVIN Q07537 POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE ;
7654	17504	27728	3.79	3.0E-82	AB029000.1	NT	Homo sapiens enkyrin-like with transmembrane domains 1 (ANKTM1), mRNA
7654	17504	27729	3.79	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
582	10520	20326	1.92	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
582	10520	20327	1.92	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1660	11562	21428	1.75	2.0E-82	AL046390.1	EST_HUMAN	Homo sapiens cDNA clone DKFZp434M117 5'
3772	13684	23466	1.14	2.0E-82	D87675.1	NT	DKFZp434M117_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434M117 5'
4140	14040	23815	1.14	2.0E-82	4504116	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4458	14352	24143	0.98	2.0E-82	AB029019.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4458	14352	24144	0.98	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
							Homo sapiens mRNA for KIAA1096 protein, partial cds
4768	14653	24441	3.18	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSCR5) and wbscr5 (WBSCR6) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5013	14887	24653	1.66	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5013	14887	24654	1.66	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5358	15278	25108	2.37	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
5746	15654	25762	4.96	2.0E-82	AF234882.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
6834	16713	26906	2.23	2.0E-82	11321670	NT	Homo sapiens slt (Drosophila) homolog 3 (SLT3), mRNA
7821	17671	27912	1.2	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
7821	17671	27913	1.2	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
8628	18493	28766	6.98	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
8628	18493	28767	6.98	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
9097	18668		2.23	2.0E-82	N94950.1	EST_HUMAN	z331d10.s1 Soares, parathyroid tumor, NblHPA Homo sapiens cDNA clone IMAGE:305203 3'
9632	19205		2.57	2.0E-82	AA011278.1	EST_HUMAN	z01g09.r1 Soares fetal liver spleen, 1NfLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
9923	19395		1.44	2.0E-82	11418097	NT	Homo sapiens SRY (sex determining region Y)-box 10 (SOX10), mRNA
577	10515	20321	1.45	1.0E-82	11546921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1190	11100		0.9	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1264	11171	21020	1.91	1.0E-82	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1265	11172	21021	0.83	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
7882	17732		1.38	1.0E-82	BF516938.1	EST_HUMAN	UHH-BW1-aca-f03-0-J1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084053 3'
8128	18016	28264	2.57	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8373	18250	28500	1.76	1.0E-82	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7057	16934	27124	4.7	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291561 5'
1392	11297	21155	1.88	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'
1656	12647	21422	1.96	8.0E-83	N66951.1	EST_HUMAN	z648f12.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:296823 3'
2836	12764		1.64	7.0E-83	AA584655.1	EST_HUMAN	nc12h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element;
4710	14596		5.49	7.0E-83	BF221613.1	EST_HUMAN	7p37a07.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y3I6 Q9Y3I6 DJ207H1.1 ;
397	10343	20169	1.34	6.0E-83	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
1747	11647	21515	1.5	6.0E-83	AW573088.1	EST_HUMAN	hf31h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to SW:YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN H10034. ;
2984	12912	22709	1.09	6.0E-83	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
3031	12659	22751	0.94	6.0E-83	AA701457.1	EST_HUMAN	z159cd05.s1 Soares fetal liver spleen_1NfLS_S1 Homo sapiens cDNA clone IMAGE:435080 3'
3515	13431	23231	0.95	6.0E-83	11430241	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5236	15160	24928	1.72	6.0E-83		NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
5669	15579	25679	2.13	6.0E-83	AJ010770.1	NT	Homo sapiens hyperfon gene, exons 1-50
6430	16291	26452	1.79	6.0E-83	11420204	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7579	17430	27644	6.77	6.0E-83	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8817	18630		6.32	6.0E-83	AA486105.1	EST_HUMAN	ab14e10.s1 Siratagene Lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THR repetitive element;
9050	18834		3.11	6.0E-83	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
931	10856		4.14	5.0E-83	U17883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2004	12649		2.1	5.0E-83	AF006305.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3586	13500	23289	0.92	5.0E-83	AL133207.2	NT	Novel human gene mapping to chromosome X
5011	14885	24651	10.99	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5011	14885	24652	10.99	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5094	14964	24739	0.86	5.0E-83	AF083827.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 11
624	10561	20373	1.47	4.0E-83	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3469	13385	23190	0.96	4.0E-83	BE888078.1	EST_HUMAN	601511580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5'
981	10904		4.5	3.0E-83	AA388311.1	EST_HUMAN	EST79542 Placenta I Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
2750	12612		1.82	3.0E-83	AA632664.1	EST_HUMAN	np87c07.s1 NC1_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR12 THR repetitive element;
1759	11658	21529	1.9	2.0E-83	AA983482.1	EST_HUMAN	ot64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216.;
1759	11658	21530	1.9	2.0E-83	AA983482.1	EST_HUMAN	ot64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614
1883	11779	21654	2.23	2.0E-83	N66951.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216.;
2821	12750	22542	1.11	2.0E-83	BE828694.1	EST_HUMAN	zad8f12.s1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
3231	13155		1.82	2.0E-83	11430834	NT	RC6-E10046-280600-013-H12 E10046 Homo sapiens cDNA
3708	13621		1	2.0E-83	AL163202.2	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
4241	14140	23915	4.47	2.0E-83	AF202879.1	NT	Homo sapiens chromosome 21 segment HS21C002
4553	14446	24230	8.13	2.0E-83	7706398	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4553	14446	24231	8.13	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
5359	15279	25109	23.35	2.0E-83	11024711	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
5359	15279	25110	23.35	2.0E-83	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6396	16258	26419	5.9	2.0E-83	AF129533.1	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6539	16539	26736	1.52	2.0E-83	U66707.1	NT	Homo sapiens F-box protein Fbl35 (FBL35) mRNA, partial cds
6839	16718	26911	2.56	2.0E-83	AF011920.1	NT	Rattus norvegicus densin-180 mRNA, complete cds
6839	16718	26912	2.56	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
6839	16718	26912	2.56	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7767	17617	27845	3.32	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
7767	17617	27846	3.32	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
7826	17676	27920	1.21	2.0E-83	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
8223	18105	28358	3.7	2.0E-83	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
8298	18177	28422	1.82	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547J135 5'
8298	18177	28423	1.82	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547J135 5'
9667	19226		3.48	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
1390	11295	21152	16.57	1.0E-83	4504326	NT	Homo sapiens hydroxycy-Coenzyme A dehydrogenase/3-ketocoyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1390	11295	21153	16.57	1.0E-83	4504326	NT	Homo sapiens hydroxycy-Coenzyme A dehydrogenase/3-ketocoyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
2620	12488	22378	1.6	1.0E-83	BE863690.1	EST_HUMAN	801507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908754 5'
3143	13071	22872	0.84	1.0E-83	7682349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
3793	13705	23491	3.55	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4151	14051	23828	2.22	1.0E-83	Z25822.1	NT	H.sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3
4789	14674	24461	1.36	1.0E-83	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
6022	15926	26057	1.75	1.0E-83	AI027614.1	EST_HUMAN	ov69b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM
3727	13639	23425	2.82	7.0E-84	BE901208.1	EST_HUMAN	PROTEIN (HUMAN);
1273	11180	21028	4.21	6.0E-84	BE838884.1	EST_HUMAN	801678023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958863 5'
1273	11180	21029	4.21	6.0E-84	BE838884.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
2348	12228	22125	4.76	6.0E-84	AA776574.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
5206	15085		6.24	6.0E-84	AL042863.2	EST_HUMAN	ae86a03.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
							DKFZp434H0322_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0322 5'
							al47g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338
5388	15307	25180	1.7	6.0E-84	AA897339.1	EST_HUMAN	VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
6415	16277	26440	3.17	6.0E-84	BE810371.1	EST_HUMAN	PM0-LT0019-190600-004-F02 LT0019 Homo sapiens cDNA
6706	16586	26774	1.9	6.0E-84	BE770196.1	EST_HUMAN	PM4-FT0054-160600-004-e10 FT0054 Homo sapiens cDNA
8821	18634		1.94	6.0E-84	AW369812.1	EST_HUMAN	IL0-BT0168-091199-139-e06 BT0168 Homo sapiens cDNA
697	10630	20456	1.06	5.0E-84	AA382811.1	EST_HUMAN	EST196094 Testis I Homo sapiens cDNA 5' end
2981	12808		1.01	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
8830	18643	28926	2.76	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
1354	11260	21116	1.08	4.0E-84	AB037735.1	NT	Homo sapiens mRNA for KIAA1314 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1389	11294	21151	4.03	4.0E-84	AI685321.1	EST_HUMAN	wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN 043847 NARDILYSIN PRECURSOR ;
4869	14749	24529	1.76	4.0E-84	AF096801.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5060	14930	24701	1.27	4.0E-84	U94982.1	NT	Human 2,4-dienoyl-CoA reductase gene, exons 3 and 4
5416	15336	25388	1.31	4.0E-84	11386188	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5416	15336	25389	1.31	4.0E-84	11386188	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5791	15697	25805	2.35	4.0E-84	AF059350.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
6507	16366	26543	12.15	4.0E-84	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
8290	18169	28413	6.56	4.0E-84	AB032956.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
313	10275	20094	1.36	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1137	11051	20891	0.89	3.0E-84	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1917	11812	21690	1.15	3.0E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1962	11856	21745	3.03	3.0E-84	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3542	13458	23251	1.18	3.0E-84	AB023898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3689	13602	23399	4.11	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRSP), mRNA, complete cds
8253	18133		7.8	3.0E-84	AI983801.1	EST_HUMAN	wu20d05.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:L05093.60S RIBOSOMAL PROTEIN L18A (HUMAN);
2058	11948	21845	5.89	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA
2058	11948	21846	5.89	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA
2913	12840	22640	9.55	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
2932	12859	22659	0.93	2.0E-84	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
4682	14568	24364	1.11	2.0E-84	BF308518.1	EST_HUMAN	601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'
4682	14568	24365	1.11	2.0E-84	BF308518.1	EST_HUMAN	601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'
6695	16575		1.67	2.0E-84	AI296674.1	EST_HUMAN	qm87c09.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895728 3'
9308	19003	25334	1.89	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1 ;
9308	19003	25335	1.89	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1 ;
309	10271	20090	1.53	1.0E-84	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN), complete cds
537	10478	20290	5.2	1.0E-84	4507952	NT	Homo sapiens tyrosine 3-monooxygenase/tyrosine 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
703	10636		0.99	1.0E-84	11427631	NT	Homo sapiens complement component 5 (C5), mRNA
1271	11178	21026	1.92	1.0E-84	AA984379.1	EST_HUMAN	am85b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2008	11900	21790	3.13	1.0E-84	BE392137.1	EST_HUMAN	601308006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3628257 5'
2176	12063	21964	1.08	1.0E-84	11427197	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
3691	13605	23391	2.14	1.0E-84	AA720851.1	EST_HUMAN	hw12e06.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
4319	14216	23998	5.59	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4601	14489	24275	3.82	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4601	14489	24276	3.82	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4823	14216	23998	4.29	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
							uterine water channel=28 kda erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
5757	15685	25773	1.52	1.0E-84	S73482.1	NT	
6113	16007	26143	1.49	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
6113	16007	26144	1.49	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
6220	16086	26236	1.96	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
6414	16276	26439	3.12	1.0E-84		NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6483	16324	26490	1.8	1.0E-84	8393994	NT	Homo sapiens NGFLA binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7495	17365		2.45	1.0E-84	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 16) (PP16) mRNA
7639	15091	24884	1.85	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
7639	15091	24885	1.85	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9190	18925		2.98	1.0E-84	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
9298	18998	25330	9.8	1.0E-84	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
951	10875		1.17	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1057	10974	20816	2.3	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1057	10974	20817	2.3	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1560	11485	21322	1.07	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1560	11465	21323	1.07	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1651	11554	21417	4.93	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4158	14058	23832	0.94	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4778	14662	24449	1.14	9.0E-85	5901979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
4825	14707	24491	1.01	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C068
9819	11554	21417	1.27	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
1120	11035	20877	3.24	7.0E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
8910	18718		5.81	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
8718	18535	28819	2.56	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8718	18535	28820	2.56	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2285	12188	22068	1.21	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
8462	18336	28598	1.9	5.0E-85	AF224699.1	NT	Homo sapiens mannosylase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9896	15094		2.45	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I) mRNA, complete cds
5738	15646	25751	1.66	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4249087 5'
5738	15646	25752	1.66	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4249087 5'
8017	17867		1.68	4.0E-85	BE079263.1	EST_HUMAN	RC1-BT0623-120200-071-c07 BT0623 Homo sapiens cDNA
9237	19549		1.97	4.0E-85	Z18867.1	EST_HUMAN	HSDHEGC03 Stratagene cDNA library Human heart, cat#936208 Homo sapiens cDNA clone HEGC03
1277	11185	21035	1.15	3.0E-85	AF096157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1741	11642	21509	3.37	3.0E-85	T97495.1	EST_HUMAN	yes909.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121504 5'
4219	14117	23894	0.94	3.0E-85	BE267189.1	EST_HUMAN	601189704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533616 5'
4805	14689	24475	1.73	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4805	14689	24476	1.73	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4864	14744	24523	8.66	3.0E-85	AB046783.1	NT	Homo sapiens mRNA for KIAA1563 protein, partial cds
4883	14764	24540	0.94	3.0E-85	7363442	NT	Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
5729	15636	25739	6.94	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
5729	15636	25740	6.94	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
6152	16025		7.04	3.0E-85	AJ404488.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
6594	16474	26663	1.61	3.0E-85	U44953.1	NT	Homo sapiens DENN mRNA, complete cds
7190	17067	27256	4.06	3.0E-85	11430899	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
8796	18610	28901	2.28	3.0E-85	5031690	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
9788	19298		2.66	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
947	10871	20719	0.87	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein Mox2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1024	10942	20786	1.85	2.0E-85	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1400	11305	21164	7.1	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1400	11305	21165	7.1	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2163	12070	21972	2.12	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2793	11222		4.24	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
4239	14138	23913	5.42	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4822	14705	24489	1.3	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7341	17209	27408	1.29	2.0E-85	A1760820.1	EST_HUMAN	w167h08.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element
2241	12125		2.44	1.0E-85	BE794306.1	EST_HUMAN	MSR1 repetitive element;
2344	12224	22121	8.09	1.0E-85	BE618392.1	EST_HUMAN	601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2344	12224	22122	8.09	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
7632	17483	27704	2.06	1.0E-85	BE257917.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
8296	18175	28419	2.56	1.0E-85	AA778785.1	EST_HUMAN	601109739F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33505653 5'
8296	18175	28420	2.56	1.0E-85	AA778785.1	EST_HUMAN	z445f03.s1 Scarses_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
8365	18242	28492	2.28	1.0E-85	BF311552.1	EST_HUMAN	z445f03.s1 Scarses_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
8365	18242	28493	2.28	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
9194	19082	25283	2.7	1.0E-85	11417862	NT	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
9448	19082	25283	3.43	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1410	11315		7.66	9.0E-86	BE274217.1	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
920	10190	20001	1.3	7.0E-86	7662247	NT	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
921	10845	20691	1.33	7.0E-86	AA860801.1	EST_HUMAN	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
921	10845	20692	1.33	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Scarses_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
6164	15121	24865	6.91	7.0E-86	11421737	NT	aj88f08.s1 Scarses_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
7078	16955	27148	2.91	7.0E-86	L38557.1	NT	Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
7693	17444		1.63	7.0E-86	5459997	NT	Homo sapiens galactose oxidase (GALO) gene, exon 15
7624	17475	27696	2.35	7.0E-86	11526307	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
8329	18206	28455	2.15	7.0E-86	11417012	NT	Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), mRNA
8329	18206	28456	2.15	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC683170), mRNA
1272	11179	21027	9.33	6.0E-86	4505492	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC683170), mRNA
204	10175	19993	1.48	4.0E-86	BE547173.1	EST_HUMAN	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH), mRNA
5677	15586	25686	10.18	4.0E-86	BE259843.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
8567	10175	19993	1.9	4.0E-86	BE547173.1	EST_HUMAN	601176865F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5'
5435	15355	25411	6.02	3.0E-86	AW340946.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
7868	17718	27963	3.31	3.0E-86	BE885479.1	EST_HUMAN	xz82h12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'
7868	17718	27964	3.31	3.0E-86	BE885479.1	EST_HUMAN	601508696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
8734	17893	28125	9.01	3.0E-86	A1699240.1	EST_HUMAN	601508696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
9163	19560		2.02	3.0E-86	BE410354.1	EST_HUMAN	tu18b02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2251371 3'
266	10231	20046	1.33	2.0E-86	AA308264.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
408	10354		1.67	2.0E-86	AL163203.2	NT	EST1717232 Jurkat T-cells VI Homo sapiens cDNA 5' end
							Homo sapiens chromosome 21 segment HS21C003

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1173	11085	20929	2.18	2.0E-86	N58977.1	EST_HUMAN	yz19a08.r1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:283478 5'
2144	12032	21930	2.37	2.0E-86	9635487	NT	Human endogenous retrovirus, complete genome
2222	12107	22011	1.12	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3369	13288	23087	1.43	2.0E-86	AW966142.1	EST_HUMAN	EST378215 MAGE resequences, MAGI Homo sapiens cDNA
3686	13599	23385	2.16	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAA1-delta) mRNA, complete cds
3686	13599	23386	2.16	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAA1-delta) mRNA, complete cds
3954	13862		2.42	2.0E-86	AW51742.1	EST_HUMAN	hd87g08.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2916542 3'
4679	14565	24360	2.8	2.0E-86	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5580	15495	25571	1.53	2.0E-86	Z16411.1	NT	H.sapiens mRNA encoding phospholipase c
5580	15495	25572	1.53	2.0E-86	Z16411.1	NT	H.sapiens mRNA encoding phospholipase c
6987	16864	27057	2.22	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
6987	16864	27058	2.22	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
7372	17241	27446	1.95	2.0E-86	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog)-like (OSE1L), mRNA
7969	17819	28061	2.69	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
7969	17819	28062	2.69	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
8276	18156	28397	1.83	2.0E-86	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA
9606	19187	28250	2.4	2.0E-86	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
9772	19290		1.81	2.0E-86	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9955	19520	25139	1.47	2.0E-86	11417883	NT	Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA
1579	11483	21343	3.1	1.0E-86	4826855	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
3125	13050	22847	2.06	1.0E-86	5453649	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3197	13122	22927	2.42	1.0E-86	L20492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3256	13179	22977	1.32	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3256	13179	22978	1.32	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3864	13775	23568	11.48	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3864	13775	23569	11.48	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4167	14067	23842	5.76	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4832	14714	24497	1.11	1.0E-86	AF100751.1	NT	Homo sapiens FK506-binding protein FKBP23 isoform mRNA, complete cds
8882	15328	25378	2.15	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5287	15209		1.47	9.0E-87	AI150703.1	EST_HUMAN	qb77c09.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6403	16264	26424	2	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6403	16264	26425	2	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
471	10414	20233	14.17	8.0E-87	X62245.1	NT	O. curculius mRNA for elongation factor 1 alpha
2250	12134	22031	2.74	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3322779 3'
2250	12134	22032	2.74	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3322779 3'
6763	16842	26829	2.67	7.0E-87	BF352776.1	EST_HUMAN	IL3-HT0619-060700-198-D10 HT0619 Homo sapiens cDNA
7794	17644	27877	3.38	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
7794	17644	27878	3.38	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
8264	18144	28384	10.88	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
8264	18144	28385	10.88	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
3482	13398	23203	0.87	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5868	15774	25893	1.73	6.0E-87	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
8107	17997		3.52	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1142	11056	20898	1.69	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis 1 Homo sapiens cDNA 5' end
9450	11056	20898	1.53	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis 1 Homo sapiens cDNA 5' end
950	10874	20721	1.33	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1155	11068	20912	10.54	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1411	11316	21179	0.86	4.0E-87	R78133.1	EST_HUMAN	y80H10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
1985	11878	21771	0.92	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
2372	12252	22142	1.07	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC31626), mRNA
2372	12252	22143	1.07	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC31626), mRNA
3419	13335	23140	2.19	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
5343	15264	25090	6.47	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
5686	15595	25696	4.36	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051
8505	18378	28644	4.35	4.0E-87	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
8994	18798	29091	2.13	4.0E-87	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (morfa1n-2) (H. sapiens) (LOC63184), mRNA
9695	19249		14.77	4.0E-87	11417812	NT	Homo sapiens putative receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
2749	12611	22502	2.99	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
3717	13629	23414	0.89	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA100307 5'
4826	14708	24492	1.17	2.0E-87	BF376311.1	EST_HUMAN	CMO-TN0038-150900-552-h08 TN0038 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4880	14780	24537	0.8	2.0E-87	BE175478.1	EST_HUMAN	RC6-H10580-200300-031-C04 HT0580 Homo sapiens cDNA
5473	15393	25457	7.87	2.0E-87	BE734190.1	EST_HUMAN	G0156904F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
5473	15393	25458	7.87	2.0E-87	BE734190.1	EST_HUMAN	G0156904F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
5819	15725		6.27	2.0E-87	BE567193.1	EST_HUMAN	G01341383F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683348 5'
6256	16122	26275	1.51	2.0E-87	BE294432.1	EST_HUMAN	G01176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531511 5'
6407	16268	26430	32.21	2.0E-87	N48128.1	EST_HUMAN	yw21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2433396 5'
6526	16385	26564	28.31	2.0E-87	N48128.1	EST_HUMAN	yw21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2433396 5'
6892	16771	26966	3.81	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
7634	17485		5.11	2.0E-87	BE531136.1	EST_HUMAN	G01278315F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610539 5'
1165	12645		2.33	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1413	11318	21181	0.94	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
1413	11318	21182	0.94	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
3649	13563	23349	3.18	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3673	13587	23374	2.47	1.0E-87	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
5057	14927	24699	1.04	1.0E-87	U50949.1	NT	Rattus norvegicus taste bud receptor protein TB 641 (TB 641) gene, complete cds
5774	15681	25788	3.39	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
5774	15681	25789	3.39	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6376	16238	26398	1.6	1.0E-87	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
6724	16604	26793	13.13	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
7165	17042	27233	1.19	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
7165	17042	27234	1.19	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
7554	17405	27620	2.77	1.0E-87	BE818183.1	EST_HUMAN	RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
7554	17405	27621	2.77	1.0E-87	BE818183.1	EST_HUMAN	RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
8114	18003	28249	2.06	1.0E-87	5729867	NT	Homo sapiens hec domain and RLD 2 (HERC2), mRNA
8367	18244		1.78	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
9599	19751		2.02	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1090	11006	20847	7.39	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1327	11234	21090	2	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1327	11234	21091	2	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
3574	13488	23279	1.13	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4172	14072	23847	2.64	9.0E-88	X91928.1	NT	H.sapiens ECE-1 gene (exon 9)
4172	14072	23848	2.64	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4934	14812	24580	1.23	9.0E-88	AB028898.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7216	17093	27284	3.69	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1787	11685		1.19	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2602	12470	22366	3	5.0E-88	N99399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
2970	12897	22696	0.92	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2978	12905	22704	0.94	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2978	12905	22705	0.94	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3343	13263		2.31	5.0E-88	AI693217.1	EST_HUMAN	wd68h08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:236799 3' similar to contains Alu repetitive element contains element MER22 MER22 repetitive element ;
3491	13407	23212	0.91	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
4631	14519	24310	0.87	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
6059	16042	26185	2.64	5.0E-88	H10932.1	EST_HUMAN	ym06b10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:47129 5'
6627	16507	26994	1.84	5.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1307	11214	21070	1.64	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1307	11214	21071	1.64	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
6295	16159	26316	1.93	4.0E-88	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
8281	18160	28402	2.84	4.0E-88	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
8780	18595	28863	2.1	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
8780	18595	28864	2.1	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
715	10647	20475	0.93	3.0E-88	11545300	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1770	11669		4.77	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2918	12845	22647	4.31	3.0E-88	N66951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296823 3'
4147	14047	23819	1.21	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4147	14047	23820	1.21	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4380	14276		3.17	3.0E-88	11429300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5242	15166	24937	4.09	3.0E-88	11429567	NT	Homo sapiens valosin-containing protein (VOP), mRNA
5429	15349	25403	3.84	3.0E-88	9966888	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5498	15417	25480	3.39	3.0E-88	11420697	NT	Homo sapiens v-rat simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA
6204	15964	26098	12.03	3.0E-88	AF279265.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
6452	16313	26479	6.66	3.0E-88	11436400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
6620	16500	26688	8.52	3.0E-88	11421726	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDFF), mRNA

Table 4

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6769	16648	26836	1.41	3.0E-88	AF034374.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein C mRNA, complete cds
7427	16440	26626	2.12	3.0E-88	11526262	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
9286	18988		4.78	3.0E-88	11417974	NT	Homo sapiens transcobalamin II, macrocytic anemia (TCN2), mRNA
1020	10988	20780	1.42	2.0E-88	7305198	NT	Homo sapiens Caldesin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1607	11512	21372	0.93	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1716	11617	21486	4.19	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4328	14225	24007	1.93	2.0E-88	5031666	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
5604	15518	25597	4.98	1.0E-88	AW139565.1	EST_HUMAN	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA
5604	15518	25598	4.98	1.0E-88	AW139565.1	EST_HUMAN	UI-H-B11-aea-d-04-0-UJ.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6004	15909	26033	17.59	1.0E-88	AB007877.1	NT	UI-H-B11-aea-d-04-0-UJ.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6004	15909	26034	17.59	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
							Homo sapiens KIAA0417 mRNA, complete cds
6263	16128	26282	4.06	1.0E-88	AA488981.1	EST_HUMAN	aa54a11.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:B0272.2
7524	17375	27584	2.95	1.0E-88	AL043314.2	EST_HUMAN	CE006511
							DKFP434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFP434N0323 5'
							os91g03.s1 NCI CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612756 3' similar to gb:M16342
							HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
8742	17891	28135	2.27	1.0E-88	AA991479.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
9502	19117		2.98	1.0E-88	AL163246.2	NT	Homo sapiens transgelin 2 (TAGLN2), mRNA
8321	18198	28447	4.12	9.0E-89	11421238	NT	Homo sapiens transgelin 2 (TAGLN2), mRNA
2705	12588	22459	1.41	8.0E-89	BE311557.1	EST_HUMAN	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'
426	10371	20194	1.35	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
426	10371	20195	1.35	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4785	14670	24457	2.94	7.0E-89	4557390	NT	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA
4847	14728	24511	5.14	7.0E-89	AL045748.1	EST_HUMAN	DKFP434E246_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFP434E246 5'
5334	15284	25076	1.35	7.0E-89	X99832.1	NT	H. sapiens CLN3 gene, complete CDS
5334	15284	25077	1.35	7.0E-89	X99832.1	NT	H. sapiens CLN3 gene, complete CDS
6428	16289	28450	1.78	7.0E-89	11420754	NT	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
8006	17856	28097	1.42	7.0E-89	X62048.1	NT	H. sapiens Wee1 hu gene
8006	17856	28098	1.42	7.0E-89	X62048.1	NT	H. sapiens Wee1 hu gene
8012	17862	28107	1.17	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
8012	17862	28108	1.17	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
9920	19393		3.07	7.0E-89	U87927.1	NT	Human acetylase hydratase (ACO2) gene, exon 2
1006	10924	20768	1.07	6.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
2166	12053	21954	1.12	6.0E-89	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2383	12263	22154	1.97	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L3 (UBE2L3) mRNA
2383	12263	22155	1.97	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L3 (UBE2L3) mRNA
3480	13996	23201	0.84	6.0E-89	7661817	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4537	14430	24211	3.5	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4537	14430	24212	3.5	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5007	14881	24646	2.77	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5007	14881	24647	2.77	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
6477	16336	26503	1.33	4.0E-89	BE762749.1	EST_HUMAN	QV3-NT0022-060600-219-g03 NT0022 Homo sapiens cDNA
2847	12775	22563	1.61	3.0E-89	AW976181.1	EST_HUMAN	EST388290 MAGE resequences, MAGN Homo sapiens cDNA
9888	19241	25215	1.92	3.0E-89	AV705749.1	EST_HUMAN	AV705749 ADB Homo sapiens cDNA clone ADBGA01 5'
121	10348	20175	1.46	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
121	10348	20176	1.46	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
402	10348	20175	0.91	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
402	10348	20176	0.91	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
519	10461	20272	0.83	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2852	12780	22569	2.01	2.0E-89	AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131
4053	13955	23731	1.45	2.0E-89	AF089897.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
4061	13963	23740	6.18	2.0E-89	X58742.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4061	13963	23741	6.18	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4396	14292	24076	1.14	2.0E-89	AJ007378.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
5368	15288	25123	2.5	2.0E-89	AB007546.1	NT	Homo sapiens GGT gene, exon 5
5338	15455	25525	1.6	2.0E-89	U03985.1	NT	Homo sapiens gene for LECT2, complete cds
6520	16379	29557	4.93	2.0E-89	U81004.1	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
6630	16510	26699	3.73	2.0E-89	11428801	NT	Human GT24 (GT24) mRNA, partial cds
8680	18568	28851	2.63	2.0E-89	11434411	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
8854	18666	28953	4.87	2.0E-89	11433673	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
8955	18762	29055	2.24	2.0E-89	U10692.1	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
							Human MAGE-7 antigen (MAGE7) pseudogene, complete cds

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8860	18672	28960	6.12	1.0E-89	BF196052.1	EST_HUMAN	hr1d09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN ;
8860	18672	28961	6.12	1.0E-89	BF196052.1	EST_HUMAN	hr1d09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN ;
6789	16668	26859	1.16	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6789	16668	26860	1.16	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1047	10965	20806	1.62	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1048	10965	20806	2.93	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1308	12690	21072	5.28	8.0E-90	BE670561.1	EST_HUMAN	7e36f08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1308	12690	21073	5.28	8.0E-90	BE670561.1	EST_HUMAN	7e36f08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
818	10748		2.65	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6907	16785		1.91	7.0E-90	AA782977.1	EST_HUMAN	ai63d08.s1 Soares testis NIH_MGC_66 Homo sapiens cDNA clone IMAGE:375503 3'
7183	17060	27250	1.88	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
7183	17060	27251	1.88	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
7833	17683	27927	1.98	7.0E-90	H68849.1	EST_HUMAN	yr86e04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
7833	17683	27928	1.98	7.0E-90	H68849.1	EST_HUMAN	yr86e04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
3029	12957	22749	1.14	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
3029	12957	22750	1.14	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
4134	14034	23809	7.33	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4134	14034	23810	7.33	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
5641	15554	25646	3.54	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
5641	15554	25647	3.54	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
6846	16725	26918	3.25	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
6846	16725	26919	3.25	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
149	10123		10.5	5.0E-90	AB036344.1	NT	Homo sapiens TOL6 gene, exon 1-10b
1175	11087	20931	1.55	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
2508	12382	22273	2.19	5.0E-90	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
4440	14334	24124	3.08	5.0E-90	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4507	14400	24186	1.07	5.0E-90	AA706222.1	EST_HUMAN	z182g10.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
4507	14400	24187	1.07	5.0E-90	AA706222.1	EST_HUMAN	z182g10.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
4571	14463	24251	0.98	5.0E-90	AL135549.1	EST_HUMAN	DKFZp762P1616_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762P1616 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5433	15353	25409	2.52	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5523	15353	25409	2.13	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6283	16147	26302	2.26	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6283	16147	26303	2.26	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6464	16323	26489	7.93	5.0E-90	4557258	NT	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA
6825	16704	26899	4.86	5.0E-90	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
7591	17432	27646	1.24	5.0E-90	11419426	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
7968	17818	28060	15.41	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
9744	19306		2.16	5.0E-90	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9789	19299		2.37	5.0E-90	AB23366.1	EST_HUMAN	ar78105.x1 Barstead actin HPLRB6 Homo sapiens cDNA clone IMAGE:2128761 3'
299	10263	20083	1.85	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
299	10263	20084	1.95	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1070	10986	20829	2.94	4.0E-90	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1663	11565	21432	9.22	4.0E-90	X99033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
4557	14449	24235	4.07	4.0E-90	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4991	14577	24372	1.97	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4713	14599	24385	1.8	4.0E-90	M95967.1	NT	Human prothrombin converting enzyme (NEC2) gene, exon 8
8901	18709	29004	103.62	3.0E-90	BE563833.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
207	10178	19995	4.28	2.0E-90	BE537913.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1156	11069	20913	3.65	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1156	11069	20914	3.65	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3771	13683	23465	2.91	2.0E-90	AI138213.1	EST_HUMAN	qc54c02.x1 Soares_placenta_8bc6weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1713410 3'
4588	14476	24264	1.13	2.0E-90	AB006627.1	NT	similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3.;
4820	14703	24488	8.33	2.0E-90	5729855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
5534	15451	25519	4.34	2.0E-90	AW672686.1	EST_HUMAN	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
7638	17489	27708	2.9	2.0E-90	11427320	NT	ba49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2899881 5' similar to TR:075208 O75208 HYPOTHETICAL 35.5 KD PROTEIN.;
7638	17489	27709	2.9	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
7722	17572	27796	1.56	2.0E-90	AU118985.1	EST_HUMAN	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7722	17572	27797	1.56	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
8765	17914	28159	49.27	2.0E-90	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
275	10241	20060	3.39	1.0E-90	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-I, Alzheimer disease) (APP), mRNA
370	12639	20148	1.21	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
371	12639	20148	1.04	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
680	10613	20435	2.03	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
680	10613	20436	2.03	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
713	10645	20472	7.71	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
713	10645	20473	7.71	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1094	11010		2.46	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1284	11192	21044	3.47	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1284	11192	21045	3.47	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1644	11548		4.02	1.0E-90	BE379884.1	EST_HUMAN	601159563F2 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3511118 5'
1860	11756	21631	4.98	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila))-like (LOC57167), mRNA
2823	12752	22545	8.4	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3777	13689	23473	1.18	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3777	13689	23474	1.18	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4326	14223	24005	1	1.0E-90	AF167340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5481	15401	25464	2.2	1.0E-90	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
6521	16380	26558	2.85	1.0E-90	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
7121	16998	27189	3.78	1.0E-90	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
7356	17224		1.22	1.0E-90	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
7371	17240	27444	1.72	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
7371	17240	27445	1.72	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9732	19268	25225	1.89	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
9732	19268	25226	1.89	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4101	14001	23780	5.48	8.0E-91	D12234.1	EST_HUMAN	HUM000S381 Liver HapG2 cell line. Homo sapiens cDNA clone s381 3'
1428	11333	21199	0.88	7.0E-91	AF063768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
6835	16714	26907	2.05	7.0E-91	11419234	NT	Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA
3429	13346	23151	1.47	5.0E-91	AA072794.1	EST_HUMAN	z90b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4415	14309	24092	1.05	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4415	14309	24093	1.05	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4703	14589	24379	0.82	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4703	14589	24380	0.82	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
7087	16964	27157	1.34	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
7087	16964	27158	1.34	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
3166	13091	22895	1.3	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAAT-delta) mRNA, complete cds
3166	13091	22896	1.3	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAAT-delta) mRNA, complete cds
8301	18180	28427	3.13	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9239	18954	25314	1.67	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCNC60 similar to Retrovirus-related gag polyprotein
9239	18954	25360	1.67	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCNC60 similar to Retrovirus-related gag polyprotein
1601	11506	21366	5.12	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1601	11506	21367	5.12	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
2624	12492	22382	0.99	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
2624	12492	22383	0.99	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
3297	13219	23020	1.77	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3416	13333	23136	2.96	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3416	13333	23137	2.96	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3720	13632	23418	0.83	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myo-like protein mRNA, complete cds
4487	14381	24168	4.02	3.0E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4905	14785	24560	1.2	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4905	14785	24561	1.2	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5488	15407	25470	1.45	3.0E-91	11434964	NT	Homo sapiens epididymal secretory protein (19.5kD) (HE1), mRNA
5807	15712		2.39	3.0E-91	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
5967	15872	25996	4.11	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
5967	15872	25997	4.11	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6502	16361	26535	4.4	3.0E-91	U96959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
6502	16361	26536	4.4	3.0E-91	U96959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7093	16970	27163	3.31	3.0E-91	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
9480	19104	25286	1.45	3.0E-91	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9812	12492	22382	3.03	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
9812	12492	22383	3.03	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
42	10030	19833	3.02	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1225	11133	20987	3.58	1.0E-91	AW449746.1	EST_HUMAN	UI-H-B18-aks-d-01-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
6090	16035	26175	1.7	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
6090	16035	26176	1.7	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
9398	19085		2.42	1.0E-91	H18212.1	EST_HUMAN	ym30603.r1 Scates infant brain 1NIB Homo sapiens cDNA clone IMAGE:49587 5'
1221	11130	20981	8.41	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1221	11130	20982	8.41	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
5353	15273	25103	3.56	9.0E-92	J03007.1	NT	Human Nat. ₄ K ₊ ATPase alpha-subunit mRNA, partial cds
5442	15362	25418	1.75	9.0E-92	11427149	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
5882	15789	25911	3.22	9.0E-92	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
6878	16757	26954	19.33	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
6878	16757	26955	19.33	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
7342	17210	27409	1.66	9.0E-92	11422086	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
87	10071	19887	2.02	8.0E-92	W26367.1	EST_HUMAN	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
283	10248	20098	5.9	8.0E-92	BE386363.1	EST_HUMAN	28f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
1778	11677	21554	1.29	8.0E-92	11434722	NT	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614687 5'
1778	11677	21555	1.29	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA
5944	15849	25973	1.29	8.0E-92	AJ000979.1	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA
6908	16786	26978	3.61	8.0E-92	L04193.1	NT	Homo sapiens MCP-4 gene
6908	16786	26979	3.61	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
7242	17119	27314	2.61	8.0E-92	AB014511.1	NT	Human lens membrane protein (mp19) gene, exon 11
7760	17610	27836	1.31	8.0E-92	Y13829.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
						NT	Homo sapiens mRNA for MBNL protein
8180	18067	28316	4.53	8.0E-92	AF074393.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
8667	18556	28841	3.21	8.0E-92	4503340	NT	Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
9572	19162	25288	1.43	8.0E-92	11434704	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
60	10046	19858	2.64	7.0E-92	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
236	12662	20020	2.51	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
236	12662	20021	2.51	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
576	10514		1.25	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Seprase truncated isoform mRNA, complete cds
1259	11166	21017	1.91	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2139	12027	21923	1.67	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2139	12027	21924	1.67	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2517	12391	22283	2.32	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2693	12558	22445	5.01	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
2724	12586	22481	1.04	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7:1 ancestral haplotype
3301	15068	23023	0.92	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3301	15068	23024	0.92	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4484	14378	24165	1.61	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4484	14378	24166	1.61	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
5110	14978	24752	1.45	7.0E-92	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
5219	15142	24836	4.87	7.0E-92	AA446206.1	EST_HUMAN	zw66d12.f1 Soares testis NHT Homo sapiens cDNA clone IMAGE:781175 5'
1569	11473		0.93	5.0E-92	BE390882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5'
2738	12600	22494	2.45	3.0E-92	BE909714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902939 5'
5583	15498	25575	3.74	3.0E-92	AA378336.1	EST_HUMAN	EST91020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13
8146	18034	28281	5.7	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
8146	18034	28282	5.7	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
23	10010	19803	1.53	2.0E-92	4501898	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
172	10143	19958	2.93	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
172	10143	19959	2.93	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
732	10664	20497	1.38	2.0E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
732	10664	20498	1.38	2.0E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1886	11588		2.74	2.0E-92	S78653.1	NT	img=mas-related [human, Genomic, 2416 nt]
1894	11789	21667	1.55	2.0E-92	A1818119.1	EST_HUMAN	wk27d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1894	11789	21668	1.55	2.0E-92	A1818119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2002	11895	21787	4.71	2.0E-92	4506860	NT	wk27d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
2623	12491	22381	37.64	2.0E-92	6912457	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
3562	13478	23265	1.02	2.0E-92	AF231919.1	NT	Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
3562	13476	23266	1.02	2.0E-92	AF231919.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
							Homo sapiens chromosome 21 unknown mRNA
							Homo sapiens chromosome 21 unknown mRNA
3631	13545	23332	4.99	2.0E-92	5803180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4191	14091	23869	1.02	2.0E-92	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4648	14534	24323	0.79	2.0E-92	AF136523.1	NT	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds
4922	14801		2.53	2.0E-92	AL040437.1	EST_HUMAN	DKFZp434C0414.1_1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434C0414.5'
5889	15894	26017	2.49	2.0E-92	AB028991.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
6420	16273		2.25	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
7141	17018	27211	1.37	2.0E-92	AW340174.1	EST_HUMAN	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711
8142	18030	28276	5.91	2.0E-92	11434900	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN;
9589	19172	28274	2.55	2.0E-92	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
9839	12491	22381	26.65	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1807	11704	21582	1.11	1.0E-92	R78078.1	EST_HUMAN	y80c08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1807	11704	21583	1.11	1.0E-92	R78078.1	EST_HUMAN	y80c08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2028	11919	21810	34.72	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
7286	17162	27360	4.04	1.0E-92	AI380356.1	EST_HUMAN	tg01b02.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element MER17 repetitive element ;
7286	17162	27361	4.04	1.0E-92	AI380356.1	EST_HUMAN	tg01b02.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element MER17 repetitive element ;
1983	11876	21769	3.14	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
1996	11890		9.21	9.0E-93	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2610	12478		1.46	9.0E-93	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3563	13477	23267	0.96	9.0E-93	BE388571.1	EST_HUMAN	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603632 5'
8911	18719		9.8	9.0E-93	11418526	NT	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
5975	15879	26003	2.49	8.0E-93	BF036364.1	EST_HUMAN	601460521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5'
246	10212	20028	6.24	7.0E-93	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1359	11295	21121	1.25	5.0E-93	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1385	11290	21145	5.39	5.0E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3'
1385	11290	21146	5.39	5.0E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3'
1459	11364		0.95	5.0E-93	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3195	13120	22925	2.42	5.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin

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6540	16398	26577	3.67	5.0E-93	AF067136.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
7549	17400	27613	2.07	5.0E-93	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7644	17494	27715	1.31	5.0E-93	5032156	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
8200	18085	28336	3.01	5.0E-93	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2) mRNA
9487	19423	25173	1.84	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
82	10066		4.72	4.0E-93	AA459933.1	EST_HUMAN	z50e09.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW:CLPA_RAT P37397 CALPONIN, ACIDIC ISOFORM
437	10381	20204	1.75	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
437	10381	20205	1.75	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
755	10685	20522	1.33	4.0E-93	7657454	NT	Homo sapiens pascadillo (zbratfish) homolog 1, containing BRCT domain (PES1) mRNA
755	10685	20523	1.33	4.0E-93	7657454	NT	Homo sapiens pascadillo (zbratfish) homolog 1, containing BRCT domain (PES1) mRNA
1166	11078	20923	2.08	4.0E-93	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731) mRNA
1934	11829	21712	5.06	4.0E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2349	12229	22126	0.84	4.0E-93	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2564	12435	22328	2.18	4.0E-93	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1) mRNA
3962	13889	23647	1.44	4.0E-93	4504664	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5465	15385	25445	4.81	4.0E-93	T46864.1	EST_HUMAN	y694c12.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN
8475	18348	28613	19.24	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GK6 Homo sapiens cDNA clone GKCDRF07 5'
3601	13515	23302	5.99	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
3601	13515	23303	5.99	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
4142	14042		2.7	3.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
5635	15452	25520	1.58	3.0E-93	AI553853.1	EST_HUMAN	tn29g03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2169076 3'
5635	15452	25521	1.58	3.0E-93	AI553853.1	EST_HUMAN	tn29g03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2169076 3'
5952	15857	25979	1.32	3.0E-93	11425182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2) mRNA
8178	18066	28314	4.15	3.0E-93	AI824829.1	EST_HUMAN	wb02d05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2304489 3'
183	10155	19970	8.31	2.0E-93	AB015610.1	NT	Chlorocibus aethiops mRNA for ribosomal protein S4X, complete cds
183	10155	19971	8.31	2.0E-93	AB015610.1	NT	Chlorocibus aethiops mRNA for ribosomal protein S4X, complete cds
320	10282	20100	6.69	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
321	10282	20100	7.68	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085

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1598	11503	21363	1.48	2.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
2093	11973	21868	1.02	2.0E-93	U40783.1	NT	Human Ctk-associated RS cyclophilin CARS-Cyp mRNA, complete cds
2436	12313	22210	0.99	2.0E-93	BE252982.1	EST_HUMAN	601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
5088	14958	24732	1.02	2.0E-93	BE253201.1	EST_HUMAN	601116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5'
5325	15245	25049	4.59	2.0E-93	AW964385.1	EST_HUMAN	EST376458 IMAGE resequences, MAGH Homo sapiens cDNA
5462	15382	25442	1.52	2.0E-93	11430039	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
6014	15918		1.32	2.0E-93	AW502002.1	EST_HUMAN	UJ-HF-BN0-aks-g-09-0-UJr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5'
8996	19476	29093	2.87	2.0E-93	AB12025.1	EST_HUMAN	qp78b10.x1 Soares fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:1929116 3'
9386	19046		1.52	2.0E-93	AA129735.1	EST_HUMAN	229c10.s1 Soares pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:503346 3'
9465	19095		1.31	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
9724	19283		2.75	2.0E-93	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
96	10081	19897	1.64	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
96	10081	19898	1.64	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
507	10449	20262	2.56	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (D328E19.C1.1), mRNA
585	10523	20330	3.75	1.0E-93	AI146755.1	EST_HUMAN	cy84b08.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384 ZINC FINGER PROTEIN. ;
854	10781	20631	3.32	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1217	11125	20974	6.41	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1217	11125	20975	6.41	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1321	11228	21083	1.55	1.0E-93	AB048783.1	NT	Homo sapiens mRNA for KIAA1563 protein, partial cds
1323	11230	21085	1.68	1.0E-93	AF167705.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
2289	12172	22070	1.01	1.0E-93	AF231981.1	NT	Homo sapiens long chain polynsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2415	12292	22190	4.16	1.0E-93	AF059066.1	NT	Homo sapiens MHC class 1 region
2459	12336		1.09	1.0E-93	AL137200.1	NT	Novel human gene mapping to chromosome 1
2792	11181	21030	2.69	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632965 5'
2792	11181	21031	2.69	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632965 5'
2903	12830	22627	4.33	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4331	14228	24010	1.44	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5417	15338	25391	1.62	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5417	15338	25392	1.62	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5607	15522	25604	9.15	1.0E-93	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6067	16051	26197	2.06	1.0E-93	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA

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6299	16163	26320	4.08	1.0E-93	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
6807	16886	28876	2.04	1.0E-93	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
6971	16848	27039	1.18	1.0E-93	Y10183.1	NT	Hi.sapiens mRNA for MEMD protein
7024	16901	27093	1.59	1.0E-93	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
7437	16450	26640	1.8	1.0E-93	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
7440	16453	26643	1.22	1.0E-93	AF091395.1	NT	Homo sapiens Trfo isoform mRNA, complete cds
7529	17380	27589	4.54	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
7529	17380	27590	4.54	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9051	19494	25132	5.92	1.0E-93	AI268262.1	EST_HUMAN	qm03c12.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1880758 3' similar to WP.T19B4.4
9716	19257		2.33	1.0E-93	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
8025	17875		1.22	8.0E-94	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3880	13791	23579	1.74	6.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
9830	19331		1.67	6.0E-94	11418351	NT	Homo sapiens mitogen-activated protein kinase 12 (MAPK12), mRNA
5296	15217	25019	3.05	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5296	15217	25020	3.05	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5689	15598	25699	1.72	5.0E-94	AA722434.1	EST_HUMAN	zgb7g06.s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:409594 3'
6183	16069	26218	1.63	5.0E-94	AI015900.1	EST_HUMAN	ot83d05.s1 Soares_fetal_fetus_Nb2HF9_9w Homo sapiens cDNA clone IMAGE:1623369 3'
9381	19736	24911	4.68	5.0E-94	T89398.1	EST_HUMAN	yd8b04.s1 Soares_fetal_liver_spleen_1NfLS Homo sapiens cDNA clone IMAGE:116239 3'
9901	19378		1.27	5.0E-94	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
9907	19384		1.26	5.0E-94	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
1799	11697		4.55	4.0E-94	LO5094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2621	12489	22379	0.86	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
4618	14506	24295	3.02	4.0E-94	AI591312.1	EST_HUMAN	tw11f10.x1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE ;
5892	15798	25921	1.84	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
5892	15798	25922	1.84	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
8749	17898	28142	1.72	4.0E-94	11545792	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA
595	10531	20339	1.17	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
704	10637	20462	1.17	3.0E-94	4602606	NT	Homo sapiens complement component 5 (C5) mRNA
1706	11607	21477	1.05	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
1706	11607	21478	1.05	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1735	11636	21504	3.45	3.0E-94	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4095	13995	23772	0.82	3.0E-94	AA464805.1	EST_HUMAN	zw63g08.r1 Soares_tetel_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5'
5484	15403	25466	3.58	3.0E-94	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
5881	15787	25909	4.16	3.0E-94	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
6771	16650	26538	1.16	3.0E-94	AF152309.1	NT	Homo sapiens probocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
6992	16869	27062	3.79	3.0E-94	AB014579.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
7533	17384	27596	4.36	3.0E-94	AF087942.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
8448	18321	28580	1.75	3.0E-94	475782.1	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
8928	18736	29029	2.27	3.0E-94	U26711.1	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds
143	10117	19937	2.24	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3050	12977	22769	1.91	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3050	12977	22770	1.91	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4261	14160	23938	1.13	1.0E-94	9506662	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
7331	17235	27439	1.93	1.0E-94	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
7636	17487	27707	1.41	1.0E-94	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872099 5'
8418	18292	28546	2.49	1.0E-94	U65590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
8635	18500	28775	2.19	1.0E-94	AI272244.1	EST_HUMAN	ap22e02.x1 Schiller oligodendroglioma Homo sapiens cDNA clone IMAGE:1958122 3' similar to TR:Q62845
9759	10117	19937	1.98	1.0E-94	BE295714.1	EST_HUMAN	Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR, ;
1461	11366	21230	1.55	9.0E-95	AF027302.1	NT	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3118	13043	22839	1.13	9.0E-95	7662027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3118	13043	22840	1.13	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
6801	16680	26869	1.87	9.0E-95	AF274763.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
4436	14331	24119	1.59	8.0E-95	AI700998.1	EST_HUMAN	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
4436	14331	24120	1.59	8.0E-95	AI700998.1	EST_HUMAN	we09e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
6294	16158	26314	1.83	8.0E-95	11426529	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
6294	16158	26315	1.83	8.0E-95	11426529	NT	we09e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
6770	16649	26837	2.05	8.0E-95	AF032897.1	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
7391	17309	27515	1.73	8.0E-95	11420944	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
7391	17309	27516	1.73	8.0E-95	11420944	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
7667	17517	27744	2.82	8.0E-95	5174644	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
							Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
							Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriplor
7681	17531		2.83	8.0E-95	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
8096	17987	28236	2.41	8.0E-95	AF112152.1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
9689	19242		8.68	8.0E-95	AA629056.1	EST_HUMAN	z184b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.t1 L1 repetitive element
274	10240	20058	9.46	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
274	10240	20059	9.46	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4270	14169	23947	5.94	7.0E-95	M95703.1	NT	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
4316	14213		1.38	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS27 C046
4982	14857	24623	1.03	7.0E-95	M95929.1	NT	Human homeobox protein (PHOX1) mRNA, 3' end
5340	15261	25087	1.76	3.0E-95	BF526041.1	EST_HUMAN	602071146F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214147 5'
922	10847	20694	0.86	2.0E-95	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
1625	11529	21387	1.6	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1625	11529	21388	1.6	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1897	11793	21672	7.79	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1900	11796	21676	3.3	2.0E-95	BE393873.1	EST_HUMAN	601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5'
2376	12256	22147	1.3	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2376	12256	22148	1.3	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2417	12294	22191	16.55	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2466	12342	22235	2.46	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2797	10846	20693	0.86	2.0E-95	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
3120	13045	22842	3.51	2.0E-95	AF015452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3517	13433	23232	2.78	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3517	13433	23233	2.78	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3565	13479	23268	0.96	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1396 protein, partial cds
3600	13604	23390	1.02	2.0E-95	AI290264.1	EST_HUMAN	qm01c02.x1 Soares_NhHMP_u_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP.T23G7.4 CE03705
4264	14163	23940	2.3	2.0E-95	7657185	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
4971	14846	24615	2.57	2.0E-95	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5022	14895	24663	0.98	2.0E-95	AA447931.1	EST_HUMAN	zxt1d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5022	14895	24664	0.98	2.0E-95	AA447931.1	EST_HUMAN	zxt1d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5367	15287	25121	3.69	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5367	15287	25122	3.69	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA

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5734	15642	25748	4.54	2.0E-95	M59724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
5957	15952	25984	2.25	2.0E-95	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6055	16038	26179	1.62	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
8106	17996	28245	2.36	2.0E-95	4757653	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI1A) mRNA
9452	19084	25285	1.98	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9840	19338	25211	4.34	2.0E-95	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
5450	15371	25427	7.73	1.0E-95	AA284651.1	EST_HUMAN	z23h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F55H2.6;
5450	15371	25428	7.73	1.0E-95	AA284651.1	EST_HUMAN	z23h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F55H2.6;
6437	16298	26480	4.85	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6437	16298	26461	4.85	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6767	16846	26835	1.67	9.0E-96	BE897289.1	EST_HUMAN	601437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922423 5'
435	12666	20201	0.82	8.0E-96	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
435	12666	20202	0.82	8.0E-96	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
5383	15302		2.66	8.0E-96	AW836047.1	EST_HUMAN	PM0-LT0019-090300-002-d09 LT0019 Homo sapiens cDNA
3834	13746	23538	0.95	7.0E-96	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
2213	12099	22003	0.85	6.0E-96	BE171984.1	EST_HUMAN	MR0-HT0559-250200-002-d07 HT0559 Homo sapiens cDNA
3276	13197	22997	0.96	6.0E-96	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3437	13354	23159	26.15	6.0E-96	M26873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end
8831	18944	28927	1.98	6.0E-96	7692289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8831	18944	28928	1.98	6.0E-96	7692289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8870	18682	28972	2.09	6.0E-96	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
317	10279	20096	2.7	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
824	10751	20569	3.06	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
824	10751	20600	3.06	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2576	12447		2.31	5.0E-96	11416767	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2991	12919	22713	0.98	5.0E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
4810	14694		1.22	5.0E-96	X60812.1	NT	H. sapiens DNA for monamine oxidase type A (7) (partial)
6065	16048	26193	4.23	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6065	16048	26194	4.23	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6719	16599	26788	1.81	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
6719	16599	26789	1.81	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5

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4097	13997		6.22	3.0E-96	H68556.1	EST_HUMAN	y87h12.1 Scores fetal liver spleen 1NF.LS Homo sapiens cDNA clone IMAGE:212327 5'
409	10355		3.49	2.0E-96	4503038	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
730	10662	20494	1.56	2.0E-96	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4651	14537	24326	1.58	2.0E-96	BE148074.1	EST_HUMAN	RC3-HT0230-040500-110-g02 HT0230 Homo sapiens cDNA
7191	17068		5.08	2.0E-96	AV689461.1	EST_HUMAN	AV689461 GK6 Homo sapiens cDNA clone GKCFMD07 5'
9151	18902		2.05	2.0E-96	AW249440.1	EST_HUMAN	2819351.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819351 5'
655	10590	20408	1.89	1.0E-96	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1742	11643	21510	2.03	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGC Homo sapiens cDNA
1742	11643	21511	2.03	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGC Homo sapiens cDNA
1806	11703	21580	0.89	1.0E-96	4503756	NT	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA
1806	11703	21581	0.89	1.0E-96	4503756	NT	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA
2181	12068	21969	1.33	1.0E-96	M75967.1	NT	Human hepatocyte growth factor gene, exon 1
2181	12068	21970	1.33	1.0E-96	M75967.1	NT	Human hepatocyte growth factor gene, exon 1
2219	12650	22009	1.88	1.0E-96	U51472.2	NT	Felis catus superfast myosin heavy chain (sMyHC) mRNA, complete cds
7058	16935	27125	20.65	1.0E-96	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
7138	17015	27208	1.98	1.0E-96	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7843	17693	27938	1.64	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
7843	17693	27939	1.64	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
3285	13206	23006	0.95	6.0E-97	BF245240.1	EST_HUMAN	601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 5'
6459	16319		2.75	6.0E-97	BE141849.1	EST_HUMAN	IL5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA
6672	16552	26747	1.76	5.0E-97	AL043314.2	EST_HUMAN	DKFZp434N0323.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
6735	16614	26804	10.79	5.0E-97	AA418026.1	EST_HUMAN	zv97e12.s1 Scores_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125
7578	17429	27643	2.76	5.0E-97	BF154912.1	EST_HUMAN	G1304125 PMS4 MRNA ;
8832	18945	28929	1.87	5.0E-97	BE148597.1	EST_HUMAN	RC0-BT0812-250900-032-a09 BT0812 Homo sapiens cDNA
8832	18945	28930	1.87	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
924	10849	20697	1.26	4.0E-97	BE004436.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
1868	11764	21638	1.08	4.0E-97	5453572	NT	CM0-BN0106-170300-293-a06 BN0106 Homo sapiens cDNA
6082	16027	26167	6.1	4.0E-97	Y11339.2	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6082	16027	26168	6.1	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
6867	16746	26939	1.41	4.0E-97	11421793	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7328	17232	27433	1.17	4.0E-97	AB011166.1	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
							Homo sapiens mRNA for KIAA0594 protein, partial cds

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7328	17232	27434	1.17	4.0E-97	AB011186.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
8503	18376	28641	1.76	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
8503	18376	28642	1.76	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
8733	17882	28124	15.68	4.0E-97	AB042557.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
8736	17885	28128	2.31	4.0E-97	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
8736	17885	28129	2.31	4.0E-97	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
9331	19012		3.83	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
243	10210	20026	1.17	3.0E-97	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
856	10783	20633	10.96	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
856	10783	20634	10.96	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1423	12694	21195	1.77	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2389	12652	22181	1.92	3.0E-97	U36255.1	NT	Human beta-prime-adaplin (BAM22) gene, exon 7
3223	13147	22948	1.14	3.0E-97	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
4670	14556	24349	12.55	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
5872	15778	25897	2.19	1.0E-97	BE566486.1	EST_HUMAN	601339520F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3881821 5'
8088	17979	28229	3.41	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
8088	17979	28230	3.41	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
8629	18494	28788	2.82	1.0E-97	AA553761.1	EST_HUMAN	nk29g02.s1 NCL CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014962 3'
8763	17912	28156	13.54	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
8763	17912	28157	13.54	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
883	10809	20655	8	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1255	11162	21012	1.29	9.0E-98	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6623	16503	26691	4.74	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
6623	16503	26692	4.74	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
7271	17148	27342	2.77	9.0E-98	X06889.1	NT	Human mRNA for amyloid A4(751) protein
7319	17195	27395	2.41	9.0E-98	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
7355	17223	27423	1.39	9.0E-98	AB037786.1	NT	Homo sapiens mRNA for KIAA1385 protein, partial cds
8369	18246	28497	2.24	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
8369	18246	28498	2.24	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
9345	10809	20688	4.97	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1350	11256	21112	0.89	8.0E-98	AB033788.1	NT	Homo sapiens hPAD-cldn10 mRNA for peptidylarginine deiminase type I, complete cds
1540	11444	21303	1.04	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1540	11444	21304	1.04	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1695	11597	21468	0.98	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1695	11597	21469	0.98	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3726	13638	23424	5.03	8.0E-98	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
5049	14921		0.88	8.0E-98	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
9717	19258	25220	1.29	4.0E-98	BE348727.1	EST_HUMAN	h8802.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151899 3'
2131	12019	21917	1.21	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
2565	12436	22329	1.85	3.0E-98	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2720	12582		2.09	3.0E-98	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
6147	16020	26159	1.7	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6147	16020	26160	1.7	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7083	16960	27153	3.31	3.0E-98	H46698.1	EST_HUMAN	yc17g09.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178240 5'
7685	17535	27759	1.6	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
7685	17535	27760	1.6	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
8322	18199	28448	5.15	3.0E-98	U59309.1	NT	Human fumarylase precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
9895	19373		2.47	3.0E-98	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
2033	11924	21816	29.05	2.0E-98	BE294281.1	EST_HUMAN	601172668F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2191	12078	21983	1.45	2.0E-98	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4199	14099	23880	0.96	2.0E-98	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4244	14143	23916	4.94	2.0E-98	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4720	14606	24390	1.51	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
4720	14606	24391	1.51	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
5069	14939	24711	6.39	2.0E-98	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI1), mRNA
5069	14939	24712	6.39	2.0E-98	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI1), mRNA
5163	15029	24795	1.09	2.0E-98	4758975	NT	Homo sapiens protein tyrosine kinase 2 beta (PTK2B) mRNA
5303	15224	25028	4.66	2.0E-98	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
7004	16881	27073	3.87	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
7004	16881	27074	3.87	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
7497	17367	27572	1.5	2.0E-98	X12664.1	NT	H. sapiens arginase gene exon 3 (EC 3.5.3.1)
7951	17801		1.18	2.0E-98	7705868	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
9350	19026	25301	1.43	2.0E-98	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
399	10345	20172	18.93	1.0E-98	AI682007.1	EST_HUMAN	tw36504.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW-RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A. ;

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
447	10391	20212	2.38	1.0E-98	AW998611.1	EST_HUMAN	PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA
1756	11655	21526	16.96	1.0E-98	N49818.1	EST_HUMAN	y23f05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243565 5' similar to PIR:S54204 S54204 ribosomal protein L29 - human ;
5256	15178	24953	6.96	1.0E-98	AA195854.1	EST_HUMAN	zp98c09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562 G806562 NEBULIN ;
7203	17080	27266	1.36	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
7203	17080	27267	1.36	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5681	15590	25692	4.29	9.0E-99	AW968635.1	EST_HUMAN	EST T380711 MAGC resequences, MAGJ Homo sapiens cDNA
8465	18338	28602	2.6	9.0E-99	AI479829.1	EST_HUMAN	tm69h07.x1 NCL_OGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BIH_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
8465	18338	28603	2.6	9.0E-99	AI479829.1	EST_HUMAN	tm69h07.x1 NCL_OGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BIH_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
8716	18533	28817	1.84	9.0E-99	AA134604.1	EST_HUMAN	zn90d02.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to TR:G662994 G662994 GPI-ANCHORED PROTEIN P137. ;
7065	16942	27134	1.19	8.0E-99	9635487	NT	Homo sapiens endogenous retrovirus, complete genome
5551	15477	25550	9.2	7.0E-99	AF035808.1	NT	Homo sapiens oscillin (hLn) gene, exon 5
8884	18695	28988	2.31	7.0E-99	AF001886.1	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
2080	11970	21863	0.93	6.0E-99	11430555	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, (LOC51232), mRNA
2080	11970	21864	0.93	6.0E-99	11430555	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, (LOC51232), mRNA
3814	13726	23517	1.87	6.0E-99	AW676364.1	EST_HUMAN	EST T388473 MAGC resequences, MAGN Homo sapiens cDNA
4642	14530	24318	1.16	6.0E-99	4502660	NT	Homo sapiens GD34 antigen (GD34) mRNA
6013	15917	26047	2.36	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
6013	15917	26048	2.36	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
6718	16598	26787	1.21	6.0E-99	X99101.1	NT	H. sapiens mRNA for estrogen receptor
7099	16966	27160	2.18	6.0E-99	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
7143	17020	27213	3.57	6.0E-99	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
7143	17020	27214	3.57	6.0E-99	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
8102	17992	28241	3.72	6.0E-99	11526298	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
902	10827	20671	0.86	5.0E-99	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
902	10827	20672	0.86	5.0E-99	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
1922	11817	21696	2.36	5.0E-99	Y11365.1	NT	H. sapiens IMPA gene, exon 8
4463	14357	24148	1.35	5.0E-99	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region
5096	14936	24709	2.46	5.0E-99	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
9360	19032		2.1	5.0E-99	BE5890177.1	EST_HUMAN	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6844	16723		5.37	3.0E-99	M95586.1	NT	Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds
1219	11128		3.46	2.0E-99	AW274792.1	EST_HUMAN	xp09e06.x1 NCI_CGAP_HIN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
3220	13144	22947	1.08	2.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4443	14337	24127	3.15	2.0E-99	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7053	16930	27121	9.75	2.0E-99	W23507.1	EST_HUMAN	zb46d06.r1 Soares_fetal_lung_Nihl19W Homo sapiens cDNA clone IMAGE:306635 5' similar to gb:M16182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
8451	18324	28583	3.83	2.0E-99	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
312	10274	20093	1.53	1.0E-99	AF114487.1	NT	Homo sapiens intersecin long isoform (TSN) mRNA, complete cds
375	10329	20152	1.04	1.0E-99	11528160	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1401	11306	21166	2.11	1.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1537	11441	21298	1.47	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1537	11441	21299	1.47	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1855	11781	21656	1.1	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
1855	11781	21657	1.1	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3046	12973	22766	0.89	1.0E-99	U03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4283	14182	23960	2.74	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4283	14182	23961	2.74	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5200	15063		1.18	1.0E-99	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
7305	17181		1.15	1.0E-99	11419721	NT	Homo sapiens ALEX1 protein (LOC51309), mRNA
7483	17353	27557	1.68	1.0E-99	AW340174.1	EST_HUMAN	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711
8683	18571	28854	2.4	1.0E-99	AB023222.1	NT	Q02711 PRO-POL-DUTPASE POLYPROTEIN;
							Homo sapiens mRNA for KIAA1005 protein, partial cds
9125	18884		3.76	1.0E-99	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1	9989	19780	1.13	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	9989	19780	1.93	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
62	10048	19859	1.48	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
62	10048	19860	1.48	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
81	10065	19883	1.62	1.0E-100	AW275237.1	EST_HUMAN	xv78b11.x1 NCI_CGAP_Bln53 Homo sapiens cDNA clone IMAGE:2824605 3'
162	10135	19950	1.16	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
314	10276	20095	1.01	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
340	10299	20114	2.43	1.0E-100	T05087.1	EST_HUMAN	EST02975 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBCR32

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
430	10375		1.53	1.0E-100	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
481	10425		7.04	1.0E-100	X89831.1	NT	G. gorilla DNA for ZNF80 gene homolog
500	10442	20255	4.17	1.0E-100	BE180609.1	EST_HUMAN	RC3-HT0625-040500-022-b09 HT0625 Homo sapiens cDNA
1002	10920	20763	2.43	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1002	10920	20764	2.43	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1528	11433		1.33	1.0E-100	AW207555.1	EST_HUMAN	UI-H-B11-afic-c-07-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
							qf62709.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA
1533	11437	21294	1.46	1.0E-100	AI200857.1	EST_HUMAN	P81061 CYSTATIN1 ;
2195	12082		1.45	1.0E-100	D83349.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2388	12267	22160	1.08	1.0E-100	X62468.1	NT	H. sapiens mRNA for IFN-gamma (pKC-0)
2674	12539	22429	1.87	1.0E-100	11418976	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
2685	12913		2.45	1.0E-100	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4116	14016	23796	1.49	1.0E-100	AF057354.1	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
4143	14043	23816	1.87	1.0E-100	4503792	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5024	14897	24665	3.07	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5024	14897	24666	3.07	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5232	15156	24924	1.8	1.0E-100	BF244218.1	EST_HUMAN	601863164F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080999 5'
5496	15415	25478	1.4	1.0E-100	AU118182.1	EST_HUMAN	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
5514	15432	25496	1.55	1.0E-100	AF135116.1	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
5915	15821	25946	5.1	1.0E-100	AU140214.1	EST_HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6015	15919	26049	1.41	1.0E-100	R10887.1	EST_HUMAN	Y38-c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
6116	16010	26146	1.4	1.0E-100	BF376478.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
6116	16010	26147	1.4	1.0E-100	BF376478.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
6119	16013	26151	6.99	1.0E-100	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
6963	16841	27033	6.19	1.0E-100	BF103853.1	EST_HUMAN	601647375F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5'
6983	16860		5.44	1.0E-100	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
7322	17198	27398	3.2	1.0E-100	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
							wr37g09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2489920 3' similar to contains element
7369	17347		1.53	1.0E-100	AI972388.1	EST_HUMAN	MER22 repetitive element ;
7426	16439	26625	1.67	1.0E-100	AW998511.1	EST_HUMAN	PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA
7527	17378	27587	1.73	1.0E-100	AB046846.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
7527	17378	27588	1.73	1.0E-100	AB046846.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
7664	17514	27740	1.69	1.0E-100	AW630487.1	EST_HUMAN	hh83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2966396 5'

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7664	17514	27741	1.69	1.0E-100	AW 630487.1	EST_HUMAN	h83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
8016	17866		1.29	1.0E-100	Y10391.1	NT	Human endogenous retrovirus HERV-K, pol gene
8141	18029	28275	5.23	1.0E-100	BF327292.1	EST_HUMAN	MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
8606	18473	28745	2.14	1.0E-100	X94633.1	NT	H.sapiens CD97 gene exon 4
8606	18473	28746	2.14	1.0E-100	X94633.1	NT	H.sapiens CD97 gene exon 4
8660	18549	28831	4.56	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
8660	18549	28832	4.56	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
8688	9989	19780	1.96	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
8930	18738		1.86	1.0E-100	AF296285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9048	18832	29114	5.59	1.0E-100	AF240786.1	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
9351	19027	25302	2.21	1.0E-100	11545732	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
9940	19409	25181	3.38	1.0E-100	11417974	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
70	10055	19871	1.22	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
70	10055	19872	1.22	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
671	10805	20422	1.16	1.0E-101	AB007915.2	NT	Homo sapiens mRNA for KIAA0448 protein, partial cds
688	10821	20447	4.45	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
688	10821	20448	4.45	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
754	10884	20521	1.32	1.0E-101	7657454	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
							Homo sapiens pscadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
							Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, mRNA
835	10762	20612	1.28	1.0E-101	4503914	NT	phosphoribosylaminimidazole synthetase (GART) mRNA
908	10832	20679	3.44	1.0E-101	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
969	10892	20741	12.74	1.0E-101	BF681218.1	EST_HUMAN	802136474FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5'
1036	10954	20796	1.63	1.0E-101	A1221878.1	EST_HUMAN	q990909.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1712	11613	21483	0.87	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1712	11613	21484	0.87	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1901	11797	21677	1.62	1.0E-101	4502996	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2010	11902	21792	1.6	1.0E-101	BE843070.1	EST_HUMAN	RC3-ST0281-160600-016-n09 ST0281 Homo sapiens cDNA
2301	12718	22080	1.66	1.0E-101	5729892	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2572	12443	22335	4.4	1.0E-101	X72993.1	NT	H.sapiens EWS gene, exon 5
2714	12576	22468	2.56	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
2714	12576	22469	2.56	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
2925	12852		12.14	1.0E-101	AJ252312.1	NT	Homo sapiens genomic downstream Rhesus box
3167	13092	22897	2.51	1.0E-101	4885270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3203	13127		2.16	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3334	13254	23059	1.67	1.0E-101	AW965556.1	EST_HUMAN	EST377629 IMAGE resequences, MAGI Homo sapiens cDNA
3354	12576	22468	1.75	1.0E-101	AJ237744.1	NT	Homo sapiens RIB1LR gene (partial), exon 12
3354	12576	22469	1.75	1.0E-101	AJ237744.1	NT	Homo sapiens RIB1LR gene (partial), exon 12
3800	13712	23499	4.83	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
4965	14840	24609	1.67	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
4965	14840	24610	1.67	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5257	15179	24954	1.4	1.0E-101	AW965139.1	EST_HUMAN	EST377212 IMAGE resequences, MAGI Homo sapiens cDNA
5651	15563	26658	3.73	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
5651	15563	26659	3.73	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6333	16196	26356	4.16	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
6333	16196	26357	4.16	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
6416	16278	26441	5.63	1.0E-101	AW008475.1	EST_HUMAN	ww55f12.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
6471	16330		1.56	1.0E-101	BE257384.1	EST_HUMAN	601109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349801 5'
6544	16402	26581	5.3	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-F12 BT0313 Homo sapiens cDNA
6633	16573	26764	2.65	1.0E-101	BF029174.1	EST_HUMAN	601764688F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996837 5'
7208	17085	27274	1.15	1.0E-101	AA038800.1	EST_HUMAN	zk29g08.r1 Soares_pregnant_uterus_NbHPJ Homo sapiens cDNA clone IMAGE:471998 5' similar to
7446	16458	26650	16.52	1.0E-101	X60069.1	NT	PIR:S54640 S54640 YD9335.03c protein - yeast;
7446	16458	26651	16.52	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
7454	17263	27468	18.4	1.0E-101	9845482	NT	Human mRNA for pancreatic gamma-glutamyltransferase
7623	17474	27694	5.64	1.0E-101	BE619667.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
7623	17474	27695	5.64	1.0E-101	BE619667.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875963 3'
7950	17800	28040	1.76	1.0E-101	11429127	NT	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875963 3'
8252	18132	28381	2.88	1.0E-101	S38327.1	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
8454	18327	28586	1.78	1.0E-101	AB020626.1	NT	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit [human, Genomic, 195 nt, segment 8 of 9]
9610	19189		11.62	1.0E-101	AW93051.1	EST_HUMAN	Homo sapiens mRNA for KIAA0819 protein, partial cds
338	10297	20111	3.24	1.0E-102	AL163303.2	NT	QV1-DT0068-240200-085-a01 DT0068 Homo sapiens cDNA
604	10540	20350	0.89	1.0E-102	BE262470.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
758	10698	20526	1.46	1.0E-102	4557534	NT	601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
1101	11017	20859	1.95	1.0E-102	M10976.1	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1247	11154	21002	1.39	1.0E-102	11437146	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1247	11154	21003	1.39	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1398	11303	21162	90.24	1.0E-102	BE408447.1	EST_HUMAN	601299982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5'
2261	12145	22044	1.34	1.0E-102	AI124669.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95;
2261	12145	22045	1.34	1.0E-102	AI124669.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95;
3026	12954	22747	1.51	1.0E-102	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3094	13021	22815	5.61	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3094	13021	22816	5.61	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4139	14039	23814	1.46	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4314	14211	23994	2.11	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
5063	14933	24705	1.09	1.0E-102	R66488.1	EST_HUMAN	y32c04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 5'
5300	15221	25025	1.88	1.0E-102	AF067133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5515	15433		7.27	1.0E-102	AB034951.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5536	15463	25522	3.46	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5536	15463	25523	3.46	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5800	15706	25818	2.54	1.0E-102	AI459825.1	EST_HUMAN	ar62f09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 Q13137 NDP52;
6351	16214	26376	6.66	1.0E-102	AJ238994.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
6495	16354	26524	2.53	1.0E-102	AV710738	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CuAAKD03 5'
6787	16666	26857	4.2	1.0E-102	BE763051.1	EST_HUMAN	QV3-NT0025-210600-236-h08 NT0025 Homo sapiens cDNA
6832	16711	26904	2.53	1.0E-102	BE910556.1	EST_HUMAN	601501107F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903145 5'
6945	16823	27014	1.36	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GK Homo sapiens cDNA clone GKCEEE11 5'
6945	16823	27015	1.36	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GK Homo sapiens cDNA clone GKCEEE11 5'
7001	16878	27069	4.06	1.0E-102	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
7374	17243	27448	1.52	1.0E-102	T70393.1	EST_HUMAN	ydl13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
7374	17243	27449	1.52	1.0E-102	T70393.1	EST_HUMAN	ydl13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
7415	17282	27490	3.58	1.0E-102	AU124629.1	EST_HUMAN	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'
7961	17811	28052	2.03	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
7961	17811	28053	2.03	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
7981	17831	28070	2.9	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
7981	17831	28071	2.9	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
8005	17855	28096	2.3	1.0E-102	AA970786.1	EST_HUMAN	on57h04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to SW:CAV2_HUMAN P51636 CAVEOLIN-2 [1];
8421	18295	28549	2.38	1.0E-102	BE897468.1	EST_HUMAN	601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924166 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8424	18298	28553	1.99	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
8424	18298	28554	1.99	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
8708	18525	28807	2.78	1.0E-102	BF359243.1	EST_HUMAN	RC6-ET0072-1:50600-011-F01 ET0072 Homo sapiens cDNA
8947	18755	29051	4.04	1.0E-102	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
9054	18837		2.82	1.0E-102	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
9601	19183	25247	4.77	1.0E-102	AW300862.1	EST_HUMAN	x407c12.x1 NCL_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2666038 3'
63	10049	19861	0.82	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
63	10049	19862	0.82	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
93	10078	19894	8.1	1.0E-103	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
201	10173	19989	0.83	1.0E-103	5453793	NT	Homo sapiens nucleolar protein (KKEJ repeat) (NOP56) mRNA
965	10888	20734	1.01	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1223	11131	20985	7.29	1.0E-103	BE877541.1	EST_HUMAN	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1578	11482	21342	2.32	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
1872	11768	21643	1.04	1.0E-103	7557562	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SNAP), mRNA
1932	11827	21708	1.27	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1932	11827	21709	1.27	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2257	12141	22040	1.57	1.0E-103	AU134991.1	EST_HUMAN	AU134991 PLACE1 Homo sapiens cDNA clone PLACE1000965 5'
2401	12278	22175	2.22	1.0E-103	AF060588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2578	12449	22340	0.86	1.0E-103	N327770.1	EST_HUMAN	ww91d08.s1 Scores_placenta_8to9weeks_2NbHP8c9W Homo sapiens cDNA clone IMAGE:259599 3'
3030	12958		2.43	1.0E-103	BE744722.1	EST_HUMAN	601578113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
3333	13283	23058	3.44	1.0E-103	AW298245.1	EST_HUMAN	UIH-BW0-aj-h-11-0-UI.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'
3393	13310	23108	1.06	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3695	13609		2.41	1.0E-103	AF023881.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3725	13637	23423	1.16	1.0E-103	AA485663.1	EST_HUMAN	ab10d12.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element ;
3757	13670	23454	1.39	1.0E-103	11430878	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
3922	13831	23611	3.02	1.0E-103	T23683.1	EST_HUMAN	seq340 b4HB3MA-Cct109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cct109+10-Bio-7 3'
5619	15534	25619	1.72	1.0E-103	AF179995.1	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
5988	15903	26027	5.37	1.0E-103	AF063490.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
6033	15936	26069	1.88	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6033	15936	26070	1.68	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
6092	15102	24878	1.68	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6092	15102	24879	1.68	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6289	16153	26310	1.64	1.0E-103	AW965776.1	EST_HUMAN	EST377849 IMAGE resequences, MAGI Homo sapiens cDNA
6338	16201	26361	3.21	1.0E-103	BE748158.1	EST_HUMAN	601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838545 5'
6568	16426	26607	3.28	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
6568	16426	26608	3.28	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
6823	16702	26896	2.95	1.0E-103	T31080.1	EST_HUMAN	EST27193 Human Brain Homo sapiens cDNA 5' end similar to None
7010	16887	27079	1.17	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
7010	16887	27080	1.17	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
7050	16927	27118	1.43	1.0E-103	BF109244.1	EST_HUMAN	7f60e03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525954 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1;
7267	17144	27337	3.08	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7267	17144	27338	3.08	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7787	17637	27870	2.02	1.0E-103	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7815	17685	27905	2.09	1.0E-103	AW963676.1	EST_HUMAN	EST375749 IMAGE resequences, MAGH Homo sapiens cDNA
7878	17728	27972	9.93	1.0E-103	AI878956.1	EST_HUMAN	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to TR:O15046 O15046 KIAA0338;
8115	18004	28250	3.08	1.0E-103	AF792759.1	EST_HUMAN	o02d06.y6 NCL CGAP_L45 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING;
8218	18101	28353	2.74	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
8218	18101	28354	2.74	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
8681	18569	28852	2.56	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
8743	17892	28136	6.49	1.0E-103	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8973	18778	29070	3.42	1.0E-103	BE644611.1	EST_HUMAN	7e68a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.i3 MER29 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9049	18833		1.72	1.0E-103	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9079	18855		2.65	1.0E-103	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
9275	18879	25323	2.21	1.0E-103	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
233	10202	20016	2.6	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072 5'
233	10202	20017	2.6	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072 5'
1845	11741	21617	1.81	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteoinductive protein 2) (BMP8) mRNA
2147	12035	21932	7.16	1.0E-104	AA132975.1	EST_HUMAN	z02c06.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587626 3' similar to gb:Z14118_mn1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2157	12044	21944	1.91	1.0E-104	BE744628.1	EST_HUMAN	601577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5'
2318	12189	22097	1.15	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2318	12189	22098	1.15	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2387	12266	22159	1.55	1.0E-104	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2842	12770	22559	7.64	1.0E-104	M34671.1	NT	Human lymphocytic antigen CD59/MEM43 mRNA, complete cds
2886	12813		2.82	1.0E-104	Y11151.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
3345	13265		1.54	1.0E-104	AA319436.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3550	13465	23260	0.99	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3550	13465	23261	0.99	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3861	13772	23584	0.91	1.0E-104	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4280	14179	23957	4.28	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4504	14397	24182	0.9	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4504	14397	24183	0.9	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
5617	15532	25615	1.33	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
5617	15532	25616	1.33	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
5891	15797	25919	8.46	1.0E-104	A1768797.1	EST_HUMAN	wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN, contains element LTR7 repetitive element ;
5891	15797	25920	8.46	1.0E-104	A1768797.1	EST_HUMAN	wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN, contains element LTR7 repetitive element ;
6073	16056	26204	1.52	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6073	16056	26205	1.52	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6288	16152	26309	2.38	1.0E-104	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
7288	17164	27363	2.24	1.0E-104	BF448230.1	EST_HUMAN	mad16g11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3'
7370	17239	27442	4.66	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
7370	17239	27443	4.66	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7430	16443	26630	3.84	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
7430	16443	26631	3.84	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
7809	17659	27898	3.14	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
7809	17659	27899	3.14	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
7947	17797	28037	1.42	1.0E-104	AV728070.1	EST_HUMAN	AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
7966	17816	28057	4.51	1.0E-104	AU130765.1	EST_HUMAN	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5'
8014	17864	28110	4.24	1.0E-104	U66355.1	NT	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
8617	18484	28755	1.84	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
8617	18484	28756	1.84	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
8641	18505	28783	4.49	1.0E-104	BF684288.1	EST_HUMAN	602141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5'
9842	19340		1.37	1.0E-104	BE393892.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3659676 5'
277	12637	20062	2.86	1.0E-105	4502156	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
419	9986	19777	16.85	1.0E-105	4505150	NT	Homo sapiens Meis1 (mouse) homologue (MEIS1) mRNA
579	10517	20323	3.22	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
579	10517	20324	3.22	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1777	11676	21553	1.16	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1884	11780	21655	1.75	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2142	12030	21928	1.64	1.0E-105	AA318369.1	EST_HUMAN	EST20609 Spleen I Homo sapiens cDNA 5' end similar to autoimmune antigen Ku, p70/p80 subunit
2689	12554		0.87	1.0E-105	AA584808.1	EST_HUMAN	no10d05.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
2975	12902		2.57	1.0E-105	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3307	13228	23032	0.93	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3307	13228	23033	0.93	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3502	13506		1.26	1.0E-105	11425532	NT	Homo sapiens dermatopontin (DPT), mRNA
4008	13914	23689	2.15	1.0E-105	AW961688.1	EST_HUMAN	EST373761 IMAGE resequences, MAGG Homo sapiens cDNA
4638	14526	24313	0.94	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4638	14526	24314	0.94	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4855	14735		3.74	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5044	14916	24690	0.95	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
5095	14965	24740	2.23	1.0E-105	AB020673.1	NT	Homo sapiens mRNA for KIAA0896 protein, complete cds
5161	14916	24690	1.3	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
6167	15124	24840	3.06	1.0E-105	11419193	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6167	15124	24841	3.06	1.0E-105	11419193	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6679	16559	26754	6.43	1.0E-105	T05087.1	EST_HUMAN	EST02975 Fetal brain, Stralagene (cat#936206) Homo sapiens cDNA clone HFBCR32

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6894	16773	26967	1.8	1.0E-105	AW007194.1	EST_HUMAN	ws50c10.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2500626 3' similar to SW:ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE ;
7234	17111	27304	2.99	1.0E-105	AW016879.1	EST_HUMAN	UI-H-B10p-ab1-b-12-Q-UI.s1 NCL_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
8303	18181	28428	5.44	1.0E-105	AF265482.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
8560	18430	28699	1.8	1.0E-105	D63548.1	NT	Homo sapiens COL4A6 gene for a6(V) collagen, exon 31
8602	18469	28740	2.06	1.0E-105	7705936	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
8867	18679	28968	2.01	1.0E-105	AW027554.1	EST_HUMAN	wv7407.x1 Soares_thymus_NHfTh Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892 P87892 PROTEASE ;
145	10119	19987	0.96	1.0E-106	AW503208.1	EST_HUMAN	UI-HF-BNO-akt-g-07-Q-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
198	10170	19987	1.54	1.0E-106	AI55055.1	EST_HUMAN	tg79c01.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2215008 3'
531	10473	20286	1.77	1.0E-106	AW96556.1	EST_HUMAN	EST377629 MAGe resequences, MAGI Homo sapiens cDNA
589	10527	20334	0.79	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psl-hd1)
590	10527	20334	1.21	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psl-hd1)
1508	11413	21272	2.66	1.0E-106	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1674	11576	21444	4.51	1.0E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1762	11661	21533	5.12	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element ;
1762	11661	21534	5.12	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element ;
2075	11965	21858	1.08	1.0E-106	BE144286.1	EST_HUMAN	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2269	12153	22052	8.39	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2456	12333	22229	1.63	1.0E-106	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2557	12429	22322	1.25	1.0E-106	U64675.2	NT	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2559	12431	22324	1.94	1.0E-106	BE260201.1	EST_HUMAN	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5'
2729	12591	22487	4.23	1.0E-106	AI276526.1	EST_HUMAN	q176h10.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
2795	11319	21183	2.97	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2795	11319	21184	2.97	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2911	12837	22635	5.01	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
2911	12837	22636	5.01	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3143	13068	22867	2.36	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3143	13068	22868	2.36	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3328	13248	23053	0.8	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3394	13311	23109	0.98	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3394	13311	23110	0.98	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3952	13860	23634	7.22	1.0E-106	AW974650.1	EST_HUMAN	EST396875 MAGE resequences, MAGN Homo sapiens cDNA
3952	13860	23635	7.22	1.0E-106	AW974650.1	EST_HUMAN	EST396875 MAGE resequences, MAGN Homo sapiens cDNA
4497	14391	24176	1.21	1.0E-106	BE144286.1	EST_HUMAN	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
5183	15047		1.21	1.0E-106	L41644.1	NT	Homo sapiens dystrophin gene, exon 41
5298	15219	25022	2.98	1.0E-106	AA781155.1	EST_HUMAN	aj24609.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN
5711	15619	25722	6.78	1.0E-106	BF679574.1	EST_HUMAN	PHPS1-2 (HUMAN);
5866	15772	25891	16.4	1.0E-106	11545913	NT	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295067 5'
5866	15772	25892	16.4	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6361	16224	26385	5.59	1.0E-106	AA663779.1	EST_HUMAN	Homo sapiens xylosyltransferase II (XT2), mRNA
6390	16252	26412	4.83	1.0E-106	11429617	NT	ae72e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X65873
6431	16292	26453	1.35	1.0E-106	BE292722.1	EST_HUMAN	KINESIN HEAVY CHAIN (HUMAN);
6490	16348	26517	7.6	1.0E-106	11425503	NT	Homo sapiens XPMC2 protein (LOC57109), mRNA
6490	16348	26518	7.6	1.0E-106	11425503	NT	601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2888345 5'
6657	16537	26733	5.33	1.0E-106	BE741408.1	EST_HUMAN	Homo sapiens sorting nexin 11 (SNX11), mRNA
6657	16537	26734	5.33	1.0E-106	BE741408.1	EST_HUMAN	Homo sapiens sorting nexin 11 (SNX11), mRNA
6754	16633	26821	1.48	1.0E-106	AF523066.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
7052	16929	27120	3.16	1.0E-106	AF654123.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
7281	17158	27353	1.86	1.0E-106	AA825307.1	EST_HUMAN	ar68a07.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233
7281	17158	27354	1.86	1.0E-106	AA825307.1	EST_HUMAN	CALGRANULIN B (HUMAN);
7351	17219	27419	2.79	1.0E-106	AF750447.1	EST_HUMAN	ty62a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
7424	17291	27501	1.86	1.0E-106	AF479569.1	EST_HUMAN	Q05084 69 KD ISLET CELL AUTOANTIGEN;
7424	17291	27502	1.86	1.0E-106	AF479569.1	EST_HUMAN	cc67e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
7803	17653	27890	1.32	1.0E-106	BF027310.1	EST_HUMAN	cc67e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
7803	17653	27891	1.32	1.0E-106	BF027310.1	EST_HUMAN	cr03a04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_on03a04 random
7880	17730	27975	5.83	1.0E-106	AA604417.1	EST_HUMAN	tm41f02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.13
7880	17730	27976	5.83	1.0E-106	AA604417.1	EST_HUMAN	TAR1 P1R5 repetitive element;
							tm41f02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.13
							TAR1 P1R5 repetitive element;
							tm41f02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.13
							TAR1 P1R5 repetitive element;
							601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
							601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
							np57b10.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
							np57b10.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7901	17751	27990	1.86	1.0E-106	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
8019	17869	28113	3.66	1.0E-106	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8269	18149	28389	5.21	1.0E-106	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
8269	18149	28390	5.21	1.0E-106	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
8415	18299	28544	2.28	1.0E-106	JO5200.1	NT	Human tyrosine receptor mRNA, complete cds
8415	18299	28545	2.28	1.0E-106	JO5200.1	NT	Human tyrosine receptor mRNA, complete cds
9122	19540		2.87	1.0E-106	AW410405.1	EST_HUMAN	fh05h11.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961644 5'
9342	19022	25298	2.31	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
9342	19022	25299	2.31	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
9554	19152		5.35	1.0E-106	BE695905.1	EST_HUMAN	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA
234	10203		3.48	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
264	10229		1.05	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alphas/beta receptor
606	10542		1.07	1.0E-107	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
614	10550	20361	1.7	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
796	10725	20565	0.86	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alphas/beta receptor
868	10794	20644	1.16	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alphas/beta receptor
953	10877	20724	10.67	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1257	11164	21015	0.78	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1551	11456	21314	2.13	1.0E-107	BF087405.1	EST_HUMAN	QY2-HT0540-120900-368-a05 HT0540 Homo sapiens cDNA
1718	11619	21488	1.47	1.0E-107	AF198275.1	NT	Homo sapiens cathepsin Z precursor (CTS2) gene, exon 3
1797	11695	21571	0.95	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1797	11695	21572	0.95	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2161	12048	21949	1.26	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2487	12362	22257	0.86	1.0E-107	BE732460.1	EST_HUMAN	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2487	12362	22258	0.86	1.0E-107	BE732460.1	EST_HUMAN	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2976	12903	22701	1.94	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2976	12903	22702	1.94	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3061	12968	22779	2.62	1.0E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
3754	13667	23450	3.92	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTMR1) gene, exon 9
5575	15490	25567	3.26	1.0E-107	BE867469.1	EST_HUMAN	601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846494 5'
6356	16219	26380	1.52	1.0E-107	AW503913.1	EST_HUMAN	U1-HF-BN0-alf-c-08-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
6356	16219	26381	1.52	1.0E-107	AW503913.1	EST_HUMAN	U1-HF-BN0-alf-c-08-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
6445	16306	26471	1.63	1.0E-107	A1765078.1	EST_HUMAN	wh56h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8087	17978	28228	2.73	1.0E-107	A1392850.1	EST_HUMAN	ig10d06.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICD1
8316	18163	28443	1.82	1.0E-107	L49141.1	NT	P05095 ALPHA-ACTININ 3, NON MUSCULAR;
8327	18204	28453	1.98	1.0E-107	BF666511.1	EST_HUMAN	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
8638	18503	28779	9.12	1.0E-107	BE540550.1	EST_HUMAN	602123693F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281039 5'
8697	17881	28122	4.21	1.0E-107	11419701	NT	601066681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
8697	17881	28123	4.21	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
9187	19673		3.94	1.0E-107	AA001415.1	EST_HUMAN	Homo sapiens HSPC049 protein (HSPC049), mRNA
939	10864	20711	1.46	1.0E-108	BE296042.1	EST_HUMAN	z645e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1
1244	11151	20989	1.55	1.0E-108	Y18000.1	NT	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632348 5'
						NT	Homo sapiens NF2 gene
2282	12166	22063	7.41	1.0E-108	A1686040.1	EST_HUMAN	tt91e10.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
						EST_HUMAN	PROTEOGLYCAN II PRECURSOR (HUMAN);
2282	12166	22064	7.41	1.0E-108	A1686040.1	EST_HUMAN	tt91e10.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
						EST_HUMAN	PROTEOGLYCAN II PRECURSOR (HUMAN);
2378	12258	22150	7.2	1.0E-108	BE206094.1	EST_HUMAN	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X53777 60S
3305	13226	23028	0.94	1.0E-108	AF032897.1	NT	RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
3305	13226	23029	0.94	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3742	13654	23437	0.92	1.0E-108	5453855	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
						NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
4065	13967	23744	1.33	1.0E-108	AW1664438.1	EST_HUMAN	hi12a11.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE
4425	14320	24106	1.99	1.0E-108	U72961.1	NT	P55194 SH3-BINDING PROTEIN 3BP-1;
4425	14320	24107	1.99	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4699	14565	24376	2.85	1.0E-108	7661979	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4868	14748	24528	2.19	1.0E-108	AJ008005.1	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5366	15286	25120	1.53	1.0E-108	AW1384094.1	EST_HUMAN	Homo sapiens PSN1 gene, alternative transcript
5393	15312	25166	2.77	1.0E-108	BE869016.1	EST_HUMAN	RCO-HT0372-241199-031-d03 HT0372 Homo sapiens cDNA
5393	15312	25167	2.77	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
						EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
5732	15640	25745	5.06	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
5732	15640	25746	5.06	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5789	15695	25904	1.37	1.0E-108	AJ133269.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6247	16113	26265	5.35	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR5B), mRNA
6399	16280	26421	3.34	1.0E-108	4758333	NT	Homo sapiens delta-6 fatty acid desaturase (FADS6), mRNA
6698	16578		1.93	1.0E-108	AF063500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8202	15099	24891	2.77	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
8593	18461	28731	4.26	1.0E-108	AW966185.1	EST_HUMAN	EST378258 IMAGE resequences, MAGI Homo sapiens cDNA
8677	18565		2.03	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
8706	12166	22063	4.14	1.0E-108	AI686040.1	EST_HUMAN	tt97e10x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
8706	12166	22064	4.14	1.0E-108	AI686040.1	EST_HUMAN	tt97e10x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
9357	19030	25303	2.79	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
9736	19270		5.59	1.0E-108	BF346356.1	EST_HUMAN	602018571F1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154297 5'
58	10044	19856	0.9	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
212	10183	19997	0.92	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
222	10192	20003	1.51	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
459	10403	20219	3.64	1.0E-109	4507712	NT	Homo sapiens tetrahydropeptide repeat domain 2 (TTC2) mRNA
583	10521	20328	14.64	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
583	10521	20329	14.64	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1184	11095	20941	9.63	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1185	11095	20941	4.89	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1831	11728	21602	1.48	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2194	12081	21985	2.03	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2204	12091	21993	1.97	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2581	12452	22344	3.88	1.0E-109	AI02328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN. ;
2581	12452	22345	3.88	1.0E-109	AI02328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN. ;
2582	12453	22346	2.75	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3020	12948	22740	1.88	1.0E-109	N85190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3342	13262	23068	1.45	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-F10 NN0009 Homo sapiens cDNA
3342	13262	23069	1.45	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-F10 NN0009 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3474	13390	23195	1.2	1.0E-109	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3767	13680		1.53	1.0E-109	BE146144.1	EST_HUMAN	MRO-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA
3911	13821	23601	1.54	1.0E-109	AB011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
3911	13821	23602	1.54	1.0E-109	AB011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
4054	13966	23732	3.67	1.0E-109	AI655417.1	EST_HUMAN	ts98e06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP.F53A2.8 CE16100 ;
4070	13972	23749	1.02	1.0E-109	AA662274.1	EST_HUMAN	nu83c12.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ;
4070	13972	23750	1.02	1.0E-109	AA662274.1	EST_HUMAN	P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ;
4304	14202	23986	2.25	1.0E-109	4604206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCY1A) mRNA
4496	14390	24175	1.19	1.0E-109	7662083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
4839	14720	24503	1.04	1.0E-109	R15400.1	EST_HUMAN	ye48a06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53057 5'
4984	14859	24626	0.86	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
4984	14859	24627	0.86	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
5254	15176	24950	2.31	1.0E-109	5174622	NT	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
5648	15364		1.48	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens cDNA
6465	16325	26491	3.66	1.0E-109	11432574	NT	Homo sapiens A.T-binding transcription factor 1 (ATBF1), mRNA
6466	16326	26492	5.01	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
6466	16326	26493	5.01	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
6753	16632	26820	1.36	1.0E-109	AL049784.1	NT	Novel human gene mapping to chromosome 13
6820	16699	26892	1.23	1.0E-109	AW749130.1	EST_HUMAN	PMO-BT0340-091299-002-e05 BT0340 Homo sapiens cDNA
7030	16907		1.72	1.0E-109	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
7071	16948	27139	5.71	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
7071	16948	27140	5.71	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
7326	17202	27402	2	1.0E-109	H84860.1	EST_HUMAN	ys00g08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP:A53491 A53491 BUMETANIDE-SENSITIVE NA-K-Cl COTRANSPORTER - SPINY ;
7462	17322	27528	1.41	1.0E-109	F06604.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1ec12
8155	18043	28294	2.93	1.0E-109	BE540909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
8155	18043	28295	2.93	1.0E-109	BE540909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
8183	18069	28318	14.2	1.0E-109	BF694831.1	EST_HUMAN	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
8335	18212	28464	2.12	1.0E-109		NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
8335	18212	28465	2.12	1.0E-109	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
8468	18341	28606	1.88	1.0E-109	AU121370.1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002690 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8676	18564	28848	2.19	1.0E-109	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
8710	18527	28810	4.83	1.0E-109	W16510.1	EST_HUMAN	zh08b12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to
9259	12091	21993	1.65	1.0E-109	Y17123.1	NT	PIR:S43969 S43969 p54-beta stress-activated protein kinases - rat ;
9594	19176	25275	2.8	1.0E-109	AB011399.1	NT	Homo sapiens SNF-5/INI1 gene, exon 6
3	9890	19781	1.48	1.0E-110	7549804	NT	Homo sapiens gene for A-F-6, complete cds
34	10021	19817	3.88	1.0E-110	5803073	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
34	10021	19818	3.88	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
75	10059	19876	30.63	1.0E-110	C04498.1	EST_HUMAN	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
104	9990	19781	1.67	1.0E-110	7549804	NT	C04498 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC3467
291	10255	20076	0.91	1.0E-110	D87291.1	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
516	10458	20269	1.16	1.0E-110	U84550.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
1163	11076	20921	1.09	1.0E-110	5031620	NT	Human dystrobrein (DTN) gene, exon 20
1258	11165	21016	1.01	1.0E-110	AB032253.1	NT	Homo sapiens calcitonin receptor-like (CALORL) mRNA
1879	11775	21650	1.5	1.0E-110	BE379477.1	EST_HUMAN	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
2012	11904		1.86	1.0E-110	BF508896.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3009683 5'
2810	12739		1.02	1.0E-110	4503098	NT	U1-H-B14-aos-b-05-O-UJ.st NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
							Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3048	12975		1.07	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3158	13083	22885	1.87	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3158	13083	22886	1.87	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3966	13673	23650	0.92	1.0E-110	BE018556.1	EST_HUMAN	bb82a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048848 5' similar to TR:O60312 O60312 KIAA0866 PROTEIN ;
4533	14426	24207	2.06	1.0E-110	AU017213.1	EST_HUMAN	ou32b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to
4556	14447	24232	2.08	1.0E-110	AU117812.1	EST_HUMAN	SW:NI21_RAT_P52591_NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4898	14778		2.34	1.0E-110	7682441	NT	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
5237	15161	24929	1.9	1.0E-110	BE259406.1	EST_HUMAN	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5511	15429	25492	7.34	1.0E-110	11419323	NT	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'
5511	15429	25493	7.34	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6032	19458	26068	4.36	1.0E-110	M55112.1	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6391	16253	26413	10.04	1.0E-110	AV714276.1	EST_HUMAN	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
6391	16253	26414	10.04	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
6409	16270	26432	2.7	1.0E-110	AB020675.1	NT	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
							Homo sapiens mRNA for KIAA0868 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7523	17374	27593	2.91	1.0E-110	AW838394.1	EST_HUMAN	QV2.L.T0063-020400-119-e04.LT0053 Homo sapiens cDNA
7915	17765	28004	4.27	1.0E-110	11432732	NT	Homo sapiens galactokinase 2 (GALK2), mRNA
8130	18018	28266	3.7	1.0E-110	Y12337.1	NT	H. sapiens mRNA for myotonic dystrophy protein kinase like protein
8334	18211	28462	3.49	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
8334	18211	28463	3.49	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
8740	17889	28133	2.43	1.0E-110	AA446529.1	EST_HUMAN	zw67g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1145816
9081	18857		4.15	1.0E-110	BE897218.1	EST_HUMAN	G1145816 FKBP54;
9204	18935		5.78	1.0E-110	AW062258.1	EST_HUMAN	6014339784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
9444	19080		1.63	1.0E-110	AB011399.1	NT	IL0-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA
9578	19684		5.07	1.0E-110	BF364546.1	EST_HUMAN	Homo sapiens gene for AF-6, complete cds
168	10140		16.85	1.0E-111	U43701.1	NT	PM3-NN1082-140900-006-f12 NN1082 Homo sapiens cDNA
189	10161	19978	1.02	1.0E-111	4758807	NT	Human ribosomal protein L23a mRNA, complete cds
718	10650		1.87	1.0E-111	BF035327.1	EST_HUMAN	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
726	10658	20489	3.58	1.0E-111	8393082	NT	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
911	10835	20684	73.62	1.0E-111	M25142.1	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
3842	13556	23342	1.17	1.0E-111	6912641	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
3842	13556	23343	1.17	1.0E-111	6912641	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
4080	13982	23760	1.08	1.0E-111	7661569	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
4235	14133	23909	4.45	1.0E-111	K02268.1	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
5364	15284	25117	2.82	1.0E-111	AA151017.1	EST_HUMAN	Human enkephalin B (enkb) gene, exon 4 and 3' flank and complete cds
5364	15284	25118	2.82	1.0E-111	AA151017.1	EST_HUMAN	z147b07.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5675	15884	25685	1.71	1.0E-111	A1344679.1	EST_HUMAN	z147b07.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
6402	16263	26423	3.03	1.0E-111	BF366228.1	EST_HUMAN	qp09g12.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M29893 RAS-RELATED PROTEIN RAL-A (HUMAN);
6579	16437	26622	2.29	1.0E-111	AA133914.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
6795	16574	26866	3.13	1.0E-111	U66533.1	NT	zn62c12.r1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:562774 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
7113	16960		10.8	1.0E-111	BF214902.1	EST_HUMAN	Human beta4-integrin (ITGB4) gene, exon 13
7149	17026	27221	13.75	1.0E-111	X17033.1	NT	601847192F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078303 5'
7149	17026	27222	13.75	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
7251	17128	27321	3.26	1.0E-111	AF091396.1	NT	Human mRNA for integrin alpha-2 subunit
							Homo sapiens T10 isoform mRNA, complete cds

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7840	17890	27935	1.51	1.0E-111	AA504180.1	EST_HUMAN	aa58g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:L09235
7893	17743	27986	6.35	1.0E-111	AA131248.1	EST_HUMAN	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
8401	18277	28529	4.52	1.0E-111	U68159.1	NT	z131f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
9038	18825	29110	3.04	1.0E-111	11417901	NT	Human thrombopodietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
9886	19489	25130	1.69	1.0E-111	W22562.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNT1), mRNA
9959	19422	25171	1.39	1.0E-111	11430450	NT	72C9 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
9959	19422	25172	1.39	1.0E-111	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
592	10528	20335	2.66	1.0E-112	4501854	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
594	10530	20337	4.49	1.0E-112	U29103.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
594	10530	20338	4.49	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
616	10552	20363	1.48	1.0E-112	BF509039.1	EST_HUMAN	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
616	10552	20364	1.48	1.0E-112	BF509039.1	EST_HUMAN	UIH-B14-aot-g-04-0-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
985	10908	20753	2.78	1.0E-112	AF157623.1	NT	UIH-B14-aot-g-04-0-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1046	10964	20805	1.72	1.0E-112	P52742	SWISSPROT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1658	11560	21424	5.88	1.0E-112	7662125	NT	ZINC FINGER PROTEIN 135
1658	11560	21425	5.88	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2460	12337	22231	2.45	1.0E-112	BE866859.1	EST_HUMAN	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3809	13721	23510	0.83	1.0E-112	BE076073.1	EST_HUMAN	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'
4646	14533	24321	5.12	1.0E-112	AB037832.1	NT	MR2-BT0690-090300-113-f09 BT0590 Homo sapiens cDNA
4646	14533	24322	5.12	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5170	15036	24804	0.94	1.0E-112	9055269	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5477	15397	25463	33.34	1.0E-112	N46046.1	EST_HUMAN	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI1), mRNA
6340	16203	26364	1.81	1.0E-112	11416777	NT	y35d07.r1 Soares_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273229 5'
6340	16203	26364	1.81	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
6766	16645	26834	1.65	1.0E-112	AU118051	EST_HUMAN	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7181	17058	27247	2.25	1.0E-112	BE867635.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
7181	17058	27248	2.25	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
7693	17543	27767	2.09	1.0E-112	BF111413.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
8159	18047	28299	4.25	1.0E-112	AW863327.1	EST_HUMAN	7130g07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to
8318	18195	28445	2.86	1.0E-112	AJ249900.1	NT	TR:Q9VW35 Q9VW35 CG8743 PROTEIN ;
							MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA
							Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8445	18319	28578	1.72	1.0E-112	BE280479.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'
8500	18373	28637	1.75	1.0E-112	AI792603.1	EST_HUMAN	qk24c08.y5 NCI_OGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
8500	18373	28638	1.75	1.0E-112	AI792603.1	EST_HUMAN	qk24c08.y5 NCI_OGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
8521	18393	28657	5	1.0E-112	AV377670.1	EST_HUMAN	PM0-CT0237-141099-001-h02 CT0237 Homo sapiens cDNA
725	10657	20487	3.71	1.0E-113	AI365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
725	10657	20488	3.71	1.0E-113	AI365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
927	10852	20700	6.32	1.0E-113	M11965.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1523	11428	21286	2.94	1.0E-113	AI365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
2048	11939	21833	1.18	1.0E-113	BF515218.1	EST_HUMAN	UIH-BW1-ant-f03-0-U1.s1 NCI_OGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
2405	12282	22179	0.96	1.0E-113	AJ006976.1	NT	Homo sapiens PLP gene
3091	13018	22813	2.34	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5035	14907	24677	0.95	1.0E-113	7657095	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
5035	14907	24678	0.95	1.0E-113	7657095	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
5211	19524		16.27	1.0E-113	BE780858.1	EST_HUMAN	601469465F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872536 5'
5377	15297	25144	6.33	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
5608	15623	25605	3.92	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
5699	15608	25710	2.05	1.0E-113	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 8 (GalNAc-1T8) (GALNT8), mRNA
7257	17134	27326	2.95	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
7257	17134	27327	2.95	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
7656	17506	27731	1.29	1.0E-113	11429367	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
8466	18339	28604	1.73	1.0E-113	AW500519.1	EST_HUMAN	UI-HF-BND-akj-b-12-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077326 5'
8550	15719	25832	2.07	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
8550	15719	25833	2.07	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
8584	18452	28721	3.44	1.0E-113	BE292968.1	EST_HUMAN	601105529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988366 5'
629	10566	20379	7.66	1.0E-114	T70551.1	EST_HUMAN	yd15co1.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
1055	10972	20815	1.31	1.0E-114	8923087	NT	Homo sapiens hypohelical protein FLJ20080 (FLJ20080), mRNA
1291	11198	21053	3.47	1.0E-114	7657529	NT	Homo sapiens thalidomide tumor deletion region protein 1 (RTDR1), mRNA
1648	11552	21413	5.53	1.0E-114	6679073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2773	10025	19823	0.82	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2773	10025	19824	0.82	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3092	13019	22814	2.29	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3135	13060	22859	1.2	1.0E-114	BF208374.1	EST_HUMAN	601869832F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
3934	13843	23621	1.95	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
5120	14988	24762	1.2	1.0E-114	AA194468.1	EST_HUMAN	zq05e05.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628832 5' similar to contains
5121	14989	24763	2.31	1.0E-114	AF004849.1	NT	MER22.13 MER22 repetitive element ;
5316	15237	25040	1.37	1.0E-114		NT	Homo sapiens PKY protein kinase mRNA, complete cds
5316	15237	25041	1.37	1.0E-114	4508880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
6316	16179	26338	7.08	1.0E-114	Y18000.1	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
6316	16179	26339	7.08	1.0E-114	Y18000.1	NT	(TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
6606	16486	26673	1.86	1.0E-114	4557800	NT	(TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
6748	16627	26814	1.73	1.0E-114	AI363139.1	EST_HUMAN	Homo sapiens NF2 gene
6748	16627	26815	1.73	1.0E-114	AI363139.1	EST_HUMAN	Homo sapiens NF2 gene
7048	16925	27116	3.39	1.0E-114	U63041.1	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
7090	16967	27161	6.35	1.0E-114	AB011133.1	NT	qy63d06.x1 NCI_OGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
7090	16967	27162	6.35	1.0E-114	AB011133.1	NT	qy63d06.x1 NCI_OGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
7418	17285		3.79	1.0E-114	AW327455.1	EST_HUMAN	Human neural cell adhesion molecule CD66 mRNA, complete cds
7447	16459	26652	3.13	1.0E-114	AF077754.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
7844	17694	27940	1.31	1.0E-114	AL163227.2	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
8167	18055		7.14	1.0E-114	BE302666.1	EST_HUMAN	Homo sapiens mRNA for KIAA0561 protein, partial cds
8527	18399	26666	4.58	1.0E-114	AV733454.1	EST_HUMAN	Homo sapiens mRNA for KIAA0561 protein, partial cds
8527	18399	26667	4.58	1.0E-114	AV733454.1	EST_HUMAN	Homo sapiens mRNA for KIAA0561 protein, partial cds
8834	18647	28932	2.86	1.0E-114	AV733454.1	EST_HUMAN	Homo sapiens mRNA for KIAA0561 protein, partial cds
8834	18647	28933	2.86	1.0E-114	AV733454.1	EST_HUMAN	Homo sapiens mRNA for KIAA0561 protein, partial cds
9479	19748		3.21	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
9729	19266	25222	3.06	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
9729	19266	25223	3.06	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
21	10008	19801	3.36	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
125	10099	19920	0.95	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
129	10103		1.99	1.0E-115	4587887	NT	Homo sapiens keratin 18 (KRT18) mRNA
289	10253	20073	2.17	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
525	10467	20278	1.08	1.0E-115	AI339206.1	EST_HUMAN	q106f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946909 3' similar to TR:O00536 O00536 TTF-1 INTERACTING PEPTIDE 5;
525	10467	20279	1.08	1.0E-115	AI339206.1	EST_HUMAN	q106f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946909 3' similar to TR:O00536 O00536 TTF-1 INTERACTING PEPTIDE 5;
769	10699	20537	1.83	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
769	10699	20538	1.83	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
771	10701	20540	49.82	1.0E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1539	11443	21301	0.92	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoacidate semialdehyde synthase mRNA, complete cds
1539	11443	21302	0.92	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoacidate semialdehyde synthase mRNA, complete cds
1795	11683	21561	3.14	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
1798	11696	21573	1.42	1.0E-115	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2034	11925	21817	0.87	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2034	11925	21818	0.87	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2820	12749		1.76	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
3077	13004	22795	2.1	1.0E-115	AJ245822.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3077	13004	22796	2.1	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3427	13344	23149	4.03	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
3956	13864	23640	4.04	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4169	14069	23844	1.09	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4301	14199	23983	3.41	1.0E-115	6912659	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4335	14232	24014	3.83	1.0E-115	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4578	14468	24254	2.58	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4578	14468	24255	2.58	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4813	14696	24482	2.96	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4813	14696	24483	2.96	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5279	15201	24977	1.75	1.0E-115	AW970335.1	EST_HUMAN	EST382416 IMAGE resequences, MAGK Homo sapiens cDNA
5330	15250	25055	7.22	1.0E-115	BF665387.1	EST_HUMAN	6021193346F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278738 5'
5402	15321	25369	2.05	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5402	15321	25370	2.05	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5852	15756	25876	12.92	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63436), mRNA
5933	15838	25960	1.93	1.0E-115	7681883	NT	Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5933	15838	25961	1.93	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6313	16176	26333	1.55	1.0E-115	AI076598.1	EST_HUMAN	oz31a06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
6313	16176	26334	1.55	1.0E-115	AI076598.1	EST_HUMAN	oz31a06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
6379	16241	26401	7.41	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
6744	16623	26811	12.78	1.0E-115	BE830187.1	EST_HUMAN	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
6744	16623	26812	12.78	1.0E-115	BE830187.1	EST_HUMAN	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
7116	16993	27184	2.2	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
7745	17595	27816	1.92	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
7745	17595	27817	1.92	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
8100	17990	28239	3.5	1.0E-115	AW571544.1	EST_HUMAN	xx32f08.x1 NCL_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAYP_CANIFA
8701	18519	28801	2.26	1.0E-115	4502528	NT	P10463 CALYPHOSINE;
560	10500	20306	1.42	1.0E-116	BE275502.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA
783	10713	20552	1.25	1.0E-116	4507334	NT	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:288875 5'
841	10768		6.89	1.0E-116	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1952	11847	21733	2.38	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
1952	11847	21734	2.38	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
1980	11873	21765	1.21	1.0E-116	AU133080.1	EST_HUMAN	AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5'
2050	12711	21834	1.01	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2050	12711	21835	1.01	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2259	12143	22042	1.88	1.0E-116	5453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2293	12175						Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds
2407	12284	22181	1.49	1.0E-116	U78308.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2704	12656	22458	2.19	1.0E-116	BE889256.1	EST_HUMAN	601513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
3137	13062	22860	4.73	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3137	13062	22861	4.73	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4281	14180	23958	2.01	1.0E-116	5031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4747	14632	24418	2.17	1.0E-116	AI907096.1	EST_HUMAN	PM-BT135-070499-016 BT135 Homo sapiens cDNA
5122	14990	24764	1.2	1.0E-116	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
							zc24d07.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR;
5637	15550	25641	5.88	1.0E-116	W42822.1	EST_HUMAN	Homo sapiens mRNA for KIAA1636 protein, partial cds
5768	15675	25781	1.65	1.0E-116	AB046856.1	NT	

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5768	15675	25782	1.65	1.0E-116	AB046886.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
5853	15759	25877	72.79	1.0E-116	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
5924	15829		1.8	1.0E-116	BE158133.1	EST_HUMAN	MR2-HT0379-270200-102-b04 HT0379 Homo sapiens cDNA
6145	16018	26155	3.59	1.0E-116	C02944.1	EST_HUMAN	C02944 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHCO567
6275	16139	26295	7.97	1.0E-116	AV716314.1	EST_HUMAN	AV716314 DGB Homo sapiens cDNA clone DCBBO306 5'
6874	16753	26949	1.99	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2
6874	16753	26950	1.99	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2
7173	17050	27239	1.43	1.0E-116	BE565507.1	EST_HUMAN	601338268F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680680 5'
							qh09c05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to
7260	17137	27330	1.98	1.0E-116	AI216352.1	EST_HUMAN	gb-X63741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
7577	17428	27642	1.77	1.0E-116	11418646	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA
8074	17965	28216	3.68	1.0E-116	BF335849.1	EST_HUMAN	CM2-CT0482-300800-349-e06 CT0482 Homo sapiens cDNA
							qq41e04.x1 Soares NthMPu_S1 Homo sapiens cDNA clone IMAGE:1935102 3' similar to WP:B0495.7
8477	18350	28615	3.23	1.0E-116	AI367140.1	EST_HUMAN	CE01765 :
9591	19741		2.08	1.0E-116	BE258593.1	EST_HUMAN	601108350F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344580 5'
9776	19614		2.68	1.0E-116	AL134889.1	EST_HUMAN	DKFZp762L1110_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762L1110 5'
546	10487	20296	1.18	1.0E-117	4826636	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1061	12684	20821	1.59	1.0E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
1719	11620	21489	6.25	1.0E-117	AF123320.1	NT	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
1790	11688	21564	2.3	1.0E-117	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
2164	12051	21952	2.99	1.0E-117	AW957689.1	EST_HUMAN	EST369769 IMAGE resequences, IMAGE Homo sapiens cDNA
3230	13154	22853	1.75	1.0E-117	AA978114.1	EST_HUMAN	op32c11.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'
							EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal
3908	13818	23599	3.62	1.0E-117	AA316723.1	EST_HUMAN	protein L29
4247	14146	23920	1.86	1.0E-117	8659564	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4475	14369	24158	1.88	1.0E-117	AL042120.1	EST_HUMAN	DKFZp434C1120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1120 5'
4622	14510	24299	1.35	1.0E-117	X89670.1	NT	H. sapiens mRNA for TPCR16 protein
4622	14510	24300	1.35	1.0E-117	X89670.1	NT	H. sapiens mRNA for TPCR16 protein
4705	14591	24382	9.22	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4705	14591	24383	9.22	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4856	14736	24516	3.36	1.0E-117	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5280	15202	24978	2.5	1.0E-117	BE730508.1	EST_HUMAN	601562557F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'
6404	16265	26426	4.99	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
6404	16265	26427	4.99	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6455	16316	26482	3.77	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
6455	16316	26483	3.77	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
6651	16531	26725	5.93	1.0E-117	A1950145.1	EST_HUMAN	wp86b07.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2488629 3' similar to TR:O75065
6837	16716	26908	1.7	1.0E-117	10834989	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
6837	16716	26909	1.7	1.0E-117	10834989	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
7361	17228	27428	2.28	1.0E-117	D16524.1	NT	Human gene for very low density lipoprotein receptor, exon 11
7635	17486	27706	1.51	1.0E-117	BE733922.1	EST_HUMAN	601569317F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843748 5'
8385	18262	28512	10.31	1.0E-117	W80605.1	EST_HUMAN	z483b11.1 Soares_fetal_heart NBHH19W Homo sapiens cDNA clone IMAGE:347229 5' similar to
8595	18462	28732	3.96	1.0E-117	AB011541.1	NT	gb:MI4219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
8595	18462	28733	3.96	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
8698	18516	28974	15.63	1.0E-117	BE269856.1	EST_HUMAN	Homo sapiens mRNA for MEGF8, partial cds
8872	18684	28974	2.22	1.0E-117	4501848	NT	601186203F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544296 5'
8872	18684	28975	2.22	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABCA1), member 3 (ABCA3), mRNA
64	10050	19863	9.54	1.0E-118	AF161500.1	NT	Homo sapiens ATP-binding cassette, sub-family A (ABCA1), member 3 (ABCA3), mRNA
90	10074	19890	2.59	1.0E-118	AL045854.1	EST_HUMAN	Homo sapiens HSPC161 mRNA, complete cds
506	10448	20261	5.09	1.0E-118	7657016	NT	DKFZp434I056_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I056 5'
896	12680	20667	0.98	1.0E-118	5174680	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
2186	12073	21975	2.39	1.0E-118	BE389705.1	EST_HUMAN	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2186	12073	21976	2.39	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2186	12073	21977	2.39	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2281	12165		3.77	1.0E-118	AW951729.1	EST_HUMAN	EST363799 IMAGE resequences, MAGB Homo sapiens cDNA
2711	12574	22465	2.38	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2711	12574	22466	2.38	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3066	12993		3.73	1.0E-118	Y13932.1	NT	Homo sapiens PRKY exon 7
3159	13084	22887	4.51	1.0E-118	A1347694.1	EST_HUMAN	qp01105.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3159	13084	22888	4.51	1.0E-118	A1347694.1	EST_HUMAN	qp01105.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3998	13904	23679	7.67	1.0E-118	D23660.1	NT	Human mRNA for ribosomal protein, complete cds
5329	15249	25053	2.02	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5329	15249	25054	2.02	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5620	15635	25620	1.88	1.0E-118	11420764	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6020	15924	26054	1.87	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6020	15924	26055	1.87	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6482	16341	26509	4.13	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
6648	16528	26722	2.23	1.0E-118	BE781223.1	EST_HUMAN	601469159F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872247 5'
6884	16763	26960	7.81	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
6884	16763	26961	7.81	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
6888	16767	26963	1.34	1.0E-118	AA443024.1	EST_HUMAN	zx98d07.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
6888	16767	26964	1.34	1.0E-118	AA443024.1	EST_HUMAN	zx98d07.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
7035	16912	27100	1.16	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
7035	16912	27101	1.16	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
7082	16939	27129	1.28	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7082	16939	27130	1.28	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7223	17100	27288	5.71	1.0E-118	BE263134.1	EST_HUMAN	601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
7936	17786	28027	1.18	1.0E-118	BF195407.1	EST_HUMAN	7n17e09.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3664785 3' similar to SW:ZP3A_HUMAN P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR ;
8598	18485	28737	3.06	1.0E-118	AA315007.1	EST_HUMAN	EST186814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
8847	18659	28947	1.75	1.0E-118	BF093687.1	EST_HUMAN	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
8847	18659	28948	1.75	1.0E-118	BF093687.1	EST_HUMAN	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
741	10672	20508	0.81	1.0E-119	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
1021	12683	20781	1.55	1.0E-119	7705607	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
1891	11788	21663	2.09	1.0E-119	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3084	12991	22783	1.81	1.0E-119	8922205	NT	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
3202	13126		1.08	1.0E-119	AA918760.1	EST_HUMAN	on10b05.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:E04F6.2 CE01214 ;
3870	13781	23573	1.15	1.0E-119	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5111	14979	24753	0.95	1.0E-119	AA077394.1	EST_HUMAN	7B14F03 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B14F03
5272	15194	24969	2.45	1.0E-119	AU133399.1	EST_HUMAN	AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001991 5'
5282	15204	24980	14.93	1.0E-119	M89914.1	NT	Human neurofibromin (NF1) gene, complete cds
5285	15207	24984	3.32	1.0E-119	BE936121.1	EST_HUMAN	RC1-NN0073-250800-018-g06 NN0073 Homo sapiens cDNA
5336	15256	25079	2.24	1.0E-119	AV693731.1	EST_HUMAN	AV693731 GKc Homo sapiens cDNA clone GKCDH803 5'
5726	15633	25736	7.19	1.0E-119	A1150703.1	EST_HUMAN	qb77c09.x1 Soares fetal heart Nbr-H19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
5887	15793	25914	2.79	1.0E-119	X06292.1	NT	Human c-fes/fps proto-oncogene
5895	15801	25925	4.26	1.0E-119	AW974193.1	EST_HUMAN	EST386296 IMAGE resequences, MAGM Homo sapiens cDNA
6381	16243	26403	1.42	1.0E-119	BE796614.1	EST_HUMAN	601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946081 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7893	17733	27977	1.48	1.0E-119	AA465124.1	EST_HUMAN	aa3205.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'
7998	17848	28089	1.42	1.0E-119	AJ29770.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
8535	18407		9.72	1.0E-119	BF569671.1	EST_HUMAN	602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
9348	19671		1.37	1.0E-119	AW847519.1	EST_HUMAN	RC3-CT0212-240999-011-f03 CT0212 Homo sapiens cDNA
237	10205	20022	1.4	1.0E-120	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
298	10282	20082	1.34	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1025	10943	20787	1.67	1.0E-120	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
1025	10943	20788	1.67	1.0E-120	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
1408	11311	21172	4.53	1.0E-120	N44873.1	EST_HUMAN	yy40g12.r1 Soares melanocyte 2N5-IM Homo sapiens cDNA clone IMAGE:273766 5'
1583	11487	21348	3.87	1.0E-120	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
2030	11950	21847	0.9	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2060	11950	21848	0.9	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2482	12358	22250	0.84	1.0E-120	4755124	NT	Homo sapiens aquaporin 4 (AQP4), splice variant b, mRNA
3267	10262	20082	1.13	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4260	14159	23936	1.17	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4260	14159	23937	1.17	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4563	14455	24242	2.79	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4563	14455	24243	2.79	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5168	15034	24801	0.89	1.0E-120	AI190903.1	EST_HUMAN	qd61f03.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1733981 3'
5508	15426	25488	13.84	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
5508	15426	25489	13.84	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6469	16328	26495	1.49	1.0E-120	D34619.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
6808	16488	26674	1.67	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
6808	16488	26675	1.67	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
6850	16729	26924	2.44	1.0E-120	BF337599.1	EST_HUMAN	602035352F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183333 5'
6898	16777	26971	2.43	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
6898	16777	26972	2.43	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
6922	16800	26993	1.33	1.0E-120	AB007934.1	NT	Homo sapiens mRNA for KIAA0465 protein, partial cds
7470	17330	27535	4.54	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
7470	17330	27536	4.54	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
7617	17468	27687	4.72	1.0E-120	BF308541.1	EST_HUMAN	601888956F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
7626	17477	27698	7.31	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
7798	17648	27885	2.53	1.0E-120	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
8469	18342	28607	6.4	1.0E-120	BE296387.1	EST_HUMAN	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632015 5'

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Table 4

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Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8914	18722	28013	2.07	1.0E-120	U94774.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, 5'UTR and exon 1
9495	19111	28288	1.36	1.0E-120	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
67	10052	19867	1.04	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
374	10328	20151	0.98	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
707	12674	20465	1.23	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1556	11461	21319	0.99	1.0E-121	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
1923	11818	21697	0.89	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
1923	11818	21698	0.89	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2055	11945	21841	1.17	1.0E-121	L76631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2530	12404	22295	1.05	1.0E-121	BF344378.1	EST_HUMAN	802014750F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150286 5'
2530	12404	22296	1.05	1.0E-121	BF344378.1	EST_HUMAN	802014750F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150286 5'
3042	12969	22763	3.09	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3042	12969	22764	3.09	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3492	13408	23213	1.09	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3492	13408	23214	1.09	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3624	13538	23325	6.61	1.0E-121	AF155156.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4236	14134	23910	1.21	1.0E-121	AI263294.1	EST_HUMAN	qx57b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'
4901	14781	24556	2.55	1.0E-121	X91937.1	NT	H. sapiens ECE-1 gene (exon 17)
5050	14922	24695	1.03	1.0E-121	AI904151.1	EST_HUMAN	CM-BT043-090299-075 BT043 Homo sapiens cDNA
6632	16512	26701	2.58	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
6632	16512	26702	2.58	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
8157	18045	28297	4.44	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
8163	18051	28303	2.28	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
8336	18213	28466	4.91	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
8363	18240	28489	3.48	1.0E-121	NS0624.1	EST_HUMAN	yv74c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248448 3'
267	10232	20047	3.99	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
333	10292	20107	2.22	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
355	10312	20132	1.54	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
864	10790	20841	2.85	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1201	11111	20957	3.41	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1667	11569	21435	1.32	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
1684	11586	21458	2.01	1.0E-122	11418424	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
1684	11586	21459	2.01	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1772	11671	21549	5.91	1.0E-122	BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898358 5'
2441	12318	22215	10.56	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126234 5'
2441	12318	22216	10.56	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126234 5'
4738	14823	24409	1.82	1.0E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
4918	14797		1.2	1.0E-122	AW504645.1	EST_HUMAN	U1-HF-BND-all-a-03-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5'
6051	15337	25390	6.41	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7219	17096	27286	1.35	1.0E-122	11424216	NT	Homo sapiens lethal giant larvae (Drosophila) homolog 2 (LLGL2), mRNA
9098	18869		4.35	1.0E-122	11418187	NT	Homo sapiens phosphomannomutase 1 (PMM1), mRNA
181	10153	19988	1.07	1.0E-123	U31519.1	NT	Human phosphoenolpyruvate carboxykinase (PCK1) gene, promoter region and partial cds
751	10881	20517	1.72	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
751	10881	20518	1.72	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
996	10916	20760	3.79	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1005	10923	20767	5.06	1.0E-123	5803114	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1218	11126	20976	3.35	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1218	11126	20977	3.35	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1439	11344	21211	1.76	1.0E-123	AJ388641.1	NT	Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN02
2052	11942	21837	2.98	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2052	11942	21838	2.98	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2052	11942	21839	2.98	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2267	12151		4.5	1.0E-123	7705962	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
5344	15265	25091	1.75	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5344	15265	25092	1.75	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5425	15346	25400	1.29	1.0E-123	BE798746.1	EST_HUMAN	601591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'
5893	15799	25923	2.27	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
6186	16071	26221	1.3	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
6509	16368	26545	1.95	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509162 5'
7392	17310	27517	4.14	1.0E-123	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7471	17331	27537	12.23	1.0E-123	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
8958	18765	29057	5	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
8958	18765	29058	5	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
268	10233	20048	1.1	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
268	10233	20049	1.1	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
273	10239		1.98	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
477	10421	20238	2.11	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
676	10609	20429	2.03	1.0E-124	AA397551.1	EST_HUMAN	z181504.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
676	10609	20430	2.03	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
742	10673	20509	3.67	1.0E-124	AF155654.1	NT	z181504.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
791	10720	20561	1.06	1.0E-124	4507500	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
886	10812	20680	1.81	1.0E-124	7705446	NT	Human putative ribosomal protein S1 mRNA
1293	11200	21056	2.59	1.0E-124	11419092	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1324	11231	21086	5.54	1.0E-124	AF274892.1	NT	Homo sapiens hypothetical protein (HSPC068), mRNA
1324	11231	21087	5.54	1.0E-124	AF274892.1	NT	Homo sapiens ring finger protein (RNF), mRNA
1773	11672	21550	2.35	1.0E-124	AJ131712.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2016	11907	21797	2.23	1.0E-124	BE879524.1	EST_HUMAN	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2408	12285	22182	0.85	1.0E-124	AB024069.1	NT	Homo sapiens mRNA for nucleolar RNA-helicase (noh61 gene)
3319	13240	23045	0.85	1.0E-124	4504116	NT	601491715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893954 5'
3446	13363	23169	0.96	1.0E-124	S78884.1	NT	Homo sapiens gene for B120, exon 11
3446	13363	23170	0.96	1.0E-124	S78884.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3598	13512	23300	2.95	1.0E-124	X13794.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3825	13737	23528	1.09	1.0E-124	4507500	NT	H. sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS)
3983	13990	23666	1.19	1.0E-124	4504116	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4639	14527	24315	1.58	1.0E-124	AB024069.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4850	14731		1.12	1.0E-124	M18178.1	NT	Homo sapiens gene for B120, exon 11
5039	14911	24685	2.72	1.0E-124	A1204535.1	EST_HUMAN	Human fibronectin gene extra type III repeat (EDII), exon x+1
5240	15164	24934	8.97	1.0E-124	8922337	NT	qf56h03.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1754069 3'
5590	15505	25580	6.43	1.0E-124	BF686135.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6185	16070	26220	3.31	1.0E-124	Y11717.1	NT	602124644F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5'
6805	16884	26874	5.66	1.0E-124	4506654	NT	M.musculus mRNA for hoxa3 gene
							Homo sapiens ribosomal protein L5 (RPL5) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6930	16808	27002	1.35	1.0E-124	AW612106.1	EST_HUMAN	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162 O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE.;
6930	16808	27003	1.35	1.0E-124	AW612106.1	EST_HUMAN	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162
7466	17326	27532	2.44	1.0E-124	AV645633.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE.;
7466	17326	27533	2.44	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
7542	17393	27604	7.8	1.0E-124	A1767133.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
7542	17393	27605	7.8	1.0E-124	A1767133.1	EST_HUMAN	wi93102.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
7676	17526	27752	1.25	1.0E-124	AW503755.1	EST_HUMAN	wi93102.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
8404	18280	28532	2.25	1.0E-124	U64776.1	NT	UHF-BND-akz-b-04-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079846 5'
8645	18509	28788	2.25	1.0E-124	AW665663.1	EST_HUMAN	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17
8767	17916	28162	1.87	1.0E-124	A1446455.1	EST_HUMAN	h05c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980906 3'
8767	17916	28163	1.87	1.0E-124	A1446455.1	EST_HUMAN	h19e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN.;
9173	10609	20429	3.98	1.0E-124	A397551.1	EST_HUMAN	h19e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN.;
9173	10609	20430	3.98	1.0E-124	AA397551.1	EST_HUMAN	z181b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT).;
9846	19626	25005	1.99	1.0E-124	11417862	NT	z181b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT).;
9846	19626	25006	1.99	1.0E-124	11417862	NT	z181b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT).;
316	10278		5.41	1.0E-125	AB032998.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
420	9987	19778	3.92	1.0E-125	BE743922.1	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
628	10565	20377	1.63	1.0E-125	A1110656.1	EST_HUMAN	Homo sapiens mRNA for KIAA1172 protein, partial cds
628	10565	20378	1.63	1.0E-125	A1110656.1	EST_HUMAN	Homo sapiens mRNA for KIAA1172 protein, partial cds
711	10643	20469	1.24	1.0E-125	AF264750.1	NT	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
842	10789	20619	2.13	1.0E-125	AA042813.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
982	10905	20750	1.53	1.0E-125	AL163210.2	NT	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
1136	11050	20890	1.63	1.0E-125	7662279	NT	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
1649	12700	21414	1.08	1.0E-125	7691867	NT	Homo sapiens ALR-like protein mRNA, partial cds
1769	11668	21545	3.81	1.0E-125	AF015450.1	NT	z183c07.s1 Soares_pregnant uterus NhlHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN).;
1769	11668	21546	3.81	1.0E-125	AF015450.1	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1769	11668	21546	3.81	1.0E-125	AF015450.1	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1769	11668	21546	3.81	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1769	11668	21546	3.81	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2455	12332	22228	1.15	1.0E-125	AA042813.1	EST_HUMAN	z163c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2551	12424	22315	1.65	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INH) mRNA
2551	12424	22316	1.65	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INH) mRNA
2555	12427	22320	2.45	1.0E-125	AI732966.1	EST_HUMAN	oh64d02.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1471779 3'
4450	14344	24136	1.98	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4450	14344	24137	1.98	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4516	14409	24195	0.84	1.0E-125	BE315412.1	EST_HUMAN	601141152F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3140796 5'
5581	15496	25573	1.41	1.0E-125	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
5612	15527	25610	3.44	1.0E-125	BE892660.1	EST_HUMAN	601433472F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3918952 5'
5965	15870	25993	1.48	1.0E-125	BE562526.1	EST_HUMAN	601335826F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3689790 5'
5965	15870	25994	1.48	1.0E-125	BE562526.1	EST_HUMAN	601335826F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3689790 5'
6201	15961	26093	6.36	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
6201	15961	26094	6.36	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
6974	16951	27043	1.22	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
6974	16951	27044	1.22	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
7272	17149	27343	4.31	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
7272	17149	27344	4.31	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
8069	17960	28211	3.15	1.0E-125	AF043458.1	NT	Homo sapiens IREL gene, exon 5
8152	18040	28289	1.86	1.0E-125	AW131202.1	EST_HUMAN	xf59f02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284 LAMBDA/IOTA PROTEIN KINASE C-INTERACTING PROTEIN. [1];
8152	18040	28290	1.86	1.0E-125	AW131202.1	EST_HUMAN	xf59f02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284 LAMBDA/IOTA PROTEIN KINASE C-INTERACTING PROTEIN. [1];
8478	18351	28616	5.13	1.0E-125	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
8609	18476	28748	2.92	1.0E-125	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
8615	18482	28754	5.15	1.0E-125	AF026029.1	NT	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
8704	18522	28804	2.49	1.0E-125	AW812899.1	EST_HUMAN	RC3-ST0186-250200-018-c11 ST0186 Homo sapiens cDNA
8793	18607	28896	4.36	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
8793	18607	28897	4.36	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
8941	18749	29044	1.96	1.0E-125	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
757	10687	20525	0.88	1.0E-126	4758007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
760	10690	20528	1.2	1.0E-126	M61936.1	NT	Human laminin B1 chain gene, exon 20

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
901	10826	20670	2.03	1.0E-126	X68735.1	NT	H.sapiens gene for alpha1-antichymotrypsin, exon 3
2552	12425	22317	2.24	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3035	12963	22757	6.07	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stratiogene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3035	12963	22758	6.07	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stratiogene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3577	13491	23281	1.21	1.0E-126	X53941.1	NT	H.sapiens DNA for liver cytochrome b5 pseudogene
3605	13519	23307	2.04	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4677	14563	24356	0.96	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4677	14563	24357	0.96	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4728	14614	24400	1.57	1.0E-126	N34078.1	EST_HUMAN	yx78c06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267850 5'
5779	15686	25795	3.68	1.0E-126	AA460075.1	EST_HUMAN	z066e03.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796444 5' similar to TR:G1145880 G1145880 TITIN;
5797	15703	25813	3.82	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
5797	15703	25814	3.82	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
6660	16540	26737	2.77	1.0E-126	X16809.1	NT	Human mRNA for ankryrin (variant 2.1)
8233	18114	28366	1.95	1.0E-126	BF683175.1	EST_HUMAN	602139138F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298240 5'
8906	18620	28910	2.41	1.0E-126	BE261680.1	EST_HUMAN	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
9635	15098	24890	4.38	1.0E-126	BE743922.1	EST_HUMAN	601677981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
165	10138	19954	3.59	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
165	10138	19955	3.59	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
166	10138	19954	2.31	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
166	10138	19955	2.31	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
272	10238	20056	2.35	1.0E-127	D87675.1	NT	Homo sapiens DNA for casein kinase I epsilon, complete cds
272	10238	20057	2.35	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
863	10789	20640	1.32	1.0E-127	AF114488.1	NT	Homo sapiens intersech short isoform (ITSN) mRNA, complete cds
898	10823	20689	1.28	1.0E-127	U72821.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1665	11567	21433	0.98	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2020	11911	21800	1.59	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2020	11911	21801	1.59	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2153	12041	21939	7.45	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2294	12176	22075	4.01	1.0E-127	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
2566	12437	22330	2.78	1.0E-127	X12881.1	NT	Human mRNA for cyclokeratin 18
2579	12450	22341	0.96	1.0E-127	AA450131.1	EST_HUMAN	z042a02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2579	12450	22342	0.96	1.0E-127	AA450131.1	EST_HUMAN	z42a02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'
3740	13652	23435	0.88	1.0E-127	AW161297.1	EST_HUMAN	au80e06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22 repetitive element ;
4026	13929	23706	1.09	1.0E-127	AF135188.1	NT	Homo sapiens delayed rectifier potassium channel subunit Isk mRNA, complete cds
4128	14028	23802	0.86	1.0E-127	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4160	14060	23833	21.46	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4160	14060	23834	21.46	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4395	14281	24075	0.92	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 retinoid metabolizing protein P450RAL-2 mRNA, complete cds
4499	14393	24178	4.16	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4532	14425		1.93	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4575	14466	24252	0.98	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5546	15462	25533	3.72	1.0E-127	X85704.1	NT	H.sapiens NOS2 gene, exon 6
5742	15650	25757	2.67	1.0E-127	X84060.1	NT	H.sapiens TCF11 gene, exon 3-6
5816	15722	25835	6.76	1.0E-127	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
6578	16436	26620	1.38	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
6578	16436	26621	1.38	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7558	17409	27624	4.97	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7558	17409	27625	4.97	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7923	17773	28012	1.17	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8498	18371	28634	6.74	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70KD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
8498	18371	28635	6.74	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70KD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
8998	18707	29001	2.46	1.0E-127	BE896415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
8998	18707	29002	2.46	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
9397	10138	19954	1.66	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
9397	10138	19955	1.66	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
9395	19177	25276	2.1	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
452	10366	20214	4.46	1.0E-128	BE385617.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'
1138	11052	20892	1.48	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1138	11052	20893	1.48	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2025	11916	21805	12.19	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2025	11916	21806	12.19	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2162	12049	21950	13.3	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2395	12273		0.85	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3348	13268	23071	1.13	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4565	14457	24245	5.46	1.0E-128	11426873	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5865	15771	25890	2.67	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
6140	15988	26123	7.23	1.0E-128	BF224345.1	EST_HUMAN	7c86b10.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
6976	16953	27046	3.28	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
6976	16953	27047	3.28	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
7834	17684	27929	1.25	1.0E-128	AA639198.1	EST_HUMAN	ns04at1.r1 NCJ_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338 CHROMOSOME SEGREGATION GENE HOMOLOG CAS.;
8092	17983	28232	5.94	1.0E-128	11425254	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
8101	17991	28240	3.87	1.0E-128	AA926959.1	EST_HUMAN	om68h08.s1 NCJ_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X54941 CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
8230	18111	28364	1.79	1.0E-128	BE384475.1	EST_HUMAN	601277826F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618750 5'
9263	18068		3.66	1.0E-128	AW955290.1	EST_HUMAN	EST367360 IMAGE resequences, MAGC Homo sapiens cDNA
116	10353	20182	2.19	1.0E-129	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
407	10353	20182	1.35	1.0E-129	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1689	11591	21461	2.86	1.0E-129	AL066880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1693	11595	21465	2.29	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1693	11595	21466	2.29	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1802	11699	21575	2.43	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
2751	12913	22503	1.19	1.0E-129	4505982	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
2751	12913	22504	1.19	1.0E-129	4505982	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
3089	13016	22808	1.35	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3089	13016	22809	1.35	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3089	13016	22810	1.35	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4073	13975	23754	2.2	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4183	14083	23856	9.7	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5
4183	14083	23857	9.7	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5706	15614	25715	2.89	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6229	16095	26245	5.17	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6267	16132	26286	7.59	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
6841	16720		3.68	1.0E-129	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
8554	18424	28693	3.52	1.0E-129	AA625526.1	EST_HUMAN	af72i07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047589 5'
8618	18132	26286	9.4	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
8888	18699	28993	2.04	1.0E-129	AU143115.1	EST_HUMAN	AU143115 Y79AA1 Homo sapiens cDNA clone Y79AA1001410 5'
8898	18699	28994	2.04	1.0E-129	AU143115.1	EST_HUMAN	AU143115 Y79AA1 Homo sapiens cDNA clone Y79AA1001410 5'
9250	18960		1.87	1.0E-129	H83155.1	EST_HUMAN	yf49c05.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:199112 5' similar to
9630	19203		1.86	1.0E-129	AL120739.1	EST_HUMAN	Yf48150 B48150 HP-25-HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN ;
1643	11547	21408	6.81	1.0E-130	BE275192.1	EST_HUMAN	DKFZ6762K171.r1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZp62K171 5'
1643	11547	21409	6.81	1.0E-130	BE275192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
1940	11835		2.06	1.0E-130	X04092.1	NT	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
2743	12605		7.7	1.0E-130	AJ010230.1	NT	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2849	12777	22564	1.1	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2849	12777	22565	1.1	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3530	13446	23243	1.07	1.0E-130	AF240698.1	NT	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3703	12777	22564	4.77	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3703	12777	22565	4.77	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3857	13768	23560	1.09	1.0E-130	AW503590.1	EST_HUMAN	601343016F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4438	14333	24122	7.48	1.0E-130	AW843993.1	EST_HUMAN	UHF-BN0-aky-g-06-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
5029	14902	24673	1.09	1.0E-130	AW363299.1	EST_HUMAN	CM4-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA
5029	14902	24674	1.09	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
6301	16165	26322	2.04	1.0E-130	11416777	NT	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
7119	16996	27187	2.45	1.0E-130	AW566242.1	EST_HUMAN	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7314	17190	27392	1.57	1.0E-130	AB037796.1	NT	EST388312 IMAGE resequences, MAGD Homo sapiens cDNA
8513	18395	28650	32.43	1.0E-130	M25140.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
4	9991	19782	2.49	0.0E+00	AA228126.1	EST_HUMAN	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 2, 3 and 4
4	9991	19783	2.49	0.0E+00	AA228126.1	EST_HUMAN	zr58c04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
7	9993	19786	1.44	0.0E+00	4885136	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
							zr58c04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
							G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
							Homo sapiens checkpoint suppressor 1 (CHEST1), mRNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
15	10001	19792	1.34	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
15	10001	19793	1.34	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
20	10007	19799	2.45	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
20	10007	19800	2.45	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
24	10011	19804	5.57	0.0E+00	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
33	10020	19816	0.97	0.0E+00	M68600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
35	10022	19819	2.41	0.0E+00	8857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
51	10038	19845	1.4	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
51	10038	19846	1.4	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
52	10039	19847	1.22	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujjiwara) Homo sapiens cDNA clone GEN-516H08 5'
52	10039	19848	1.22	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujjiwara) Homo sapiens cDNA clone GEN-516H08 5'
53	10040	19849	4.14	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
55	10042	19852	8.1	0.0E+00	AW069634.1	EST_HUMAN	cr48e07.x1 Jila bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
55	10042	19853	8.1	0.0E+00	AW069634.1	EST_HUMAN	cr48e07.x1 Jila bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
59	10045	19857	5.8	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
61	10047		2.75	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
69	10054	19869	1.77	0.0E+00	4759977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
69	10054	19870	1.77	0.0E+00	4759977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
71	10054	19869	1.49	0.0E+00	4759977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
71	10054	19870	1.49	0.0E+00	4759977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
74	10058	19875	42.13	0.0E+00	AA953770.1	EST_HUMAN	on89e04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563870 3' similar to SW.TMOD_HUMAN P28269 TROPOMODULIN ;
76	10060	19877	1.09	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
77	10061		14.77	0.0E+00	4504444	NT	Homo sapiens heterologous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
86	10070	19886	47.55	0.0E+00	5010088	NT	Homo sapiens actin, beta (ACTB) mRNA
89	10073	19889	13.39	0.0E+00	U89277.1	NT	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds
94	10079	19895	1.46	0.0E+00	A1114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
95	10080	19896	1.03	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1368 protein, partial cds
102	10085	19901	6.13	0.0E+00	X91213.1	NT	H. sapiens ncx1 gene (exon 2)
110	10091	19906	1.39	0.0E+00	AI623701.1	EST_HUMAN	ts38b05.x1 NC1 CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
111	10091	19906	1.88	0.0E+00	AI623701.1	EST_HUMAN	ts38b05.x1 NC1 CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
112	12636	19907	1.83	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5'
112	12636	19908	1.83	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5'
115	10094	19913	0.86	0.0E+00	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
126	10100	19921	3.17	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
126	10100	19922	3.17	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
135	10108	19929	1.49	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
135	10108	19930	1.49	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
147	10121		9.05	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
151	10125	19943	2.42	0.0E+00	BF036881.1	EST_HUMAN	601480375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
153	10127		15.84	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
156	10130	19946	1.36	0.0E+00	AF111169.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
158	10132	19947	1.1	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
159	10132	19947	1.18	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
160	10133	19948	2.99	0.0E+00	W73973.1	EST_HUMAN	zd62b05.r1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
161	10134	19949	1.51	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
164	10137	19952	18.37	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
164	10137	19953	18.37	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
174	10145	19960	4.25	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
174	10145	19961	4.25	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
179	10150	19964	1.98	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
179	10150	19965	1.98	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
187	10159	19976	130.42	0.0E+00	D50699.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
192	10164	19981	2.83	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
192	10164	19982	2.83	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
194	10166	19984	2.92	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
194	10166	19985	2.92	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
203	12661	19991	9.33	0.0E+00	AI587308.1	EST_HUMAN	tq04f08.x1 NCI_CGAP_Uk3 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
203	12661	19992	9.33	0.0E+00	AI587308.1	EST_HUMAN	tq04f08.x1 NCI_CGAP_Uk3 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
205	10176	19994	1.94	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
208	10179		16.66	0.0E+00	4506692	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
209	10180		3.46	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
215	10186	19999	2.48	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
216	10186	19999	1.95	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
217	10187	20000	1.61	0.0E+00	6678444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspy), mRNA
							TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
224	10195	20004	3.43	0.0E+00	BE246780.1	EST_HUMAN	cDNA clone TCBAP4466
							TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
224	10195	20005	3.43	0.0E+00	BE246780.1	EST_HUMAN	cDNA clone TCBAP4466
							TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
224	10195	20006	3.43	0.0E+00	BE246780.1	EST_HUMAN	cDNA clone TCBAP4466
							TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
225	10195	20004	3.99	0.0E+00	BE246780.1	EST_HUMAN	cDNA clone TCBAP4466
							TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
225	10195	20005	3.99	0.0E+00	BE246780.1	EST_HUMAN	cDNA clone TCBAP4466
							TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
225	10195	20006	3.99	0.0E+00	BE246780.1	EST_HUMAN	cDNA clone TCBAP4466
							TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
226	10195	20004	12.62	0.0E+00	BE246780.1	EST_HUMAN	cDNA clone TCBAP4466
							TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
226	10195	20005	12.62	0.0E+00	BE246780.1	EST_HUMAN	cDNA clone TCBAP4466
							TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
226	10195	20006	12.62	0.0E+00	BE246780.1	EST_HUMAN	cDNA clone TCBAP4466
							TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
238	10206	20023	4.66	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
240	10208		6.54	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
247	10213	20029	3.75	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
249	10215	20032	1.46	0.0E+00	X89772.1	NT	H.sapiens mRNA for interferon alpha/beta receptor (long form)
257	10223		6.81	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
269	10234	20050	1.14	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
269	10234	20051	1.14	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
270	10236	20053	2.57	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
281	10246	20066	1.11	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
281	10246	20067	1.11	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
282	10247		0.86	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
290	10254	20074	5.26	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
290	10254	20075	5.26	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
301	10265	20085	4.03	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
302	10266	20086	3.11	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
303	12664		5.3	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
304	10267	20087	1.99	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
305	10268		2.03	0.0E+00	AA480002.1	EST_HUMAN	zvf18c06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:763994 5'
306	10269	20088	13.28	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
307	10269	20088	9.68	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
311	10273	20092	2.23	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
324	10285	20101	0.9	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
324	10285	20102	0.9	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
325	10286	20103	4.18	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
326	10286	20103	2.31	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
341	10300	20115	3.67	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLL T4) mRNA
342	10301	20116	0.86	0.0E+00	4505256	NT	Homo sapiens moesin (MSN), mRNA
345	10304	20120	3.76	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
348	10307	20125	0.8	0.0E+00	U71600.1	NT	Human zinc finger protein zfp31 (zfp31) mRNA, partial cds
353	10311	20129	2.15	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
353	10311	20130	2.15	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
354	12665	20131	3.4	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
356	10313	20133	0.89	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
358	10315	20136	1.4	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
359	10316	20137	1.37	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
360	10316	20137	1.52	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
372	10326	20149	1.13	0.0E+00	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLAGE1000899 5'
381	10365	20188	5.35	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
382	10366	20189	1.01	0.0E+00	A1363014.1	EST_HUMAN	qy61h05.x1 NCL_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54199
387	10334	20156	3.43	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN);
390	10336	20159	1.38	0.0E+00	4503660	NT	RC2-CT0320-300100-016-a09 CT0320 Homo sapiens cDNA
391	10337	20160	2.04	0.0E+00	4503660	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
							Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
391	10337	20161	2.04	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FQ(GAMMA)BP) mRNA
392	10338	20162	1.17	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FQ(GAMMA)BP) mRNA
393	10339	20163	1.64	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FQ(GAMMA)BP) mRNA
393	10339	20164	1.64	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FQ(GAMMA)BP) mRNA
394	10340	20165	2.43	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FQ(GAMMA)BP) mRNA
395	10341	20166	0.9	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FQ(GAMMA)BP) mRNA
396	10342	20167	0.84	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
396	10342	20168	0.84	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
400	10346		43.09	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
414	9881	19772	1.31	0.0E+00	R17795.1	EST_HUMAN	yg09a02.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:31652 5'
422	10367		2.61	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
423	10368	20190	2.42	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
424	10369	20191	4.7	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
424	10369	20192	4.7	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
425	10370	20193	3.51	0.0E+00	AF193607.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
438	10382	20206	2.01	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
443	10387		0.98	0.0E+00	AA324262.1	EST_HUMAN	EST27054 Cerebellum II Homo sapiens cDNA 5' end
444	10388		0.91	0.0E+00	BE254447.1	EST_HUMAN	601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
460	10404	20220	3.15	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
460	10404	20221	3.15	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
465	10408	20228	1.27	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
465	10408	20229	1.27	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
475	10419	20235	2.26	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
476	10420	20236	7.05	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
476	10420	20237	7.05	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
485	10428	20242	2.59	0.0E+00	AB030305.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
487	10430	20244	1.64	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
485	10438	20250	2.17	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
496	12668	20251	1.05	0.0E+00	AWG88825.1	EST_HUMAN	PM0-DT0065-130400-002-c06 DT0065 Homo sapiens cDNA
498	10440	20253	1.07	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
499	10441	20254	1.64	0.0E+00	8923955	NT	Homo sapiens PC326 protein (PC326), mRNA
508	10450	20263	3.91	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
515	12669	20267	1.97	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
520	10462	20273	1.13	0.0E+00	BF028005.1	EST_HUMAN	601764858F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996969 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
526	10468	20280	1.16	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
529	10471	20283	11.27	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TOEB1L) mRNA
530	10472	20284	3.96	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
530	10472	20285	3.96	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
536	10477		5.78	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
544	10485	20295	1.79	0.0E+00	AW135324.1	EST_HUMAN	U1-H-B11-acb-h-04-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
554	10495		3.15	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
571	10510	20318	2.65	0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
584	10522		5.28	0.0E+00	J04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
587	10525	20332	1.73	0.0E+00	BF104888.1	EST_HUMAN	601822627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
593	10529	20336	1.46	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
598	10534	20342	1.05	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
598	10534	20343	1.05	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
607	10543	20351	1.38	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
610	10546	20354	0.96	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
611	10547	20355	2.22	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
611	10547	20356	2.22	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
612	10548	20357	0.93	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
612	10548	20358	0.93	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
619	10556	20368	1.34	0.0E+00	AA339496.1	EST_HUMAN	zf60c07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'
623	10560	20372	6.37	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
627	10564	20375	3.17	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
627	10564	20376	3.17	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
630	10567		3.28	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
637	10574	20388	2.89	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
638	10576	20391	1.06	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
642	10579	20395	1.41	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
646	10583	20398	2.18	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
646	10583	20399	2.18	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
652	10588	20404	3.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
662	10588	20405	3.98	0.0E+00	4828947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
668	12672		0.95	0.0E+00	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
667	10601	20419	4.66	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA
672	10606	20423	4.35	0.0E+00	AB029012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
682	10615	20438	2.03	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
692	10625	20450	19.46	0.0E+00	AA614537.1	EST_HUMAN	np49d01.s1 NCI_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352
696	10629	20454	7.66	0.0E+00	M60675.1	NT	INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN); Human von Willebrand factor gene, exons 23 through 34
696	10629	20455	7.66	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
706	10639	20464	1.45	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
712	10644	20470	3.89	0.0E+00	AF264760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
712	10644	20471	3.89	0.0E+00	AF264760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
714	10646	20474	9.78	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
719	10651	20481	1.7	0.0E+00	BE241577.1	EST_HUMAN	TCAAP-ID0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA
739	10670	20505	1.12	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
739	10670	20506	1.12	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
740	10671	20507	2.4	0.0E+00	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
743	10674	20510	1.55	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
743	10674	20511	1.55	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
745	10676	20512	0.78	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
746	10677	20513	1.12	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
747	12676	20514	0.81	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
748	10678	20515	2.17	0.0E+00	BE869735.1	EST_HUMAN	60144564/F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
752	10682	20519	3.38	0.0E+00	R48915.1	EST_HUMAN	y69g08.1 Soares breast 2NblHst Homo sapiens cDNA clone IMAGE:154046 5'
753	10683	20520	2.4	0.0E+00	5032086	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
762	10692	20529	1.58	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
765	10696	20533	2.97	0.0E+00	7661968	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
775	10705	20544	1.17	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
775	10705	20545	1.17	0.0E+00	D90006.1	NT	Human mRNA for KIAA0184 gene, partial cds
780	10710	20549	2.64	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
784	10714	20553	2.37	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
784	10714	20554	2.37	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
789	10718	20560	6.84	0.0E+00	5174478	NT	Homo sapiens pericentriem (PCNT) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
790	10719		7.06	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
807	10736	20581	1.51	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
808	10737	20582	4.43	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
810	10739	20584	3.91	0.0E+00	4557686	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA
816	10744	20590	1.24	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
816	10744	20591	1.24	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
821	10749	20596	1.14	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
825	10752	20601	1.55	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
825	10752	20602	1.55	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
832	10759		1.57	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
836	10763	20613	3.37	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
836	10763	20614	3.37	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
837	10764	20615	7.38	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
838	10765	20616	3.03	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
839	10766	20617	2.02	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
843	10770	20620	1.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
843	10770	20621	1.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
844	10771	20622	1.97	0.0E+00	AA533272.1	EST_HUMAN	U68407.s1 NCI_CGAP_P110 Homo sapiens cDNA clone IMAGE:997453
844	10771	20623	1.97	0.0E+00	AA533272.1	EST_HUMAN	U68407.s1 NCI_CGAP_P110 Homo sapiens cDNA clone IMAGE:997453
845	10772		7.39	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
849	10776	20624	1.3	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
849	10776	20625	1.3	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	10777	20626	2.16	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	10777	20627	2.16	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
873	10799	20650	0.87	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
880	10806	20655	1.85	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
880	10806	20656	1.85	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
890	10816	20665	3.93	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
900	10825		7.45	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
903	10825		3.29	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
904	10828	20673	1.5	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
905	10829	20674	0.99	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
905	10829	20675	0.99	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
905	10829	20676	0.99	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
906	10830	20677	2.14	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (P14) gene, exons 1-4, complete cds
909	10833	20680	105.13	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
909	10833	20681	105.13	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
910	10834	20682	167.64	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
910	10834	20683	167.64	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
935	10860	20706	36.3	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
936	10861	20707	13.25	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
937	10862	20708	53.71	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
938	10863	20709	1.9	0.0E+00	4507430	NT	Homo sapiens thymotrophic embryonic factor (TEF), mRNA
938	10863	20710	1.9	0.0E+00	4507430	NT	Homo sapiens thymotrophic embryonic factor (TEF), mRNA
946	12681	20717	2.46	0.0E+00	A1001948.1	EST_HUMAN	os98e03.s1 NCJ_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
946	12681	20718	2.46	0.0E+00	A1001948.1	EST_HUMAN	os98e03.s1 NCJ_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
948	10872	20720	7.21	0.0E+00	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT), homolog (KIAA0929), mRNA
959	10882	20730	2.52	0.0E+00	AB030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
967	10890	20736	4.64	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
967	10890	20737	4.64	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
967	10890	20738	4.64	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
968	10891	20739	1.27	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
968	10891	20740	1.27	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
977	10900	20747	1.25	0.0E+00	4757969	NT	Homo sapiens chirodomain protein, Y chromosome-like (CDYL) mRNA
988	10910	20755	1.05	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
989	10911	20756	7.48	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
990	10911	20756	6.69	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
993	10914		1.99	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
994	10914		3.49	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
997	10917	20761	0.84	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
998	10917	20761	1.43	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
999	10917	20761	1.81	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1000	10918	20762	2.23	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1003	10921	20765	2.28	0.0E+00	7651685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1007	10925	20769	2.66	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1009	10927		1.94	0.0E+00	AA468990.1	EST_HUMAN	aa86g07.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1012	10930	20774	1.04	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1012	10930	20775	1.04	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1013	10931	20776	0.97	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1013	10931	20777	0.97	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1017	10935		4.44	0.0E+00	8922933	NT	Homo sapiens hypothetical protein FLJ11196 (FLJ11196), mRNA
1031	10949	20792	2.19	0.0E+00	4758599	NT	Homo sapiens heat shock 70kD protein 93 (mortalin-2) (HSPA9B) mRNA
1049	10966	20807	1.88	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1049	10966	20808	1.88	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1053	10970	20812	2.52	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1053	10970	20813	2.52	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1054	10971	20814	38.24	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1056	10973		0.93	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1058	10975	20818	3.28	0.0E+00	5174384	NT	Homo sapiens alkylation repair, akB homolog (ABH), mRNA
1066	10982	20827	3.58	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1080	10988	20837	3.6	0.0E+00	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-H08 BN0115 Homo sapiens cDNA
1103	11019	20861	3.79	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1103	11019	20862	3.79	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1118	11031	20872	1.12	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1116	11031	20873	1.12	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1117	11032	20874	5.7	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1119	11034	20876	0.96	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1121	11036	20878	10.18	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1123	11038	20879	12.02	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1124	11039	20880	2.03	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1124	11039	20881	2.03	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1128	11042	20884	0.95	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1129	11043	20885	1	0.0E+00	A1147650.1	EST_HUMAN	qb22d10.x1 Soares pregnant uterus NbtIPU Homo sapiens cDNA clone IMAGE:1697011 3'
1131	11045	20887	1.44	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1140	11054	20896	1.13	0.0E+00	9966844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1152	11065	20908	2.31	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1152	11065	20909	2.31	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1154	11067	20911	1.59	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1161	11074	20920	1.02	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1191	11101		1.13	0.0E+00	7657336	NT	Homo sapiens mult. (E. coli) homolog 3 (MLH3), mRNA
1206	11116	20962	1.14	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1206	11116	20963	1.14	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1207	11117	20964	1.31	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1208	12687	20965	0.95	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1226	11134	20988	3.62	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1227	11135	20989	1.3	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1245	11152		1.48	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1253	11180	21009	45.69	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1260	11197	21018	3.66	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR9) mRNA, complete cds
1266	11173	21022	1.71	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1266	11173	21023	1.71	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1278	11186	21036	6.42	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1278	11186	21037	6.42	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1278	11186	21038	6.42	0.0E+00	5174748	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1279	11187		2.6	0.0E+00	AF096195.1	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1289	12689	21050	1.1	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1289	12689	21051	1.1	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1295	11202	21057	1.71	0.0E+00	5803146	NT	Homo sapiens zinc finger protein 9 (ZNF9), mRNA
1296	11203	21058	0.82	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 9 (ZNF9), mRNA
1298	11205	21059	1.07	0.0E+00	5803146	NT	Homo sapiens zinc finger protein 9 (ZNF9), mRNA
1300	11207	21061	4.1	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1301	11208	21062	1.06	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1302	11209	21063	4.64	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1303	11210	21064	4.1	0.0E+00	8567387	NT	Homo sapiens perox (Drosophila) homolog 3 (PER3), mRNA
1303	11210	21065	4.1	0.0E+00	8567387	NT	Homo sapiens perox (Drosophila) homolog 3 (PER3), mRNA
1315	11221	21078	1.35	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1366	11291	21147	0.89	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyd gene
1393	11298	21156	9.13	0.0E+00	AJ277892.1	NT	Homo sapiens partial ITN gene for titin
1396	11301	21160	0.96	0.0E+00	AJ208756.1	EST_HUMAN	qg38b06.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:127A1.5
1397	11302	21161	8.18	0.0E+00	6042206	NT	RAN, member RAS oncogene family; Homo sapiens RAN, member RAS oncogene family (RAN), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
1407	11312	21173	1.4	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1407	11312	21174	1.4	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1409	11314	21177	2.54	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1409	11314	21178	2.54	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1412	11317	21180	5.25	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1421	11327	21192	3.51	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-6fucosyltransferase (alpha1-6FucT) gene, exon 7
1432	11337	21203	9.7	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1432	11337	21204	9.7	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1437	11342	21208	1.02	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1437	11342	21209	1.02	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1445	11350	21214	3.05	0.0E+00	AL132999.1	NT	Novel human gene on chromosome 20
1447	11352	21215	1.03	0.0E+00	AL137764.1	NT	Novel human gene mapping to chromosome 1
1451	11356	21220	1.22	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1454	11359	21223	4.97	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1456	11361	21225	1.51	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1456	11361	21226	1.51	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1457	11362		0.97	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1462	11367	21231	3.65	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1462	11367	21232	3.65	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1495	11399	21259	1.32	0.0E+00	7706434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51896), mRNA
1509	11414	21273	0.95	0.0E+00	AA481172.1	EST_HUMAN	aa34a03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815116 5'
1515	11420	21276	11.95	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1515	11420	21277	11.95	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1517	11422	21280	0.97	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1519	11424		2.03	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1520	11425	21283	3.9	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1520	11425	21284	3.9	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1521	11426	21285	3.12	0.0E+00	7662405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1522	11427		8.41	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1527	11432	21289	5.02	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1530	11435	21291	5.75	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1530	11435	21292	5.75	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1531	12697		10.12	0.0E+00	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1532	11436	21293	11.11	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1541	11446	21306	5.81	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1541	11446	21307	5.81	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1543	11448	21308	12.91	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1562	11467	21325	1.66	0.0E+00	Z83738.1	NT	H. sapiens H2B/e gene
1563	11468	21326	1.38	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1563	11468	21327	1.38	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1564	11469	21328	5.5	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKCC Homo sapiens cDNA clone GKCB0F02 5'
1564	11469	21329	5.5	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKCC Homo sapiens cDNA clone GKCB0F02 5'
1566	12698	21330	1.5	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1570	11474	21331	0.98	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1572	11476	21334	2.49	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1572	11476	21335	2.49	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1574	11478	21336	14.05	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1574	11478	21337	14.05	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1576	11480	21339	0.94	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1591	11495	21355	4.67	0.0E+00	H26973.1	EST_HUMAN	yo76c05.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1602	11507	21368	1.4	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1602	11507	21369	1.4	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1645	11549	21410	1.27	0.0E+00	A1768104.1	EST_HUMAN	wg81b07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN.;
1646	11550	21411	3.33	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1650	11553	21415	1.56	0.0E+00	M29590.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1650	11553	21416	1.56	0.0E+00	M29590.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1652	11555	21418	1.22	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1653	11556	21419	0.92	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1657	11559	21423	1.11	0.0E+00	4557610	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1659	11561	21426	2.99	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NBHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
1659	11561	21427	2.99	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1661	11563	21429	1.21	0.0E+00	Z80780.1	NT	yo59e08.r1 Soares breast 3NBHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
1661	11563	21430	1.21	0.0E+00	Z80780.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1664	11566		7.85	0.0E+00	5031748	NT	H. sapiens H2B/h gene
						NT	H. sapiens H2B/h gene
						NT	(Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1672	11574	21442	4.55	0.0E+00	8923841	NT	Homo sapiens FOXJ2 forkhead factor (LOC58810), mRNA
1677	11579	21448	1.02	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1677	11579	21449	1.02	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1680	11582	21453	1.43	0.0E+00	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1685	11587	21460	2.59	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1687	11589		2.6	0.0E+00	S94400.1	NT	TCR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8]
1699	12702	21472	0.87	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
1710	11611	21481	1.75	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1745	12703		13.91	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1749	11649	21517	0.9	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1749	11649	21518	0.9	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1751	11651	21521	1.23	0.0E+00	U63963.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1754	11654		1.13	0.0E+00	W76571.1	EST_HUMAN	z66g09.r1 Scores_fetal_heart_NH919W Homo sapiens cDNA clone IMAGE:345684 5'
1755	12704	21525	3.89	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1765	11664	21538	7.25	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
1767	11666	21541	4.6	0.0E+00	AB002331.1	NT	Human mRNA for KIA0333 gene, partial cds
1768	11667	21542	4.34	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1768	11667	21543	4.34	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1768	11667	21544	4.34	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1781	11680	21558	1.04	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1781	11680	21559	1.04	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1793	11691	21566	10.22	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1793	11691	21567	10.22	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1804	11701	21576	3.19	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1804	11701	21577	3.19	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1805	11702	21578	4.52	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1805	11702	21579	4.52	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1809	11706	21584	1.47	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-atn-f-07-o-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1809	11706	21585	1.47	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-atn-f-07-o-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1832	11729	21603	2.08	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1832	11729	21604	2.08	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1832	11748	21623	0.99	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0126-200300-012-504 BN0126 Homo sapiens cDNA
1881	11777	21651	3.52	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1881	11777	21652	3.52	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1889	11785		1.65	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1890	12707	21661	4.06	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1890	12707	21662	4.06	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1895	11790	21669	2.28	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1895	11790	21670	2.28	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1898	11794		5.25	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GST T2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1903	11799		1.9	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
1905	12708	21678	0.94	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
1913	11808	21685	1.97	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1913	11808	21686	1.97	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1924	11819		1.12	0.0E+00	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
1926	11821	21700	1.15	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1926	11821	21701	1.15	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1927	11822	21702	8.13	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1927	11822	21703	8.13	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1937	11832	21715	1.21	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1937	11832	21716	1.21	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1943	11838	21720	2.01	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1943	11838	21721	2.01	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1945	11840	21722	1.33	0.0E+00	AW193024.1	EST_HUMAN	x169b01.x1 NCI CGAP_Par1 Homo sapiens cDNA clone IMAGE:2679913 3'
1945	11840	21723	1.33	0.0E+00	AW193024.1	EST_HUMAN	x169b01.x1 NCI CGAP_Par1 Homo sapiens cDNA clone IMAGE:2679913 3'
1946	11841	21724	8.4	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1946	11841	21725	8.4	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1948	11843	21727	0.92	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1948	11843	21728	0.92	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1955	11850	21737	2.31	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
1975	11868	21759	0.96	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1975	11868	21760	0.96	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2011	11903	21793	1.09	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2011	11903	21794	1.09	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2013	11905	21795	0.96	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2014	11906	21796	5.46	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2015	11314	21177	1.01	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2015	11314	21178	1.01	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2017	11908	21798	1.95	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2017	11908	21799	1.95	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2019	11910		2.34	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2021	11912		1.6	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2022	11913	21802	0.92	0.0E+00	Z42399.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-0ic02
2024	11915		1.94	0.0E+00	A1244247.1	EST_HUMAN	q60f08.x1 NC1_CGAP_U2 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element
2029	11920	21811	2.59	0.0E+00	BE377225.1	EST_HUMAN	601485146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2031	11922	21813	1.5	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2031	11922	21814	1.5	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2035	11926	21819	2.42	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2035	11926	21820	2.42	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2040	11931	21826	2.53	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2040	11931	21827	2.53	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2045	11936	21831	1.32	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2077	11957		2.63	0.0E+00	BE767964.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2088	11958		1.13	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR51) gene, exon 6 and complete cds
2070	11960	21854	3.09	0.0E+00	BF027592.1	EST_HUMAN	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2071	11961	21855	2	0.0E+00	4503766	NT	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA
2073	11963	21856	0.99	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2074	11964	21857	1.16	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271039-022-G10 CT0219 Homo sapiens cDNA
2076	11966	21859	1.96	0.0E+00	AI904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2076	11966	21860	1.96	0.0E+00	AI904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2112	12001		1.19	0.0E+00	7657262	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNNMB3L), mRNA
2132	12020		1.6	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3'end

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2138	12026	21922	1.02	0.0E+00	BE274696.1	EST_HUMAN	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346688 5'
2140	12028	21925	1.09	0.0E+00	D87695.1	NT	Human mRNA for KIAA0244 gene, partial cds
2141	12029	21926	10.46	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2141	12029	21927	10.46	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2143	12031	21929	1.4	0.0E+00	AA931691.1	EST_HUMAN	cc32e01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896 3'
2145	12033		0.9	0.0E+00	MT9828.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29
2148	12036	21933	17.1	0.0E+00	BF344434.1	EST_HUMAN	602014820F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4160734 5'
2149	12037	21934	11.29	0.0E+00	BE748899.1	EST_HUMAN	601672186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
2152	12040	21937	2.35	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2152	12040	21938	2.35	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2156	12714	21943	1.77	0.0E+00	BF313617.1	EST_HUMAN	601900261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129622 5'
2159	12046	21946	1.92	0.0E+00	BE018750.1	EST_HUMAN	bb84e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;
2160	12047	21947	0.92	0.0E+00	AA042813.1	EST_HUMAN	zk63c07.s1 Soares_pregnant_uterus_Nb1PU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X68857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2160	12047	21948	0.92	0.0E+00	AA042813.1	EST_HUMAN	zk63c07.s1 Soares_pregnant_uterus_Nb1PU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X68857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2168	12055	21956	2.32	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2168	12055	21957	2.32	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2169	12056	21958	2.63	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2169	12056	21959	2.63	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2174	12061		1.04	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2193	12080	21984	7.56	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2199	12086	21988	1.44	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2206	12093	21996	1.09	0.0E+00	BE895281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3818607 5'
2209	12096	21999	0.87	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2209	12096	22000	0.87	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2212	12098	22002	1.36	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2253	12137	22034	4.16	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2253	12137	22035	4.16	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2254	12138	22036	2.51	0.0E+00	A1076404.1	EST_HUMAN	oz09c07.x1 Soares_fetal_liver脾_NFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2256	12140	22038	2.21	0.0E+00	AA429001.1	EST_HUMAN	zv78a11.r1 Soares_total_fetus_Nb2HF8_sw Homo sapiens cDNA clone IMAGE:759740 5'
2256	12140	22039	2.21	0.0E+00	AA429001.1	EST_HUMAN	zv78a11.r1 Soares_total_fetus_Nb2HF8_sw Homo sapiens cDNA clone IMAGE:759740 5'
2258	12142	22041	2.23	0.0E+00	BF347039.1	EST_HUMAN	602021846F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157339 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2263	12147	22047	1.19	0.0E+00	L02840.1	NT	Homo sapiens potassium channel Kv2.1 mRNA, complete cds
2264	12148	22048	2.03	0.0E+00	6325466	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2271	12155	22054	1	0.0E+00	BE676095.1	EST_HUMAN	7f22a02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:O94939 OB4939 KIAA0857 PROTEIN;
2274	12158	22056	10.08	0.0E+00	AF044571.1	NT	Homo sapiens phosphotyrosine kinase alpha subunit (PHKA2) gene, exon 32
2275	12159	22057	2.72	0.0E+00	AI625542.1	EST_HUMAN	y57c08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3'
2280	12164	22061	1.76	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2280	12164	22062	1.76	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2291	12173	22072	4.26	0.0E+00	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
2291	12173	22073	4.26	0.0E+00	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
2300	12182	22079	2.88	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2304	12185	22083	1.75	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2305	12186		5.71	0.0E+00	BE794026.1	EST_HUMAN	601586843f1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2306	12187	22084	0.98	0.0E+00	AW867076.1	EST_HUMAN	MR1-SN0033-120400-002-a04 SN0033 Homo sapiens cDNA
2307	12188	22085	1.97	0.0E+00	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2308	12189	22086	1.44	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2308	12189	22087	1.44	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2309	12190					NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2310	12191	22088	2.31	0.0E+00	AF280107.1	NT	
2310	12191	22089	7.57	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2310	12191	22090	7.57	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2327	12208		0.96	0.0E+00	BE814424.1	EST_HUMAN	MRO-BN0070-090600-029-d12 BN0070 Homo sapiens cDNA
2363	12243	22138	1.34	0.0E+00	AU119582.1	EST_HUMAN	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2366	12246		3.64	0.0E+00	AJ042035.1	EST_HUMAN	ox60b02.x1 Soares_NHMP_u_S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:O08662 O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE.;
2369	12249	22141	0.98	0.0E+00	AW303998.1	EST_HUMAN	xv15f07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR:O54924 O54924 EXO84.;
2371	12251		2.03	0.0E+00	BE895605.1	EST_HUMAN	601432808f1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2382	12262		1.69	0.0E+00	AB005622.1	EST_HUMAN	AB005622 HeLa cDNA (T.Noma) Homo sapiens cDNA similar to adenylylate kinase isozyme 2
2386	12265	22158	5.63	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2390	12268	22162	2.48	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystikinin type-A receptor, complete cds
2390	12268	22163	2.48	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystikinin type-A receptor, complete cds

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2398	12276	22172	2.28	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2402	12279	22176	0.98	0.0E+00	BF345274.1	EST_HUMAN	602018059F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
2410	12287	22185	3.95	0.0E+00	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2414	12291	22188	0.87	0.0E+00	BE831003.1	EST_HUMAN	CM0-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2414	12291	22189	0.87	0.0E+00	BE831003.1	EST_HUMAN	CM0-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2419	12296	22193	2.27	0.0E+00	BF569144.1	EST_HUMAN	602184558T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2428	12305	22201	2.66	0.0E+00	AW466922.1	EST_HUMAN	ha04h04.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
2430	12307	22202	3.45	0.0E+00	AW501010.1	EST_HUMAN	U1-HF-BPOp-als-c-07-0-U1.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2444	12321	22219	2.08	0.0E+00	5453966	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2444	12321	22220	2.08	0.0E+00	5453966	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2457	12334		2.35	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2462	12339	22233	16.13	0.0E+00	BE795542.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2463	11792	21671	1.18	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2464	12340	22234	1.8	0.0E+00	BF509482.1	EST_HUMAN	U1-H-BI4-aoz-b-05-0-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2467	12343	22236	2.25	0.0E+00	732684.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2469	12345		5.57	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2471	12347	22239	1.99	0.0E+00	BE910378.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2472	12348	22240	1.96	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2473	12349	22241	55.78	0.0E+00	BE150865.1	EST_HUMAN	RC4-HT0276-160200-073-d05 HT0276 Homo sapiens cDNA
2474	12350	22242	1.14	0.0E+00	8923340	NT	Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA
2475	12351	22243	3.21	0.0E+00	U93239.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2481	12357	22249	1.64	0.0E+00	BE886490.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
2486	12361	22255	4.39	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2486	12361	22256	4.39	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2488	12363	22259	0.97	0.0E+00	AF245505.1	NT	Homo sapiens adiclin mRNA, complete cds
2504	12379	22267	1.27	0.0E+00	BE538921.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2509	12383	22274	3.8	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2509	12383	22275	3.8	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2510	12384	22276	1.19	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
2510	12384	22277	1.19	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
2511	12385	22278	0.99	0.0E+00	BF223041.1	EST_HUMAN	7q27h12.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:3' similar to TR:O00246 O00246
2514	12388	22280	7.65	0.0E+00	AF245505.1	NT	HYPOHETICAL 9.3 KD PROTEIN ;
2540	12414	22304	1.05	0.0E+00	BE299613.1	EST_HUMAN	Homo sapiens adiclin mRNA, complete cds
							601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'

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2553	12654	22318	2.37	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2553	12654	22319	2.37	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2554	12426		3.85	0.0E+00	BF513835.1	EST_HUMAN	U1-HBW1-amp-f-12-o-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2560	12432	22325	2.8	0.0E+00	BF672818.1	EST_HUMAN	602152653F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283612 5'
2562	12434		1.16	0.0E+00	BE616695.1	EST_HUMAN	601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3821786 5'
2569	12440	22332	1.34	0.0E+00	AB037742.1	NT	Homo sapiens mRNA for KIAA1321 protein, partial cds
2570	12441	22333	0.97	0.0E+00	AI571737.1	EST_HUMAN	tr19b08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2168055 3' similar to gb.L20977 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN);
2571	12442	22334	2.27	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, l, 28kd (TAF2l) mRNA
2573	12444	22336	5.78	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2574	12445	22337	1.03	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2574	12445	22338	1.03	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2577	12448	22339	1.1	0.0E+00	BE293328.1	EST_HUMAN	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5'
2585	12456		10.42	0.0E+00	BE792472.1	EST_HUMAN	601584930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2595	12465	22358	2.46	0.0E+00	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2601	12727	22365	7.02	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
2608	12476		1.09	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2609	12477	22369	5.19	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2613	12481	22370	1.17	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
2616	12484	22373	0.98	0.0E+00	AU133385.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001964 5'
2617	12485	22374	1.41	0.0E+00	M69225.1	NT	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds
2619	12487	22376	1.21	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2619	12487	22377	1.21	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2622	12490	22380	1.29	0.0E+00	AW887015.1	EST_HUMAN	RC1-OT0086-220300-011-d07 OT0086 Homo sapiens cDNA
2626	12494	22385	1	0.0E+00	BF000018.1	EST_HUMAN	7n15n05.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316089 3'
2627	12495	22386	3.25	0.0E+00	BE383165.1	EST_HUMAN	601298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2628	12496		2.74	0.0E+00	BE531263.1	EST_HUMAN	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5'
2656	12523	22413	1.74	0.0E+00	8922843	NT	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA
2690	12565		8.72	0.0E+00	AA316723.1	EST_HUMAN	EST:88414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2691	12566	22443	0.88	0.0E+00	BE794894.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2698	12562	22452	3.59	0.0E+00	U36253.1	NT	Human beta-prime-adaplin (BAM22) gene, exon 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2700	12564	22454	1.08	0.0E+00	769517	NT	Homo sapiens neuregulin 1 (NRG1), transcript variant SMD1, mRNA
2701	12565	22455	10.23	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2708	12571	22462	10.37	0.0E+00	BE796376.1	EST_HUMAN	601591991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2709	12572	22463	3.2	0.0E+00	BF680632.1	EST_HUMAN	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 5'
2712	12731	22467	13.51	0.0E+00	BE563433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2713	12575		1.28	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2715	12577	22470	2.17	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2716	12577	22471	2.17	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2716	12578	22472	0.9	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2716	12578	22473	0.9	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2717	12579	22474	2.2	0.0E+00	AF290195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2718	12580		15.67	0.0E+00	AV651066.1	EST_HUMAN	AV651066 GLC Homo sapiens cDNA clone GLCCLD07 3'
2719	12581	22475	1.72	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2719	12581	22476	1.72	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2723	12585	22479	3.21	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34KD) (CDR1) mRNA
2723	12585	22480	3.21	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34KD) (CDR1) mRNA
2727	12589	22485	2.2	0.0E+00	BE747193.1	EST_HUMAN	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2730	12592	22488	0.97	0.0E+00	BE176836.1	EST_HUMAN	RC4-HT0587-170300-012-d11 HT0587 Homo sapiens cDNA
2741	12603		1.3	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2742	12604	22498	3.47	0.0E+00	BF514110.1	EST_HUMAN	U1-HBW1-armw-e-07-Q.U1.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2748	12610		1.07	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2754	12616	22507	4.95	0.0E+00	BF677694.1	EST_HUMAN	60208579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2758	12620	22513	1.73	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2761	12623	22515	9.56	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTG Homo sapiens cDNA clone HTCCCA03 5'
2761	12623	22516	9.56	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTG Homo sapiens cDNA clone HTCCCA03 5'
2763	12625		11.15	0.0E+00	AB79163.1	EST_HUMAN	au55d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to
2766	12628	22521	1.97	0.0E+00	BF530661.1	EST_HUMAN	suwR13A, HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
2767	12629	22522	2.91	0.0E+00	BE872768.1	EST_HUMAN	602071957F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214679 5'
2769	12631	22523	1.11	0.0E+00	AU131494.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3954642 5'
2769	12631	22524	1.11	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2770	12632	22525	10.1	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2770	12632	22526	10.1	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2775	10151	19966	4.6	0.0E+00	ST6830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3068 nt]

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2778	12638		1.94	0.0E+00	A5033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2784	10649	20479	1.37	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2784	10649	20480	1.37	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2789	10941	20784	3.58	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2789	10941	20785	3.58	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2805	12735	22534	2.39	0.0E+00	X85980.1	NT	H.sapiens serine hydroxymethyltransferase pseudogene
2806	12736		1.27	0.0E+00	AF068624.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
2808	12738		1.1	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2814	12743		1.07	0.0E+00	AJ238852.1	NT	Homo sapiens partial rpl3 gene for ribosomal protein L3, U82 snoRNA, U83a snoRNA and U83b snoRNA genes
2815	12744	22538	2.24	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2819	12748	22541	5.94	0.0E+00	M80902.1	NT	Human AHNAK nucleoprotein mRNA, 5' end
2822	12751	22543	1.58	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2822	12751	22544	1.58	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2824	12763		1.38	0.0E+00	X73428.1	NT	H.sapiens Id3 gene for HLH type transcription factor
2826	12765		2.84	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2828	12767	22547	2.58	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
2833	12761	22551	43.46	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2833	12761	22552	43.46	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2837	12766	22555	1.34	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2838	12766		4.62	0.0E+00	Y10658.1	NT	H.sapiens mRNA for nuclear DNA helicase II
2839	12767		0.96	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2840	12768	22556	25.08	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2840	12768	22557	25.08	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2851	12779	22563	2.42	0.0E+00	4507280	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2854	12782	22572	1.35	0.0E+00	AL047599.1	EST_HUMAN	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2855	12783	22573	1.25	0.0E+00	7661883	NT	DKFZp586G0621_r1 586 (synonym: huter) Homo sapiens cDNA clone DKFZp586G0621
2855	12783	22574	1.25	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2856	12784		3.42	0.0E+00	4503098	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2858	12786	22576	4.95	0.0E+00	BE081896.1	EST_HUMAN	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2858	12786	22577	4.95	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2866	12794	22588	1.64	0.0E+00	AL163206.2	NT	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2866	12794	22689	1.64	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2867	12795	22690	1.08	0.0E+00	AA215579.1	EST_HUMAN	z96b11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:363517 3' similar to contains Alu repetitive element;
2874	12801		3.09	0.0E+00	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
2877	12804	22699	1.16	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2878	12805	22600	18.66	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2879	12806	22601	1.25	0.0E+00	AI561002.1	EST_HUMAN	tn18d07.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2879	12806	22602	1.25	0.0E+00	AI561002.1	EST_HUMAN	O16247 F44E7.2 PROTEIN.;
2881	12808	22604	1.87	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
2882	12809	22605	1.5	0.0E+00	AF152338.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2887	12824	22617	1.34	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2897	12824	22618	1.34	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2898	12825	22619	4.98	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2898	12825	22620	4.98	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2901	12828	22623	2.66	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2901	12828	22624	2.66	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2902	12829	22625	3.23	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2902	12829	22626	3.23	0.0E+00	5174574	NT	(MLLT4) mRNA
2907	12833	22630	1.27	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9V/LN1
2907	12833	22631	1.27	0.0E+00	BF110702.1	EST_HUMAN	Q9V/LN1 CG17293 PROTEIN.;
2915	12842	22642	2.03	0.0E+00	4505084	NT	7n40d03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9V/LN1
2915	12842	22643	2.03	0.0E+00	4505084	NT	Q9V/LN1 CG17293 PROTEIN.;
2917	12844	22645	0.94	0.0E+00	4885214	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2917	12844	22646	0.94	0.0E+00	4885214	NT	Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA
2924	12851	22651	1.6	0.0E+00	4758827	NT	Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA
2927	12854	22654	1.3	0.0E+00	X15309.1	NT	Homo sapiens neurexin III (NRXN3) mRNA
2927	12854	22655	1.3	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2929	12856	22657	7.93	0.0E+00	AF105275.1	NT	H. sapiens NF-H gene, exon 4
2929	12856	22657	7.93	0.0E+00	AF105275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4' (ILT1c) gene, exon 6

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2943	12870		1.13	0.0E+00	AI149880.1	EST_HUMAN	qf43f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
2952	12879	22677	0.84	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
2962	12879	22678	0.84	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
2953	12880	22679	0.97	0.0E+00	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
2954	12881	22680	2.15	0.0E+00	AB004894.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
2964	12891	22689	1.33	0.0E+00	7662273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
2965	12892	22690	1.59	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2966	12892	22691	1.59	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2990	12918		0.89	0.0E+00	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2992	12920	22714	1.04	0.0E+00	M74099.1	NT	Human displacement protein (CCAA1) mRNA
3001	12929	22721	0.82	0.0E+00	4506882	NT	Homo sapiens semenogelin 1 (SEMG1) mRNA
3006	12934		4.85	0.0E+00	AF195983.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3009	12937	22730	7.86	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3009	12937	22731	7.86	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3011	12939		5.08	0.0E+00	AL359403.1	NT	Isoform 2 of a novel human mRNA from chromosome 22
3014	12942	22735	2.02	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
							Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α)
3017	12945		1.74	0.0E+00	AF196779.1	NT	Homo sapiens interleukin 2 receptor, beta (IL2RB) mRNA
3019	12947	22739	0.99	0.0E+00	4504664	NT	Human germline gene 16.1 for Ig lambda L-chain C region (IgL-C16.1)
3038	12966	22730	2.79	0.0E+00	X03529.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3043	12970		1.85	0.0E+00	AF199355.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3047	12974	22767	1.89	0.0E+00	AF084589.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3068	12995	22786	2.85	0.0E+00	AF265208.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3069	12996	22787	3.97	0.0E+00	AF149773.1	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3074	13001	22791	4.21	0.0E+00	7662139	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3075	13002	22792	1.64	0.0E+00	AF042075.1	NT	
							Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3102	13028	22824	3.45	0.0E+00	4826783	NT	Human ferritin heavy chain mRNA, complete cds
3111	13036	22832	19.64	0.0E+00	L20941.1	NT	
3115	13040	22836	1.79	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3115	13040	22837	1.79	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
							ye32f03.s1 Stralagene lung (#637210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SF.S29539
3123	13048	22845	9.41	0.0E+00	T94870.1	EST_HUMAN	S29539 BASIC PROTEIN, 23k -;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3138	13063	22862	1.1	0.0E+00	BF243336.1	EST_HUMAN	601978507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3140	13065	22863	1.03	0.0E+00	AI958086.1	EST_HUMAN	wu12h10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2618803 3'
3145	13070	22870	3.99	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3145	13070	22871	3.99	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3156	13081	22883	1.5	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3156	13081	22884	1.5	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3163	13088	22892	7.73	0.0E+00	4504658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3164	13089	22893	3.26	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3164	13089	22894	3.26	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3180	13105	22910	2.44	0.0E+00	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3183	13108	22912	2.23	0.0E+00	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3188	13113	22918	0.82	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3188	13113	22919	0.92	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3190	13115	22920	26.3	0.0E+00	AA747483.1	EST_HUMAN	ae87b11.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3198	13123	22928	4.53	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3198	13123	22929	4.53	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3210	13134	22935	1.56	0.0E+00	4557590	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3215	13139	22942	3.35	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3224	13148		4.39	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
3225	13149	22949					Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
3227	13151	22951	1.19	0.0E+00	AF019413.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3237	15066	22959	4.15	0.0E+00	AF056084.1	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3237	15066	22960	3.46	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3252	13175	22973	2	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3253	13176	22974	0.89	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3282	13203	23003	4.86	0.0E+00	AI599264.1	EST_HUMAN	t58f08.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222535 3' similar to SWI:RL11_RAT P25121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element;
3289	13211	23011	2.98	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3289	13211	23012	2.98	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3290	13212	23013	1	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3290	13212	23014	1	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3292	13214	23015	1.01	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3292	13214	23016	1.01	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3296	13218	23019	11.07	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3298	13220	23021	0.96	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3303	13224	23026	0.99	0.0E+00	BE779039.1	EST_HUMAN	601464995F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5'
3350	13270	23073	3.01	0.0E+00	AU123664.1	EST_HUMAN	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'
3357	13276	23076	1.66	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10G1), mRNA
3357	13276	23077	1.66	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3360	13279	23079	1.43	0.0E+00	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
3361	13280	23080	0.99	0.0E+00	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I) mRNA, complete cds
3377	13295	23094	1.35	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3377	13295	23095	1.35	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3378	13296	23096	0.96	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3381	13299	23098	1.71	0.0E+00	5803067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3390	12565	22455	6.04	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3395	13312	23111	2.08	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3398	13315	23115	1.53	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3398	13315	23116	1.53	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3400	13317	23118	5.53	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and incA, incB, and incC incompatibility determinants
3402	13319	23120	1.21	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR1), mRNA
3409	13326	23126	3.68	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE. ;
3409	13326	23127	3.68	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE. ;
3413	13330	23132	2.67	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3420	13337	23141	2.86	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3420	13337	23142	2.86	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3426	13343	23148	1.14	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
3431	13348	23153	6.18	0.0E+00	U43293.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3436	13353	23157	1.01	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3436	13353	23158	1.01	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3440	13367	23163	2.06	0.0E+00	AF045482.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3440	13367	23164	2.06	0.0E+00	AF045482.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3448	13366	23172	1.23	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3455	13371	23175	0.94	0.0E+00	AA626677.1	EST_HUMAN	ab51f12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3455	13371	23176	0.94	0.0E+00	AA626677.1	EST_HUMAN	ab51f12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3455	13371	23177	0.94	0.0E+00	AA626677.1	EST_HUMAN	ab51f12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3458	13374	23180	1.11	0.0E+00	4508028	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45) mRNA
3461	13377	23182	2.23	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3461	13377	23183	2.23	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3463	13379	23185	1.43	0.0E+00	4826795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KONE2) mRNA
3470	13386	23191	0.92	0.0E+00	AI384007.1	EST_HUMAN	te35g12.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498
3473	13389	23194	0.96	0.0E+00	MT10976.1	NT	O00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ; Human endogenous retroviral DNA (4-1), complete retroviral segment
3495	13412	23217	0.82	0.0E+00	4508884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
3497	13414		1.3	0.0E+00	AF078868.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3505	13422	23225	1.39	0.0E+00	AL133204.1	NT	Novel human gene mapping to chromosome X
3507	13423	23226	0.96	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3527	13443		0.98	0.0E+00	AI081907.1	EST_HUMAN	ox77c11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1662356 3' similar to WP:119B4.4 CE13742 ;
3529	13445	23242	1.26	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3533	13449		4.53	0.0E+00	AW852217.1	EST_HUMAN	QY0-C.T0225-230300-169-e01 CT0225 Homo sapiens cDNA
3540	13456		0.95	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3541	13457	23250	7.43	0.0E+00	BF676393.1	EST_HUMAN	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248596 5'
3564	13478		1.1	0.0E+00	4826967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3566	13480	23269	0.98	0.0E+00	AW664693.1	EST_HUMAN	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3566	13480	23270	0.98	0.0E+00	AW664693.1	EST_HUMAN	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3569	13483	23274	1.13	0.0E+00	4826763	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3571	13485	23277	0.98	0.0E+00	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3578	13492	23282	0.79	0.0E+00	4557752	NT	Homo sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA
3578	13492	23283	0.79	0.0E+00	4557752	NT	Homo sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA
3586	13510	23297	1.51	0.0E+00	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3600	13514		28.67	0.0E+00	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3616	13530	23316	4.26	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3619	13533	23318	3.26	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3619	13533	23319	3.26	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3623	13537	23323	1.5	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3623	13537	23324	1.5	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3626	13540	23326	2.2	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3626	13540	23327	2.2	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3630	13544	23331	1.79	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3632	13546	23333	1.25	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
3645	13559	23344	3.53	0.0E+00	AW298134.1	EST_HUMAN	UIH-BW0-ajs-e-12-0-UI.s1 NCI CGAP Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3645	13559	23345	3.53	0.0E+00	AW298134.1	EST_HUMAN	UIH-BW0-ajs-e-12-0-UI.s1 NCI CGAP Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3668	13582	23369	0.99	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen a1 chain, exon 6
3669	13583	23370	1.03	0.0E+00	AA463659.1	EST_HUMAN	aa06g01.r1 Soares NIHMP.U. S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4. [1];
3687	13591	23377	3.35	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3689	13613	23397	3.88	0.0E+00	7662183	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3701	13615	23399	7.88	0.0E+00	4506718	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3705	13618	23401	1.02	0.0E+00	7657065	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3705	13618	23402	1.02	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3746	13659	23441	1.13	0.0E+00	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
3747	13660		1.01	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3748	13661	23442	2.3	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (P TR208) gene, partial cds
3751	13664	23446	1.69	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3751	13664	23447	1.69	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3752	13665	23448	1.45	0.0E+00	AF020091.1	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds
3756	13669	23453	1.1	0.0E+00	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
3758	13671	23455	1.1	0.0E+00	AI377699.1	EST_HUMAN	te02f10.x1 Soares_NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3759	13672		1.7	0.0E+00	AF162496.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3760	13673	23456	4.46	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
3763	13676	23458	11.67	0.0E+00	S78685.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds
3764	13677	23459	2	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3765	13678	23460	2.39	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3768	13681	23462	1.31	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3768	13681	23463	1.31	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3769	13682	23464	1.97	0.0E+00	4504534	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D) mRNA
3773	13685	23467	1.61	0.0E+00	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3775	13687	23470	1.12	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3780	13692	23478	5.67	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3780	13692	23479	5.67	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3782	13694	23482	3.93	0.0E+00	U09412.1	NT	Human Zinc finger protein ZNF134 mRNA, complete cds
3784	13696	23483	1.63	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3787	13699	23486	0.99	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3788	13700	23487	1.87	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3790	13702	23489	0.82	0.0E+00	AF099117.1	NT	Homo sapiens amphiphysin gene, partial cds
3799	13711	23498	2.54	0.0E+00	A1864727.1	EST_HUMAN	wk01f01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O43340
3802	13714	23502	6.08	0.0E+00	4506742	NT	O43340 R28830_2, contains element PTR7 repetitive element;
3807	13719	23508	1.41	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3813	13725	23515	1	0.0E+00	6005887	NT	DKFZp434N0413_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0413 5'
3813	13725	23516	1	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3815	13727	23518	2.45	0.0E+00	4504138	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1 GBP1), mRNA
3816	13728		1.8	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3820	13732	23521	0.87	0.0E+00	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3830	13742	23534	1.27	0.0E+00	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
3833	13745	23537	1.62	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
3840	13751	23544	1.75	0.0E+00	BF365295.1	EST_HUMAN	RC3-HT0860-170800-011-a12 HT0860 Homo sapiens cDNA
3842	13753	23546	1.4	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone lrcyte 1996726 similar to MXRA5
3842	13753		1.4	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone lrcyte 1996726 similar to MXRA5
3848	13759	23547	1.78	0.0E+00	AF129533.1	NT	Matrix remodeling associated gene 5
3848	13759	23552	1.78	0.0E+00	AF129533.1	NT	Homo sapiens F-box protein FBX3b (FBX3B) mRNA, partial cds
3853	13764	23557	3.2	0.0E+00	BE378602.1	EST_HUMAN	601236966F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
3854	13765	23558	1.27	0.0E+00	BE313146.1	EST_HUMAN	601153727F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509743 5'
3860	13771	23563	0.97	0.0E+00	AW580740.1	EST_HUMAN	PM3-LT0031-100100-003-009 LT0031 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3893	13803	23587	4.6	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3893	13803	23588	4.6	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3903	13813		3.93	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
3905	13815		5.44	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
3912	13822	23603	1.53	0.0E+00	AL118494.1	NT	Novel human gene mapping to chromosome 20
3916	13825	23605	2.89	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3924	13833	23613	1.46	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
3935	13844		25.75	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
3939	13847	23623	1.18	0.0E+00	7592183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3940	13848	23624	2.05	0.0E+00	U09366.1	NT	Human zinc finger protein ZNF133
3960	13867	23645	6.24	0.0E+00	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
3968	13875		3.79	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
3976	13883	23658	3.28	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3976	13883	23659	3.28	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3981	13888	23663	5.63	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
3981	13888	23664	5.63	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
3993	13900	23677	0.81	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
4000	13906	23682	4.89	0.0E+00	4885306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4001	13907	23683	1.94	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4003	13909	23684	1.28	0.0E+00	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4004	13910	23685	6.1	0.0E+00	11419297	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4005	13911	23686	1.58	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4013	13919	23695	2.7	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4017	15071	23697	0.85	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4022	11031	20872	0.8	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4022	11031	20873	0.8	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4028	13931	23707	0.99	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
4029	13932	23708	1.16	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4029	13932	23709	1.16	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4032	13935	23711	1.05	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4032	13935	23712	1.05	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4041	13944	23722	4.59	0.0E+00	A1982597.1	EST_HUMAN	wu04d04.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2515975 3'
4041	13944	23723	4.59	0.0E+00	A1982597.1	EST_HUMAN	wu04d04.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2515975 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4044	13946	23725	0.88	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4044	13946	23726	0.88	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4048	13950		1.99	0.0E+00	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
4055	13957	23733	0.97	0.0E+00	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
4056	13958	23734	1.98	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4064	13966		6.19	0.0E+00	AW675599.1	EST_HUMAN	ba51f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:29000095 3' similar to SW:TH12_BOVIN
4069	13971	23748	1.52	0.0E+00	AW408788.1	EST_HUMAN	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4071	13973	23751	1.33	0.0E+00	8922466	NT	UI-HF-BM0-adx-c-02-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4071	13973	23752	1.33	0.0E+00	8922466	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4081	13983		1.96	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homology)-like (PKDREJ) mRNA
4098	13998	23775	7.82	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element ;
4098	13998	23776	7.82	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element ;
4113	14013	23791	3.79	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4113	14013	23792	3.79	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4126	14026	23801	0.87	0.0E+00	4506982	NT	Homo sapiens semenogelin I (SEMG1) mRNA
4130	14030	23803	8.21	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
4130	14030	23804	8.21	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
4137	14037		0.88	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4163	14063	23837	1.13	0.0E+00	AJ003145.1	NT	Homo sapiens mRNA for olfactory receptor protein, pseudogene
4176	14076	23851	7.84	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds
4190	14090	23869	0.95	0.0E+00	AW936889.1	EST_HUMAN	PM2.DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4196	14096	23876	0.88	0.0E+00	4826827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4196	14096	23877	0.88	0.0E+00	4826827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4198	14098	23879	5.73	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein Fbx4 (FBL4) mRNA, partial cds
4206	14105		1.92	0.0E+00	AI189844.1	EST_HUMAN	qd23f06.x1 Soares_placenta_8to9weeks_2Nb1P8to9W Homo sapiens cDNA clone IMAGE:1724579 3' similar to contains MER20_b2 MER20 repetitive element ;
4210	14108		4.09	0.0E+00	U14520.1	NT	Human CBFA3 (Osr33) gene, partial cds
4224	14122	23897	0.98	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
4230	14128	23904	0.87	0.0E+00	6553384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4230	14128	23905	0.87	0.0E+00	6563384	NT	Homo sapiens protein kinase C, α (PRKCN), mRNA
4237	14135	23911	1.17	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4237	14135	23912	1.17	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4245	14144	23917	10.2	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4263	14162		1.15	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4268	14167	23943	1.56	0.0E+00	U03901.1	NT	Human Ig light chain VL1 region germline (hum1v1c2c) gene, partial cds
4274	14173	23950	5.17	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4278	14177	23955	2.78	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4278	14177	23956	2.78	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4284	14183	23962	1.58	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4284	14183	23963	1.58	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4289	14187	23969	8.95	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4289	14187	23970	8.95	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4299	14197	23982	10.81	0.0E+00	4885126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4302	14200	23984	0.98	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4333	14230	24012	1.1	0.0E+00	7019456	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4341	14238		5.85	0.0E+00	AF105953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4346	14243	24025	8.1	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4346	14243	24026	8.1	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4368	14284		1.92	0.0E+00	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
4401	14286	24080	40.23	0.0E+00	AW084864.1	EST_HUMAN	xc68e08.x1 NCJ CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW:AHNK_HUMAN
4403	15073		1.91	0.0E+00	8051619	NT	Q09666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNK ;
4405	14299	24083	1.38	0.0E+00	AF016050.1	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4408	14302		7.5	0.0E+00	AL163207.2	NT	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGFR165) mRNA, complete cds
4410	14304	24087	1.29	0.0E+00	AW381570.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
4416	14310	24094	1.83	0.0E+00	AJ278120.1	NT	PM1-HT0305-101199-002-003 HT0305 Homo sapiens cDNA
4416	14310	24095	1.83	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4418	14312	24097	3.91	0.0E+00	4758467	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4419	14313	24098	2.3	0.0E+00	AF108830.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4424	14318	24104	1.47	0.0E+00	Z66526.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4429	14324	24111	1.12	0.0E+00	S78684.1	NT	H. sapiens pancreatic polypeptide receptor PP1 gene
							Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4430	14325	24112	1.95	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4430	14325	24113	1.95	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4439	15074	24123	3.08	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4444	14338	24128	5.37	0.0E+00	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4449	14343	24135	1.92	0.0E+00	AF152337.1	NT	Homo sapiens protobacterin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4452	14348	24139	1.36	0.0E+00	5454179	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4462	14356	24147	15.15	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4473	14367	24156	1.47	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4477	14371	24161	1.58	0.0E+00	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4481	14375		2.78	0.0E+00	L35485.1	NT	Homo sapiens iduronate sulphate (IDS) gene, complete cds
4483	14377	24163	9.78	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4483	14377	24164	9.78	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4498	14392	24177	2.04	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4500	14394	24179	8.67	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4500	14394	24180	8.67	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4511	14404		0.84	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4523	14416		1.5	0.0E+00	AA174072.1	EST_HUMAN	zp18g08.s1 Statagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4526	14419		1.55	0.0E+00	7657410	NT	Homo sapiens odz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA
4528	14421		1.22	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4529	14422	24205	1.71	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4530	14423	24206	4.37	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4531	14424		1.89	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4541	14434	24216	1.91	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4541	14434	24217	1.91	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4542	14435	24218	1.3	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4542	14435		1.3	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4543	14436	24220	1.18	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4554	14013	23791	7.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4554	14013	23792	7.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4560	14452	24238	21.96	0.0E+00	Y18990.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4566	14458	24246	2.32	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
4574	14465		2.01	0.0E+00	AF086411.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4580	14470	24257	2.65	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4580	14470	24258	2.65	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4581	14471	24259	2.55	0.0E+00	M74099.1	NT	Human displacement protein (GCAAT) mRNA
4585	14474	24262	1.82	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4585	14474	24263	1.82	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4588	10108	19929	1.03	0.0E+00	T56945.1	EST_HUMAN	ya83g04.12 Strategene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4586	10108	19930	1.03	0.0E+00	T56945.1	EST_HUMAN	ya83g04.12 Strategene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4597	14475		0.99	0.0E+00	BE278730.1	EST_HUMAN	601158935F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3505521 5'
4593	14481	24267	1.11	0.0E+00	BE390050.1	EST_HUMAN	601285246F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3607067 5'
4514	14502	24290	37.36	0.0E+00	M80902.1	NT	Human AHNK nucleoprotein mRNA, 5' end
4517	14505	24293	3.14	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4517	14505	24293	3.14	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4517	14505	24294	3.14	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4620	14508	24297	1.12	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4621	14509	24298	1.34	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4636	14524		1.54	0.0E+00	X58467.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D6
4644	14532	24319	0.95	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4644	14532	24320	0.95	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4652	14538	24327	1.09	0.0E+00	AF026801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-26
4655	14541	24330	0.92	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4655	14541	24331	0.92	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4676	14562	24355	1.78	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B13-ajw-c-04-0-UI.s1 NCJ_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
4681	14567	24363	1.11	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4686	14572		1.8	0.0E+00	AF083242.1	NT	Homo sapiens HSP C024-iso mRNA, complete cds
4697	14583		2.04	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
4735	14620		2.83	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4737	14622	24408	2.79	0.0E+00	X87205.1	NT	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4739	14624	24410	1.3	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR9) mRNA, complete cds
4740	14625	24411	1.47	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4741	14626	24412	3.51	0.0E+00	4503766	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4743	14628	24414	61.82	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4744	14629	24415	1.4	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4746	14631	24417	0.97	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA
4748	14633	24419	0.8	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4752	14637	24424	7.78	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4756	14641	24428	0.95	0.0E+00	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4757	14642	24429	1.66	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4757	14642	24430	1.66	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4759	14644	24432	1.69	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4759	14644	24433	1.69	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4762	14647	24436	1.08	0.0E+00	M55582.1	NT	Human collagenase type IV (CLG4) gene, exon 2
4763	14648	24437	3.22	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4776	14680	24447	0.99	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF2I)
4786	14671	24458	0.82	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4788	14673	24460	1.44	0.0E+00	X92841.1	NT	H.sapiens MICA gene
4791	14676	24463	1.97	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4792	14677	24464	1.18	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4794	14679	24466	2.26	0.0E+00	6677648	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA
4795	14680	24467	1.05	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (called-coil proline-rich) (MGEA6), mRNA
4797	14682	24469	8.64	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
4799	14684	24471	1.2	0.0E+00	Y16723.1	NT	Homo sapiens gene encoding filensin, exon 8
4800	14685	24472	1.61	0.0E+00	7705546	NT	Homo sapiens zinc-finger DNA-binding protein (HUMHOXY1), mRNA
4801	14686		1.33	0.0E+00	AJ010442.1	NT	Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RhD, therad 7
4806	14690	24477	24.91	0.0E+00	AF055066.1	NT	Homo sapiens MHC class 1 region
4808	14692		2.43	0.0E+00	4505508	NT	Homo sapiens oploid receptor, delta 1 (OPRD1) mRNA
4809	14693	24480	2.46	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4812	14013	23791	5.48	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4812	14013	23792	5.48	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4814	14697	24484	0.86	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4824	14706	24490	12.01	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4827	14709	24493	0.95	0.0E+00	D63562.1	NT	Homo sapiens COL4A6 gene for a6(V) collagen, exon 44 and partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4831	14713	24496	1.52	0.0E+00	4503684	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPF) mRNA
4837	14319	24105	1.06	0.0E+00	4506952	NT	Homo sapiens sialyltransferase B (alpha-N-acetylneuraminase: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT6) mRNA
4845	14726	24508	1.31	0.0E+00	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4845	14726	24509	1.31	0.0E+00	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4854	14734	24515	0.86	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4871	14751	24530	1.34	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4879	14759	24536	1.45	0.0E+00	AW452728.1	EST_HUMAN	UJH-B13-alc-f-02-Q-UJ.s1 NCI_OGAP_Sub6 Homo sapiens cDNA clone IMAGE:3068691 3'
4885	14766	24542	1.2	0.0E+00	8922928	NT	Homo sapiens hypothetical protein FLJ11190 (FLJ11190), mRNA
4886	14706	24490	7.99	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4888	14768	24544	2.81	0.0E+00	AF056332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
4888	14768	24545	2.81	0.0E+00	AF056332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
4894	14774	24552	2.95	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4897	14777		4.34	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
4910	14789		2.88	0.0E+00	BE408863.1	EST_HUMAN	601303729F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3638118 5'
4915	14794	24569	5.37	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL1) (DSP) mRNA
4925	14804	24574	0.99	0.0E+00	AB028966.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
4939	14817	24584	1.66	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
4939	14817	24585	1.66	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
4953	14830	24596	1.06	0.0E+00	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltracitin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
4953	14830	24597	1.06	0.0E+00	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltracitin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
4957	14013	23791	5.81	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4957	14013	23792	5.81	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4959	14834	24602	3.51	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4960	14835	24603	7.78	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4988	14843		1.17	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
4978	14853	24619	1.35	0.0E+00	AF016705.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3
4987	14862		1.33	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4990	14865		37.78	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
5000	14875	24639	2.29	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
5001	14876	24640	3.02	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5003	14878	24642	4.23	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5005	14013	23791	2.89	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5005	14013	23792	2.89	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5018	14892	24660	2.43	0.0E+00	X52988.1	NT	Bacillus amyloquelaciens sacB gene for levansucrase (EC 2.4.1.10)
5037	14909	24681	1.84	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5037	14909	24682	1.84	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5040	14912	24686	1.01	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5054	14926	24698	1.22	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
5055	14013	23791	11.22	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5055	14013	23792	11.22	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5056	14013	23791	14.9	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5056	14013	23792	14.9	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5065	14935	24708	1.33	0.0E+00	4557362	NT	Homo sapiens PR domain containing 1, with ZNF domain (PRDM1) mRNA
5070	14940	24713	1.03	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5070	14940	24714	1.03	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5071	14941	24715					Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5080	14950	24726	1.06	0.0E+00	U91328.1	NT	Homo sapiens titin (TTN) mRNA
5096	14013	23791	3.04	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5096	14013	23792	6.27	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5098	14967	24743	6.27	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5098	14967	24743	1.34	0.0E+00	L35475.1	NT	Human olfactory receptor-like gene, complete cds
5098	14967	24744	1.34	0.0E+00	L35475.1	NT	Human olfactory receptor-like gene, complete cds
5099	14013	23791	9.38	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5099	14013	23792	9.38	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5124	14992	24765	0.94	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5126	14993	24766	1.35	0.0E+00	5360213	NT	Homo sapiens glyican 3 (GPC3) mRNA
5130	14997	24768	0.8	0.0E+00	AE000327.1	NT	Escherichia coli K-12 MG1655 section 217 of 400 of the complete genome
5140	15007	24778	1.06	0.0E+00	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
5159	15026	24793	0.96	0.0E+00	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
5162	15028	24794	1.59	0.0E+00	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5165	15031	24797	1.12	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5165	15031	24798	1.12	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5186	15050	24814	1.72	0.0E+00	AF006061.1	NT	Homo sapiens placental growth hormone isoform hGH-V3 (hGH-V) mRNA, complete cds
5187	14013	23791	10.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5187	14013	23792	10.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5189	15052	24816	6.75	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5193	15056		1.38	0.0E+00	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5195	15058	24822	3.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5195	15058	24823	3.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5196	15059	24824	0.96	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
5208	15086		15.06	0.0E+00	AF093093.1	NT	Homo sapiens acinifase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5214	15137	24830	2.25	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5214	15137	24831	2.25	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5226	15150	24917	2.99	0.0E+00	9256579	NT	Homo sapiens protocadherin alpha 13 (PODHA13) mRNA
5234	15158	24926	3.82	0.0E+00	BE931080.1	EST_HUMAN	RC3-GN0076-310800-013-503 GN0076 Homo sapiens cDNA
5238	15162	24930	3.12	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5238	15162	24931	3.12	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5245	15168	24940	1.92	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5245	15168	24941	1.92	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5307	15228	25032	5.8	0.0E+00	BE675498.1	EST_HUMAN	7f10c06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294250 3'
5308	15229	25033	1.77	0.0E+00	BE220753.1	EST_HUMAN	h89a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165194 3' similar to SW:Y054_HUMAN
5309	15230	25034	1.67	0.0E+00	BE794412.1	EST_HUMAN	P42694 HYPOTHETICAL PROTEIN KIAA0054. ;
5309	15230	25035	1.67	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5311	15232	25037	5.46	0.0E+00	M29908.1	NT	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5313	15234	25038	1.81	0.0E+00	AF91363.1	EST_HUMAN	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5319	19442	25044	5.42	0.0E+00	11421038	NT	oh68a09.y5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1472152 5' similar to gb:M18512 IG
5324	15244		2.91	0.0E+00	BE669962.1	EST_HUMAN	HEAVY CHAIN PRECURSOR V-J REGION (HUMAN);
5327	15247	25052	1.92	0.0E+00	BE538857.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4) mRNA
5333	15253	25075	1.31	0.0E+00	BE292784.1	EST_HUMAN	602118928F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276254 5'
5337	15257	25080	1.8	0.0E+00	BF526328.1	EST_HUMAN	601061489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5337	15257	25081	1.8	0.0E+00	BF526328.1	EST_HUMAN	601105891F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988310 5'
5348	15987	26122	1.71	0.0E+00	4557364	NT	602071372F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214272 5'
							602071372F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214272 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5352	15272	25101	5.24	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5352	15272	25102	5.24	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5362	15282	25114	1.45	0.0E+00	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
5362	15282	25115	1.45	0.0E+00	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
5374	15294	25141	1.67	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5385	15305	25158	3.26	0.0E+00	BF526931.1	EST_HUMAN	602042322F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179988 5'
5385	15305	25159	3.26	0.0E+00	BF526931.1	EST_HUMAN	602042322F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4179988 5'
5389	15308	25161	2.35	0.0E+00	BF313139.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5396	15315	25362	4.21	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5420	15341		2.43	0.0E+00	AW867316.1	EST_HUMAN	MRO-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA
5431	15351	25405	3.05	0.0E+00	BE292899.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5431	15351	25406	3.05	0.0E+00	BE292899.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5444	15365	25420	1.31	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5444	15365	25421	1.31	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5451	15372	25429	5.35	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5451	15372	25430	5.35	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5455	15376	25435	2.9	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5455	15376	25436	2.9	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5470	15390	25453	6.69	0.0E+00	M85719.1	EST_HUMAN	EST02238 Fetal brain, Striatogene (cat#936206) Homo sapiens cDNA clone HFBCM48
5474	15394	25459	3.67	0.0E+00	AW405472.1	EST_HUMAN	UI-HF-BL0-adj-d-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5'
5489	15408	25471	5.74	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5489	15408	25472	5.74	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5489	15408	25473	5.74	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5491	15410	25475	1.88	0.0E+00	U36261.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13
5531	15448	25515	3.26	0.0E+00	AA165905.1	EST_HUMAN	zp56b11.r1 Striatogene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740
5532	15449	25516	1.5	0.0E+00	AJ006345.1	NT	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
5532	15449	25517	1.5	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5537	15454	25524	2	0.0E+00	AJ207616.1	EST_HUMAN	Homo sapiens KVLQT1 gene
5548	15464	25534	3.98	0.0E+00	11416801	NT	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
5555	15471	25542	6.76	0.0E+00	BE560082.1	EST_HUMAN	Homo sapiens protocadherin beta 2 (PCDH2), mRNA
5556	15472	25543	1.58	0.0E+00	10048478	NT	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'
5557	15473	25544	3.03	0.0E+00	U86961.1	NT	Mus musculus aczonin (Acz), mRNA
							Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5557	15473	25545	3.03	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5564	15480	25553	2.1	0.0E+00	BF338835.1	EST_HUMAN	602036272F1 NCL CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4184321 5'
5566	15482	25555	2.93	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5574	15489	25556	1.74	0.0E+00	BF56905.1	EST_HUMAN	602185852F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4310076 5'
5596	15510	25588	2.47	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
5597	15511	25589	1.89	0.0E+00	BE828144.1	EST_HUMAN	RC5-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA
5601	15515	25593	1.41	0.0E+00	BE958636.1	EST_HUMAN	601646287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930453 5'
5615	15530	25613	1.66	0.0E+00	BF031742.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
5615	15530	25614	1.66	0.0E+00	BF031742.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
5631	15545	25633	1.54	0.0E+00	W33069.1	EST_HUMAN	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
5631	15545	25634	1.54	0.0E+00	W33069.1	EST_HUMAN	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
5632	15546		2.16	0.0E+00	AF012618.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14
5634	15548	25636	3.57	0.0E+00	BE280197.1	EST_HUMAN	601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3508323 5'
5638	15551	25642	2.74	0.0E+00	BE889610.1	EST_HUMAN	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'
5649	15561	25654	1.63	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
5649	15561	25655	1.63	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
5660	19450	25668	10.66	0.0E+00	9789986	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
5663	15574	25671	1.29	0.0E+00	AA193506.1	EST_HUMAN	zr40h01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5.;
5663	15574	25672	1.29	0.0E+00	AA193506.1	EST_HUMAN	zr40h01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5.;
5680	15589	25690	13.03	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
5680	15589	25691	13.03	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
5730	15638	25742	1.41	0.0E+00	AU137772.1	EST_HUMAN	AU137772 PLACE1 Homo sapiens cDNA clone PLACE1007201 5'
5741	15649	25756	3.4	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds
5755	15663	25770	4.14	0.0E+00	AA204740.1	EST_HUMAN	zq81d03.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN.;
5756	15664	25771	3.57	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
5759	15664	25772	3.57	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
5775	15682	25790	2.8	0.0E+00	BE257173.1	EST_HUMAN	601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5'
5784	15690	25800	1.47	0.0E+00	L35930.1	NT	Human anion exchanger (AE1) gene, exons 1-20
5795	15701	25811	1.38	0.0E+00	11435630	NT	Homo sapiens peptide transporter 3 (LOC51296), mRNA

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5826	15732		8.1	0.0E+00	AV650020.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLCAD09 3'
5830	15736	25848	2.81	0.0E+00	AW575598.1	EST_HUMAN	UI-HF-BLO-acc-g-12-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'
5832	15738	25850	4.21	0.0E+00	H01255.1	EST_HUMAN	Y27b03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933 5'
5838	15744	25857	1.99	0.0E+00	X15377.1	NT	Human gene for the light and heavy chains of myeloperoxidase
5843	15749	25862	4.25	0.0E+00	BE735999.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
5843	15749	25863	4.25	0.0E+00	BE735999.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
5847	15753	25869	11.57	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
5847	15753	25870	11.57	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
5854	15760	25878	1.56	0.0E+00	AB989483.1	EST_HUMAN	ws25c07.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498220 3'
5859	15765	25882	4.81	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'
5859	15766	25883	4.91	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'
5901	15807	25931	1.36	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BLO-acc-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'
5901	15807	25932	1.36	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BLO-acc-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'
5921	15826	25951	1.69	0.0E+00	AV719444.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone GLOEHC08 5'
5930	15835	25958	2.24	0.0E+00	AF190860.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G) mRNA, complete cds
5936	15841	25964	3.45	0.0E+00	AW163640.1	EST_HUMAN	au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 G.T24. [3] TR:O43840 TR:O43206;
5936	15841	25965	3.45	0.0E+00	AW163640.1	EST_HUMAN	au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 G.T24. [3] TR:O43840 TR:O43206;
5951	15856	25978	4.79	0.0E+00	BE799873.1	EST_HUMAN	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
5955	15860	25981	7.23	0.0E+00	BE89813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
5955	15860	25982	7.23	0.0E+00	BE89813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
5961	15866	25988	3.71	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2
5964	15869	25991	2.15	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5964	15869	25992	2.15	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5970	15875	25999	3.54	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
5973	15877	26001	4.13	0.0E+00	AB38412.1	EST_HUMAN	tt31f11.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE
5974	15878	26002	1.79	0.0E+00	L32832.1	NT	P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR.;
5980	15885	26007	3.58	0.0E+00	AA434584.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
5991	15896	26017	1.48	0.0E+00	BE925875.1	EST_HUMAN	zw62c03.r1 Soares fetal fetus Nb2HF9_9w Homo sapiens cDNA clone IMAGE:773688 5'
6011	15916	26044	1.44	0.0E+00	AU125928.1	EST_HUMAN	QV3-BN0047-300800-278-c06 BN0047 Homo sapiens cDNA
6041	15944	26076	7.44	0.0E+00	BE169131.1	EST_HUMAN	AU125928 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6042	15945	26077	1.81	0.0E+00	BF085667.1	EST_HUMAN	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA
6063	16046	26191	3.15	0.0E+00	AA190755.1	EST_HUMAN	zp88e03.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627292 5'
6071	16054	26201	6.08	0.0E+00	A1940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6071	16054	26202	6.08	0.0E+00	A1940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6076	16059	26208	3.07	0.0E+00	11435626	NT	Homo sapiens CD6 antigen (CD6), mRNA
6094	15104	24867	1.98	0.0E+00	BE566381.1	EST_HUMAN	607339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682267 5'
6099	15109	24872	13.15	0.0E+00	BE867889.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
6099	15109	24873	13.15	0.0E+00	BE867889.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
6101	15995	26130	2.07	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
6101	15995	26131	2.07	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
6118	16012	26150	1.46	0.0E+00	BF088376.1	EST_HUMAN	Q08379 GOLGIN-95. ;
6121	16015	26153	3.84	0.0E+00	AA195106.1	EST_HUMAN	CM1-HT0877-060900-397-g11 HT0877 Homo sapiens cDNA
6126	15973		10.28	0.0E+00	11034810	NT	z344903.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:3665332 5'
6135	15982	26118	2.57	0.0E+00	BF569905.1	EST_HUMAN	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
6142	15990		2.32	0.0E+00	J03069.1	NT	602186852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
6146	16019	26157	2.8	0.0E+00	AF217289.1	NT	Human MYCL2 gene, complete cds
6146	16019	26158	2.8	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6154	15112	24876	2.75	0.0E+00	11420775	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6168	15125	24842	5.63	0.0E+00	BE262941.1	EST_HUMAN	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
6169	15128	24843	2.32	0.0E+00	Z37976.1	NT	601148954F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501829 5'
6169	15128	24844	2.32	0.0E+00	Z37976.1	NT	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
6170	15127	24845	2.83	0.0E+00	AF257737.1	NT	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
6170	15127	24846	2.83	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6175	15132	24851	1.35	0.0E+00	AF310105.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6178	16094	26213	2.18	0.0E+00	BF569905.1	EST_HUMAN	Homo sapiens NALP1 mRNA, complete cds
6181	16087	26217	3.58	0.0E+00	L01978.1	NT	602186852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
6190	16076	26224	5.61	0.0E+00	BF306996.1	EST_HUMAN	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
6193	16078	26227	1.76	0.0E+00	U41302.1	NT	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
6225	16091	26241	1.34	0.0E+00	AW954806.1	EST_HUMAN	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
6226	16092	26242	1.41	0.0E+00	BE254103.1	EST_HUMAN	EST366876 IMAGE resequences, MAGC Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6237	16103	26253	5.9	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001566 5'
6253	16119		2.44	0.0E+00	AU143706.1	EST_HUMAN	AU143706 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5'
6260	16126	26279	1.31	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
6260	16126	26280	1.31	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
6273	15137	24830	1.97	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6273	15137	24831	1.97	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6286	16180	26305	3.63	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA
6286	16150	26306	3.63	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA
6302	16166	26323	25.51	0.0E+00	AH128344.1	EST_HUMAN	qc87a07.x1 Soares_placenta_8to9weeks_2NBHP8to9W Homo sapiens cDNA clone IMAGE:1714844 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ; contains element HGR repetitive element;
6302	16166	26324	25.51	0.0E+00	AH128344.1	EST_HUMAN	qc87a07.x1 Soares_placenta_8to9weeks_2NBHP8to9W Homo sapiens cDNA clone IMAGE:1714844 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ; contains element HGR repetitive element;
6304	16168	26326	18.73	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6304	16168	26327	18.73	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6306	16170		14.06	0.0E+00	BF337375.1	EST_HUMAN	602035089F1 NCJ_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4182839 5'
6308	16172	26329	5.1	0.0E+00	AA128453.1	EST_HUMAN	zn60f09.r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:562801 5' similar to TR:G806562 G806562 NEBULIN.;
6328	16191	26353	6.72	0.0E+00	AF003213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
6328	16191	26354	6.72	0.0E+00	AF003213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
6337	16200	26360	7.55	0.0E+00	X70172.1	NT	H. sapiens DNA for ZNGP2 pseudogene, exon 4
6339	16202	26362	11.09	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
6339	16202	26363	11.09	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
6347	16210	26372	1.43	0.0E+00	AW956903.1	EST_HUMAN	EST368573 IMAGE resequences, MAGD Homo sapiens cDNA
6349	16212	26374	2.54	0.0E+00	AW950516.1	EST_HUMAN	EST362586 IMAGE resequences, MAGA Homo sapiens cDNA
6389	16251	26411	1.87	0.0E+00	AW239326.1	EST_HUMAN	xb39a05.y1 NCJ_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050 HNF3FH TRANSCRIPTION FACTOR GENESIS.;
6400	16261		1.8	0.0E+00	AU117553.1	EST_HUMAN	AU117553 HEMBA1 Homo sapiens cDNA clone HEMBA1007661 5'
6401	16262	26422	3.64	0.0E+00	11427135	NT	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
6411	16272	26434	54.66	0.0E+00	AA211663.1	EST_HUMAN	zn50f02.r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
6482	16321	26486	4.25	0.0E+00	AI752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random

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6462	16321	26487	4.25	0.0E+00	AI752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
6499	16358	26530	1.59	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
6499	16358	26531	1.59	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
6515	16374	26551	1.3	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
6530	16389	26569	1.98	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6534	16392	26571	5.37	0.0E+00	BF217905.1	EST_HUMAN	601885465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5'
6539	16397	26576	2.98	0.0E+00	AU129622.1	EST_HUMAN	AU129622 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'
6550	16408	26586	6.49	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
6555	16413	26590	4.97	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
6555	16413	26591	4.97	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
6556	16414	26592	60.88	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
6556	16414	26593	60.88	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
6574	16432	26614	1.52	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
6574	16432	26615	1.52	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
6622	16502	26690	1.29	0.0E+00	AA149791.1	EST_HUMAN	zco1c06.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566410 5'
6645	16525	26719	3.72	0.0E+00	BE736046.1	EST_HUMAN	601305658F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639903 5'
6654	16534	26729	3.97	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
6654	16534	26730	3.97	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
6674	16554	26749	1.65	0.0E+00	AA397551.1	EST_HUMAN	z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
6677	16557	26750	7.54	0.0E+00	AU142402.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
6688	16568	26750	8.73	0.0E+00	BF673096.1	EST_HUMAN	AU142402 Y79AA1 Homo sapiens cDNA clone Y79AA1000277 5'
6714	16594	26783	1.96	0.0E+00	AL120124.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294128 5'
6714	16594	26784	1.96	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
6730	16610	26784	1.96	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
6742	16621	26810	1.35	0.0E+00	BE877693.1	EST_HUMAN	601485254F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887773 5'
6742	16621	26810	1.35	0.0E+00	AW500549.1	EST_HUMAN	UI-HF-BN0-aj-f-01-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077496 5'
6747	16626	26813	14.35	0.0E+00	AW157233.1	EST_HUMAN	au93b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to
6775	16654	26842	1.16	0.0E+00	BE745597.1	EST_HUMAN	TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];
6775	16654	26843	1.16	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6793	16662	26852	2.72	0.0E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
6810	16689	26878	2.2	0.0E+00	BE674157.1	EST_HUMAN	7d76a04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O95793 O95793 STAUFEN PROTEIN.;
6811	16690	26879	1.36	0.0E+00	AI885671.1	EST_HUMAN	w60b10.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to
6817	16696	26887	1.31	0.0E+00	BE563650.1	EST_HUMAN	SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR.;
6817	16696	26888	1.31	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
6924	16703	26897	1.44	0.0E+00	11427235	NT	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
6924	16703	26898	1.44	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
6851	16730		3.89	0.0E+00	AA398511.1	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
6856	16735	26928	1.45	0.0E+00	AW364874.1	EST_HUMAN	z73a08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:S85655 PROHIBITIN (HUMAN);
6856	16735	26929	1.45	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
6859	16748	26942	1.21	0.0E+00	BE612586.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
6859	16748	26943	1.21	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
6879	16758	26956	1.25	0.0E+00	AL163209.2	NT	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
6879	16758	26957	1.25	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
6899	16778		2.01	0.0E+00	BE890797.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
6913	16791	26984	2.4	0.0E+00	4758695	NT	601431239F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'
6913	16791	26985	2.4	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
6955	16833	27026	2.85	0.0E+00	X98922.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
6955	16833	27027	2.85	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
6955	16833	27028	2.85	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
6993	16870		1.36	0.0E+00	AW1513513.1	EST_HUMAN	601431239F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'
6995	16872	27063	3.64	0.0E+00	D52650.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
7011	16888	27081	4.46	0.0E+00	BE378495.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-08-C02 5'
7015	16892	27083	1.31	0.0E+00	AA410545.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
7016	16933		4.32	0.0E+00	BF313946.1	EST_HUMAN	z32a04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724062 5'
7021	16998	27088	1.41	0.0E+00	AW139673.1	EST_HUMAN	601900571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5'
7021	16998	27089	1.41	0.0E+00	AW139673.1	EST_HUMAN	601900571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5'
7038	16915	27104	2.39	0.0E+00	BE260272.1	EST_HUMAN	UI-H-B11-adr-e-12-Q-JL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
7040	16917	27106	1.83	0.0E+00	BF700166.1	EST_HUMAN	UI-H-B11-adr-e-12-Q-JL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7040	16917	27107	1.83	0.0E+00	BF700165.1	EST_HUMAN	602127864F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
7040	16917	27108	1.83	0.0E+00	BF700165.1	EST_HUMAN	602127864F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
7069	16946	27137	6.35	0.0E+00	AA962527.1	EST_HUMAN	0680g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
7073	16950	27142	3.54	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
7073	16950	27143	3.54	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
7088	16965	27159	1.28	0.0E+00	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
7095	16972		1.45	0.0E+00	AV718377.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAA11 5'
7099	16976	27169	3.64	0.0E+00	AW337277.1	EST_HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
7102	16979	27171	1.57	0.0E+00	AU124051.1	EST_HUMAN	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001575 5'
7147	17024	27218	2.64	0.0E+00	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
7148	17025	27219	4.41	0.0E+00	AW592233.1	EST_HUMAN	hf48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
7148	17025	27220	4.41	0.0E+00	AW592233.1	EST_HUMAN	hf48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
7176	17053	27241	2.84	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
7176	17053	27242	2.84	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
7177	17054	27243	1.17	0.0E+00	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
7178	17055	27244	18.6	0.0E+00	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
7198	17075	27261	3.97	0.0E+00	11422857	NT	Homo sapiens tumor protein p73 (TP73), mRNA
7204	17081	27268	1.25	0.0E+00	K01241.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
7207	17084	27272	2.65	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
7207	17084	27273	2.65	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
7210	17087	27277	1.96	0.0E+00	AV660739.1	EST_HUMAN	AV660739 GLC Homo sapiens cDNA clone GLCGK12 3'
7213	17090	27280	3.43	0.0E+00	7706638	NT	Homo sapiens polycystin-L (PKDL), mRNA
7231	17108	27298	3.86	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
7231	17108	27299	3.86	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
7241	17118	27313	1.91	0.0E+00	X14766.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
7250	17127	27320	2.12	0.0E+00	A1954607.1	EST_HUMAN	wq34a12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MB83_HUMAN
7254	17131	27324	4.49	0.0E+00	9255695	NT	O15480 MELANOMA-ASSOCIATED ANTIGEN B3 ;
7263	17140	27333	1.54	0.0E+00	AW988311.1	EST_HUMAN	Homo sapiens protocadherin alpha 8 (PCDH8), mRNA
7269	17146	27340	1.49	0.0E+00	9635487	NT	EST370381 IMAGE resequences, IMAGE Homo sapiens cDNA
7280	17157	27352	6.88	0.0E+00	11436965	NT	Human endogenous retrovirus, complete genome
							Homo sapiens MAP-kinase activating death domain (MADD), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7290	17166	27365	1.44	0.0E+00	AB011150.1	NT	Homo sapiens mRNA for KIAA0578 protein, partial cds
7291	17167	27366	2.56	0.0E+00	BE794823.1	EST_HUMAN	601589294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943463 5'
7298	17174	27374	1.24	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
7298	17174	27375	1.24	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
7308	17184	27383	1.6	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder I Homo sapiens cDNA 5' end
7308	17184	27384	1.6	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder I Homo sapiens cDNA 5' end
7360	17227	27426	1.38	0.0E+00	BE207063.1	EST_HUMAN	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:135049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
7360	17227	27427	1.38	0.0E+00	BE207063.1	EST_HUMAN	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:135049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
7368	17346	27551	2.71	0.0E+00	BF348013.1	EST_HUMAN	602023150F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4168300 5'
7383	17252	27457	3	0.0E+00	BE712515.1	EST_HUMAN	QV2-HT0698-250700-282-b08 HT0698 Homo sapiens cDNA
7406	17273	27479	11.81	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5'
7425	17292	27503	1.27	0.0E+00	AI088043.1	EST_HUMAN	ow60h01.x1 Scores NSF_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to TR:Q14677 Q14677 KIAA0171 PROTEIN.;
7429	16442	26628	2.06	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
7429	16442	26629	2.06	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
7431	16444	26632	8.96	0.0E+00	AI290909.1	EST_HUMAN	qm09e06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A.;
7431	16444	26633	8.86	0.0E+00	AI290909.1	EST_HUMAN	qm09e06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A.;
7432	16445	26634	1.99	0.0E+00	AW953836.1	EST_HUMAN	EST366026 MAGC resequences, MAGC Homo sapiens cDNA
7450	17259	27464	3.92	0.0E+00	AF163486.1	NT	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8
7461	17321		4.9	0.0E+00	BE255829.1	EST_HUMAN	601109942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'
7463	17323	27529	1.37	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
7463	17323	27530	1.37	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
7484	17324	27531	7.21	0.0E+00	AW163779.1	EST_HUMAN	au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072
7475	17335	27541	2.85	0.0E+00	BE263191.1	EST_HUMAN	60S RIBOSOMAL PROTEIN L7A (HUMAN);
7488	17358	27562	3.98	0.0E+00	C06158.1	EST_HUMAN	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5'
7488	17358	27563	3.98	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
7490	17360	27566	3.22	0.0E+00	BE746215.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
7499	17369	27574	1.93	0.0E+00	11437282	NT	601576883F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
7499	17369	27575	1.93	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA

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7499	17369	27576	1.93	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
7514	17302	27509	1.47	0.0E+00	BE900549.1	EST_HUMAN	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'
7530	17381	27591	2.59	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
7530	17381	27592	2.59	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
7548	17399	27612	1.47	0.0E+00	BE082977.1	EST_HUMAN	RC2-BT0642-130300-017-g01 BT0642 Homo sapiens cDNA
7559	17410	27626	1.76	0.0E+00	AW500293.1	EST_HUMAN	U1HF-BN0-ekg-b-12-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
7559	17410	27627	1.76	0.0E+00	AW500293.1	EST_HUMAN	U1HF-BN0-akg-b-12-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
7563	17414	27629	1.25	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7563	17414	27630	1.25	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7580	17431	27645	2.45	0.0E+00	AW500526.1	EST_HUMAN	U1HF-BN0-akg-c-07-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5'
7607	17458	27673	1.34	0.0E+00	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
7621	17472	27691	2.56	0.0E+00	S78466.1	NT	AlGF=androgen-induced growth factor AlGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
7621	17472	27692	2.56	0.0E+00	S78466.1	NT	AlGF=androgen-induced growth factor AlGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
7622	17473	27693	2.57	0.0E+00	BE563320.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688680 5'
7630	17481	27701	1.62	0.0E+00	AW363135.1	EST_HUMAN	CM2-CT0311-301199-043-h11 CT0311 Homo sapiens cDNA
7650	17500	27722	2.17	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
7650	17500	27723	2.17	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
7659	17509	27734	7.73	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
7659	17509	27735	7.73	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
7666	17516	27743	1.76	0.0E+00	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
7682	17532	27756	2.22	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
7683	17533	27757	1.86	0.0E+00	AF162308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
7701	17551	27776	2.72	0.0E+00	AF009220.1	NT	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds
7701	17551	27777	2.72	0.0E+00	AF009220.1	NT	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds
7708	17558	27784	1.65	0.0E+00	BF092898.1	EST_HUMAN	NR4-TN0114-110300-101-e04 TN0114 Homo sapiens cDNA
7720	17570	27795	2.44	0.0E+00	BE280793.1	EST_HUMAN	601155227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138798 5'
7728	17578	27800	1.74	0.0E+00	AW236269.1	EST_HUMAN	xn72b01.xt NCJ CGAP_GML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02152_cds1 L-
7736	17586	27810	1.91	0.0E+00	11427235	NT	LACTATE DEHYDROGENASE M CHAIN (HUMAN);
7753	17603	27826	5.98	0.0E+00	AU143673.1	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
							AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7753	17603	27827	5.98	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
7756	17606	27830	7.52	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
7758	17608	27832	2.48	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
7758	17608	27833	2.48	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
7785	17635	27868	2.96	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
7785	17635	27869	2.96	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
7795	17645	27879	2.13	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
7795	17645	27880	2.13	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
7804	17654	27892	4.01	0.0E+00	AA196387.1	EST_HUMAN	zp97h11.r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:628197 5'
7823	17673	27915	1.17	0.0E+00	AA131248.1	EST_HUMAN	z31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
7823	17673	27916	1.17	0.0E+00	AA131248.1	EST_HUMAN	z31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
7842	17692	27937	1.46	0.0E+00	AF179308.1	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
7865	17715	27959	3.45	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
7865	17715	27960	3.45	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
7892	17742	27985	1.24	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
7897	17747	27987	1.64	0.0E+00	AB029290.1	NT	Homo sapiens mRNA for actin binding protein ABP620, complete cds
7903	17753	27991	5.19	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
7903	17753	27992	5.19	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
7904	17754	27993	3.27	0.0E+00	AA194770.1	EST_HUMAN	zq06h11.r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:628965 5' similar to TR:G407097
7905	17755	27994	5.43	0.0E+00	BF340331.1	EST_HUMAN	G407097 165KD PROTEIN ;
7905	17755	27995	5.43	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184939 5'
7946	17796	28036	1.37	0.0E+00	T03078.1	EST_HUMAN	602037045F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184939 5'
7972	17822	28065	2.35	0.0E+00	BF436218.1	EST_HUMAN	FB23A4 Fetal brain, Stragene Homo sapiens cDNA clone FB23A4 3'end
7973	17823		2.05	0.0E+00	AV654765.1	EST_HUMAN	nab45e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
7982	17832	28072	3.55	0.0E+00	AW517930.1	EST_HUMAN	AV654765 GLC Homo sapiens cDNA clone GLODZC07 3'
7984	17834	28074	6.06	0.0E+00	BE549213.1	EST_HUMAN	xu74b01.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:MG9066 MOESIN (HUMAN);
8001	17851	28092	1.65	0.0E+00	BE781742.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
8008	17858	28101	2.23	0.0E+00	BE082720.1	EST_HUMAN	601467419F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870700 5'
8008	17858	28102	2.23	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-d03 BT0642 Homo sapiens cDNA
8015	17865	28111	1.69	0.0E+00	BE743215.1	EST_HUMAN	RC2-BT0642-150200-012-d03 BT0642 Homo sapiens cDNA
8015	17865	28112	1.69	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
8032	17924	28170	2.33	0.0E+00	AV711075.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8032	17924	28171	2.33	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
8034	17926		6.11	0.0E+00	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
8040	17931	28178	6.43	0.0E+00	AW963563.1	EST_HUMAN	EST375636 MAGE resequences, MAGH Homo sapiens cDNA
8051	17942	28191	2.5	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8051	17942	28192	2.5	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8054	17945	28195	1.99	0.0E+00	AW057621.1	EST_HUMAN	wy6109.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2533085 3' similar to TR:Q00566 Q00566 VDX;
8059	17950	28200	1.92	0.0E+00	BE249270.1	EST_HUMAN	TCAAP3D00917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0917
8060	17951	28201	4.86	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
8060	17951	28202	4.86	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
8068	17959	28209	2.91	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
8068	17959	28210	2.91	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
8081	17972	28221	2.01	0.0E+00	AW404795.1	EST_HUMAN	UI-HF-BLO-ecm-d-04-0-UJ.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'
8084	17975	28224	4.8	0.0E+00	11424829	NT	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
8085	17976	28225	9.16	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
8085	17976	28226	9.16	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
8086	17977	28227	2.73	0.0E+00	AI991827.1	EST_HUMAN	wb32b06.x1 Soares Dieckgraefe colon_NHCD Homo sapiens cDNA clone IMAGE:2521715 3'
8089	17980	28231	3.04	0.0E+00	BE882109.1	EST_HUMAN	601506204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5'
8093	17984	28233	10.56	0.0E+00	BE891630.1	EST_HUMAN	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919636 5'
8095	17986	28234	22.36	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
8095	17986	28235	22.36	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
8110	18000	28247	1.91	0.0E+00	BE903304.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
8113	15448	25515	4.05	0.0E+00	AA195905.1	EST_HUMAN	zp95b11.r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740
8134	18022	28269	4.69	0.0E+00	BE793498.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
8143	18031	28277	6.8	0.0E+00	AV727362.1	EST_HUMAN	601588829F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
8143	18031	28278	6.8	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
							AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
8156	18044	28296	17.96	0.0E+00	AW516055.1	EST_HUMAN	xy04g10.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S
8161	18049	28301	2.17	0.0E+00	AU135741.1	EST_HUMAN	RIBOSOMAL PROTEIN S16 (HUMAN);
							AU135741 PLACE1 Homo sapiens cDNA clone PLACE1002794 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8166	18054	28304	3.45	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element ;
8166	18054	28305	3.45	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element ;
8166	18054	28306	3.45	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element ;
8168	18056	28307	1.82	0.0E+00	Z34897.1	NT	H.sapiens mRNA for H1 histamine receptor
8169	18057	28308	2.8	0.0E+00	F13099.1	EST_HUMAN	HSC3IC031 normalized Infant brain cDNA Homo sapiens cDNA clone c-3ic03
8176	18064	28313	2.12	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
8191	18077	28328	2.92	0.0E+00	AW338094.1	EST_HUMAN	xi66f01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17115 (G MU CHAIN C REGION (HUMAN);
8192	18078	28329	5.64	0.0E+00	AW451230.1	EST_HUMAN	UI-H-B13-alf-a-01-0-UI.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
8192	18078	28330	5.64	0.0E+00	AW451230.1	EST_HUMAN	UI-H-B13-alf-a-01-0-UI.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
8194	10179		14.21	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
8196	18081	28332	2.03	0.0E+00	AB014567.1	NT	Homo sapiens mRNA for KIAA0687 protein, partial cds
8208	18092	28346	2.35	0.0E+00	BE298449.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
8224	18106	28359	1.88	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0545 protein, partial cds
8227	18109	28363	59.52	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
8240	18120	28371	3.47	0.0E+00	BE792155.1	EST_HUMAN	601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936639 5'
8241	18121		25.37	0.0E+00	BF884061.1	EST_HUMAN	602141405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5'
8244	18124	28374	6.16	0.0E+00	AU118386.1	EST_HUMAN	AU118386 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
8245	18125		2.72	0.0E+00	AW236289.1	EST_HUMAN	xi72601.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
8250	18130	28378	6.77	0.0E+00	A1149809.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
8250	18130	28379	6.77	0.0E+00	A1149809.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
8251	18131	28380	3.05	0.0E+00	AW391937.1	EST_HUMAN	QV4-ST0234-121199-032-506 ST0234 Homo sapiens cDNA
8262	18142		4.62	0.0E+00	AU116908.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
8265	18145	28386	18.63	0.0E+00	11424726	NT	Homo sapiens insulin receptor (INSR), mRNA
8271	18151	28392	1.78	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM00093-170400-191-406 UM0093 Homo sapiens cDNA
8271	18151	28393	1.78	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM00093-170400-191-406 UM0093 Homo sapiens cDNA
8272	18152	28394	2.14	0.0E+00	BF940308.1	EST_HUMAN	602037014F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4184979 5'
8273	18153	28395	49.5	0.0E+00	BE261209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
8282	18161	28403	2.53	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKSH) gene, exon 15-17
8283	18162	28404	68.7	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8287	18166	28409	3.52	0.0E+00	BE73036.1	EST_HUMAN	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA
8287	18166	28410	3.52	0.0E+00	BE73036.1	EST_HUMAN	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA
8307	18184	28431	24.55	0.0E+00	AA740782.1	EST_HUMAN	cd32e07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element
8313	18190	28439	3.12	0.0E+00	AF252303.1	NT	MSR1 repetitive element;
8326	18203	28452	149.55	0.0E+00	C05088.1	EST_HUMAN	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
8333	18210	28460	2.17	0.0E+00	AA746375.1	EST_HUMAN	C05089 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC4817
8333	18210	28461	2.17	0.0E+00	AA746375.1	EST_HUMAN	cd56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
8341	18218	28470	2.41	0.0E+00	M78448.1	EST_HUMAN	cd56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
8341	18218	28471	2.41	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBCC26
8344	18221	28472	1.82	0.0E+00	BF353625.1	EST_HUMAN	EST00596 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBCC26
8345	18222	28473	8.08	0.0E+00	AL157608.1	EST_HUMAN	QV2-H-T0698-020800-295-d07 HT0698 Homo sapiens cDNA
8357	18234	28482	10.53	0.0E+00	AJ116988.1	EST_HUMAN	DKFp761J2116_r1 761 (synonym: hary2) Homo sapiens cDNA clone DKFZp761J2116 5'
8375	18252	28503	1.86	0.0E+00	BF366553.1	EST_HUMAN	AJ116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
8395	18271	28523	3.78	0.0E+00	BE182360.1	EST_HUMAN	IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
8395	18271	28524	3.78	0.0E+00	BE182360.1	EST_HUMAN	PMO-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
8405	18281	28533	3.46	0.0E+00	BE996423.1	EST_HUMAN	PMO-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
8410	18285	28539	1.74	0.0E+00	AW500307.1	EST_HUMAN	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
8410	18285	28540	1.74	0.0E+00	AW500307.1	EST_HUMAN	U1-HF-BN0-akg-d-02-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
8442	18316	28574	4	0.0E+00	BE997953.1	EST_HUMAN	U1-HF-BN0-akg-d-02-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
8443	18317	28575	1.96	0.0E+00	A1459545.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
8443	18317	28576	1.96	0.0E+00	A1459545.1	EST_HUMAN	ac86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
8455	18328	28597	88.73	0.0E+00	F00884.1	EST_HUMAN	ac86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
8455	18328	28598	88.73	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215 Homo sapiens cDNA clone
8480	18353	28618	3.88	0.0E+00	4759827	NT	77E12
8481	18354	28619	4.54	0.0E+00	BF206661.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215 Homo sapiens cDNA clone
8483	18356	28620	16	0.0E+00	AW207734.1	EST_HUMAN	Homo sapiens neurexin III (NRXN3) mRNA
8484	18357	28621	3.77	0.0E+00	AW604975.1	EST_HUMAN	601870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'
8484	18357	28622	3.77	0.0E+00	AW604975.1	EST_HUMAN	U1-H-B12-age-h-01-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
8488	18361	28625	6.91	0.0E+00	AB018260.1	NT	RC0-CT0380-210100-032-c10 CT0380 Homo sapiens cDNA
8488	18361	28626	6.91	0.0E+00	AB018260.1	NT	RC0-CT0380-210100-032-c10 CT0380 Homo sapiens cDNA
8488	18361	28626	6.91	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8490	18363	28628	2.59	0.0E+00	BE206846.1	EST_HUMAN	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;
8490	18363	28629	2.59	0.0E+00	BE206846.1	EST_HUMAN	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;
8511	18383	28648	2.85	0.0E+00	1102471.1	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
8514	18386	28651	2.01	0.0E+00	BF093687.1	EST_HUMAN	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
8518	18390	28653	2.9	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-104 HT0230 Homo sapiens cDNA
8518	18390	28654	2.9	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-104 HT0230 Homo sapiens cDNA
8526	18398	28665	6.47	0.0E+00	AA195905.1	EST_HUMAN	zp95b11.11 Stratiene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
8546	18418	28687	4.47	0.0E+00	BF507876.1	EST_HUMAN	UHH-B14-aok-b-10-0-UI.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
8546	18418	28688	4.47	0.0E+00	BF507876.1	EST_HUMAN	UHH-B14-aok-b-10-0-UI.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
8553	18423	28692	2.16	0.0E+00	AU135170.1	EST_HUMAN	AU135170 PLACE1 Homo sapiens cDNA clone PLACE1001381 5'
8557	18427	28696	5.62	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
8557	18427	28697	5.62	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
8566	18435		10.32	0.0E+00	BF240536.1	EST_HUMAN	601875630F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099710 5'
8577	18445	28713	3.05	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
8577	18445	28714	3.05	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
8581	18449	28717	3.49	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
8581	18449	28718	3.49	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
8596	18463	28734	6.1	0.0E+00	4503544	NT	Homo sapiens eukaryotic translation initiation factor 5A (EIF5A) mRNA
8603	18470	28741	2.49	0.0E+00	BF576267.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
8605	18472	28744	5.44	0.0E+00	AW328173.1	EST_HUMAN	dr04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'
8608	18475		120.65	0.0E+00	M55083.1	NT	Human gamma actin-like pseudogene, complete cds
8612	18479	28750	3.18	0.0E+00	A1680968.1	EST_HUMAN	wf20e11.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351180 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
8614	18481	28752	3.64	0.0E+00	BF306996.1	EST_HUMAN	601898823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
8614	18481	28753	3.64	0.0E+00	BF306996.1	EST_HUMAN	601898823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
8620	18486	28758	26.88	0.0E+00	BF362452.1	EST_HUMAN	QV2-NN0054-230800-333-e04 NN0054 Homo sapiens cDNA
8639	18504		4.07	0.0E+00	BE897051.1	EST_HUMAN	601439605F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
8648	18512	28793	2.89	0.0E+00	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
8650	18514		2.24	0.0E+00	BF207662.1	EST_HUMAN	601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5'
8661	18550	28833	4.61	0.0E+00	BE206846.1	EST_HUMAN	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8661	18550	28834	4.61	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-
8663	18552	28836	3	0.0E+00	AW763028.1	EST_HUMAN	56KDA-ASSOCIATED PROTEIN. ; QVQ-CT0225-101299-071-f06 CT0225 Homo sapiens cDNA
8668	18557		2.36	0.0E+00	AA558707.1	EST_HUMAN	hl42c08.s1 NCL_CGAP_P74 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-
8669	15148	24915	5	0.0E+00	A1934954.1	EST_HUMAN	ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN); wp06g08.x1 NCL_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2464094 3'
8670	18558	28842	7.41	0.0E+00	AW327895.1	EST_HUMAN	dr02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846619 5'
8700	18518	28900	4.73	0.0E+00	BE185656.1	EST_HUMAN	IL5-HT0731-020500-077-405 HT0731 Homo sapiens cDNA
8712	18529	28812	4.74	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178.t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
8712	18529	28813	4.74	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178.t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
8722	18539	28823	12.53	0.0E+00	A1923116.1	EST_HUMAN	wn83q03.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
8724	18580	28863	4.18	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCL_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686 Q13686 ALKB HOMOLOG PROTEIN. ;
8724	18580	28864	4.18	0.0E+00	AA760913.1	EST_HUMAN	Q13686 ALKB HOMOLOG PROTEIN. ;
8728	18584	28869	2.33	0.0E+00	BE910546.1	EST_HUMAN	601501090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902926 5'
8737	17886	28130	5.67	0.0E+00	BE976347.1	EST_HUMAN	7127f12.x1 NCL_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:3295919 3' similar to TR:O00409 O00409 CHECKPOINT SUPPRESSOR 1. ;
8772	18589	28875	2.78	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
8772	18589	28876	2.78	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
8784	18599	28888	4.02	0.0E+00	AU138211.1	EST_HUMAN	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5'
8797	18611	28902	1.91	0.0E+00	BE922317.1	EST_HUMAN	601441096F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
8827	18640	28924	10.47	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
8827	18640	28925	10.47	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
8837	18650	28937	2.97	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYROT1 Homo sapiens cDNA clone THYRO1001398 5'
8837	18650	28938	2.97	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYROT1 Homo sapiens cDNA clone THYRO1001398 5'
8840	18653	28941	2.35	0.0E+00	AW006022.1	EST_HUMAN	wz9/th01.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:F53H10.2 OE11040 ZINC FINGER, C2H2 TYPE ;
8843	19474	28943	3.84	0.0E+00	BF002333.1	EST_HUMAN	7h22b10.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316696 3' similar to TR:Q13458 Q13458 TRIO. ;
8861	18673	28962	3.19	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA
8861	18673	28963	3.19	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA
8879	18690	28982	2.57	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8878	18690	28983	2.57	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
8883	18694	28987	5.52	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
8885	18696	28989	2.04	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
8885	18696	28990	2.04	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
8896	16272	26434	63.21	0.0E+00	AA211663.1	EST_HUMAN	zn56f02.r1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:862203 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
8900	15883	26006	4.08	0.0E+00	AW505430.1	EST_HUMAN	U1-HF-BND-ama-c-01-0-UL:r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5'
8902	18710	29005	3.25	0.0E+00	BE794758.1	EST_HUMAN	501590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
8903	18711	29006	37.53	0.0E+00	BE879633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
8904	18712	29007	2.93	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
8915	18723	29014	6.35	0.0E+00	BE409993.1	EST_HUMAN	501299403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629544 5'
8916	18724	29015	1.93	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8916	18724	29016	1.93	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8916	18724	29017	1.93	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8917	18725	29018	2.32	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8917	18725	29019	2.32	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8919	18727	29020	5.66	0.0E+00	BF681641.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5'
8919	18727	29021	5.66	0.0E+00	BF681641.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5'
8924	18732	29026	3.22	0.0E+00	BE903372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958935 5'
8933	18741	29034	6.15	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
8933	18741	29035	6.15	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
8934	18742	29036	3.02	0.0E+00	X61755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8934	18742	29037	3.02	0.0E+00	X61755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8964	19475		20.36	0.0E+00	BF309120.1	EST_HUMAN	601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
8965	18771	29062	1.98	0.0E+00	BE698861.1	EST_HUMAN	RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA
8965	18771	29063	1.98	0.0E+00	BE698861.1	EST_HUMAN	RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA
8969	18775	29066	31.56	0.0E+00	BE297175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532968 5'
8981	18786	29076	36.47	0.0E+00	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
8981	18786	29077	36.47	0.0E+00	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
8982	18787	29078	34.29	0.0E+00	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
8987	18792	29081	31.52	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #36215. Homo sapiens cDNA clone 77E12

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8987	18792	29082	31.52	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone
9000	18803	29096	7.35	0.0E+00	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
9002	18805	29098	92.9	0.0E+00	Z20656.1	NT	Homo sapiens cf cardiac alpha-myosin heavy chain gene
9017	19747	24893	2.54	0.0E+00	BE312542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'
9031	19594		2.67	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9033	19605		3.43	0.0E+00	AI190993.1	EST_HUMAN	qe17b12.x1 Soares fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
9043	18829		2.24	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9052	18843		2.2	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9071	18849		2.73	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9090	18864		5.48	0.0E+00	5802973	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
9123	19563	25066	1.63	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9133	19571		2.82	0.0E+00	AL041931.1	EST_HUMAN	DKFZp434K0819_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434K0819 5'
9158	19711		3.07	0.0E+00	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GSTSET), mRNA
9167	18910		4.39	0.0E+00	AL046544.1	EST_HUMAN	DKFZp434G218_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G218 5'
9180	19610		2.36	0.0E+00	AI903497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sapiens cDNA
9218	19732		1.3	0.0E+00	N54484.1	EST_HUMAN	yv40e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW_POL_BAEVM P10272 POL POLYPROTEIN ;
9233	18952		3.36	0.0E+00	AF106656.1	NT	Homo sapiens adenylsuccinate lyase gene, complete cds
9236	10752	20601	3.21	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
9236	10752	20602	3.21	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
9246	19612		2.75	0.0E+00	10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
9276	10477		2.7	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
9309	19412	25183	2.48	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9370	19544	25064	3.23	0.0E+00	AW590082.1	EST_HUMAN	hg31e06.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
9382	19595		1.61	0.0E+00	BE090210.1	EST_HUMAN	RC6-BT0711-290300-011-D05 BT0711 Homo sapiens cDNA
9426	19607		2.33	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
9461	19092		1.56	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
9498	19600		1.59	0.0E+00	AI204914.1	EST_HUMAN	an05h04.x1 Stratagene scizoo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
9529	19136		1.58	0.0E+00	AI904646.1	EST_HUMAN	QV-BT065-020399-103 BT065 Homo sapiens cDNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9540	19596		1.88	0.0E+00	BE439792.1	EST_HUMAN	HTM1-654F HTM1 Homo sapiens cDNA
9551	11841	21724	1.98	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9551	11841	21725	1.98	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9571	19161	25267	2.33	0.0E+00	AF036365.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds
9584	11561	21426	2.87	0.0E+00	H30132.1	EST_HUMAN	y059e08.r1 Soares breast 3NbhBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 (GAMMA-GLUTAMYLTRANSEPTIDASE 5 PRECURSOR (HUMAN))
9584	11561	21427	2.87	0.0E+00	H30132.1	EST_HUMAN	y059e08.r1 Soares breast 3NbhBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 (GAMMA-GLUTAMYLTRANSEPTIDASE 5 PRECURSOR (HUMAN))
9597	19179		32.21	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
9599	19181	25244	3.99	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
9599	19181	25245	3.99	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
9685	19239	25214	5.21	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC projectTCBA Homo sapiens cDNA clone TCBAP4466
9692	15089	24829	1.64	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
9693	19249		2.39	0.0E+00	11528291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
9721	15092	24886	3.19	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
9734	19269		2.21	0.0E+00	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9773	19291	25233	1.5	0.0E+00	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
9794	19757		2.79	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9800	19546	20354	1.41	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9878	19364		2.13	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
9913	19388	25177	2.42	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
9938	19407		1.51	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
9946	19621		1.29	0.0E+00	11434874	NT	Homo sapiens oxytocin receptor (OXTR), mRNA
9966	19591		1.56	0.0E+00	BE177449.1	EST_HUMAN	RC1-HT0595-200400-012-F12 HT0595 Homo sapiens cDNA
9971	19431		1.28	0.0E+00	AL048911.1	EST_HUMAN	DKFZp434J0618_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0618

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CLAIMS

1. A spatially-addressable set of single exon nucleic-acid probes for measuring gene expression in a sample derived
5 from human heart comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 9,981 - 19,771.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

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average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 9,980 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human heart.

35

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14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 9,981 - 19,771 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of
10 SEQ ID NOs.: 19,772 - 29,119, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

16. A single exon nucleic acid probe as claimed in any one
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one
35 of claims 13 - 20, wherein said probe lacks homopolymeric

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stretches of A or T.

22. A method of measuring gene expression in a sample derived from human heart, comprising:

5 contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then measuring the label detectably bound to each probe of
10 said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from
15 genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said probe is a
20 single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

25

24. A method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence according to the method of claim 23; and
30 then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,
35 wherein a common pattern of expression of said exons in

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said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID
5 NOs: 1 - 19,771 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of
SEQ ID Nos: 1 - 19,771.

10 27. A peptide comprising a sequence as set out in any of
SEQ ID Nos: 19,772 - 29,119.

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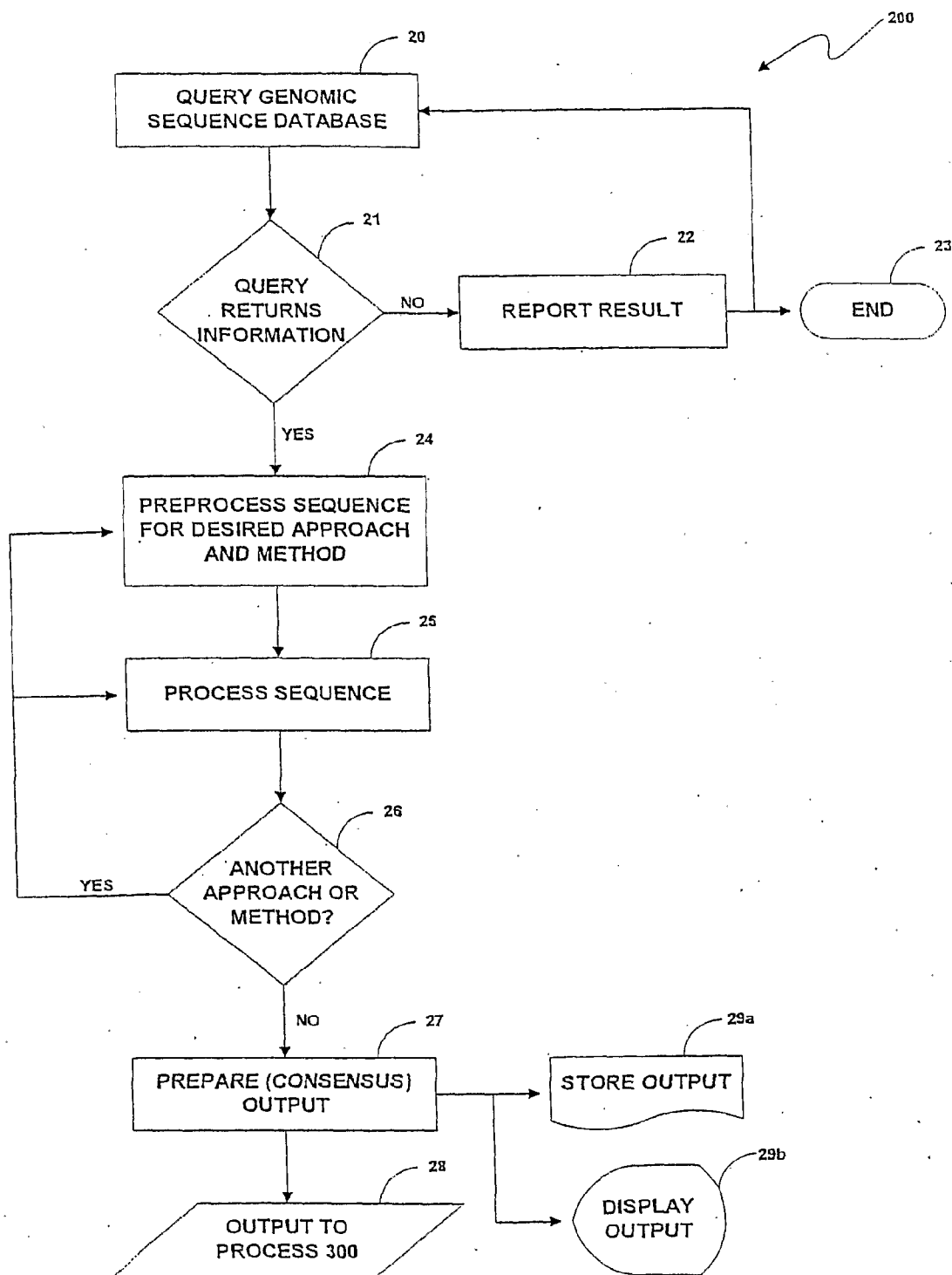


Fig. 2

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Fig. 3

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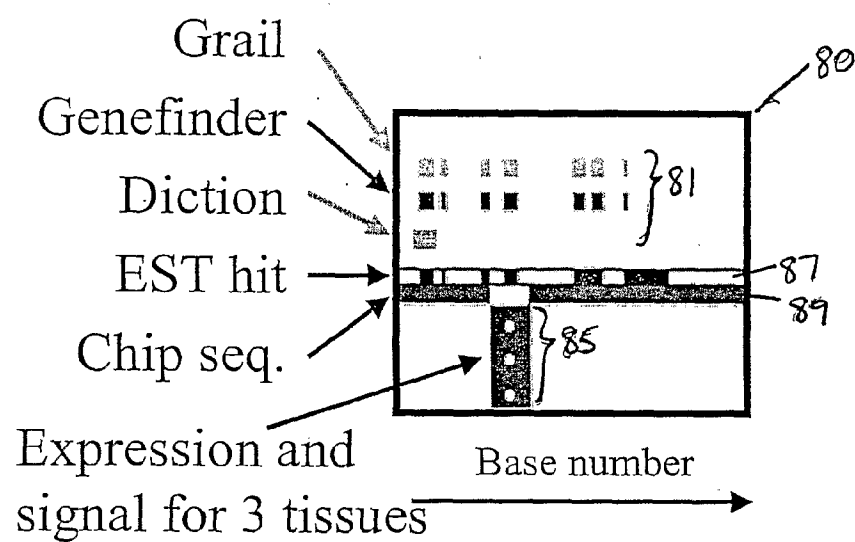


Fig. 4

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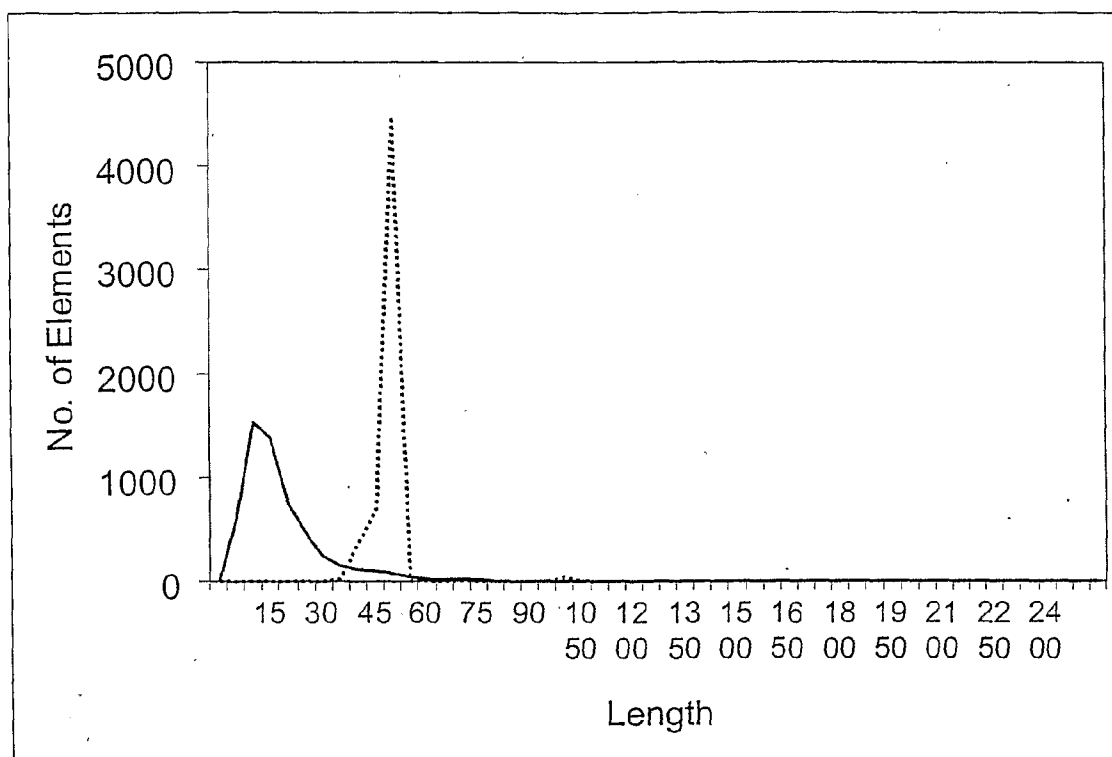


Fig. 5

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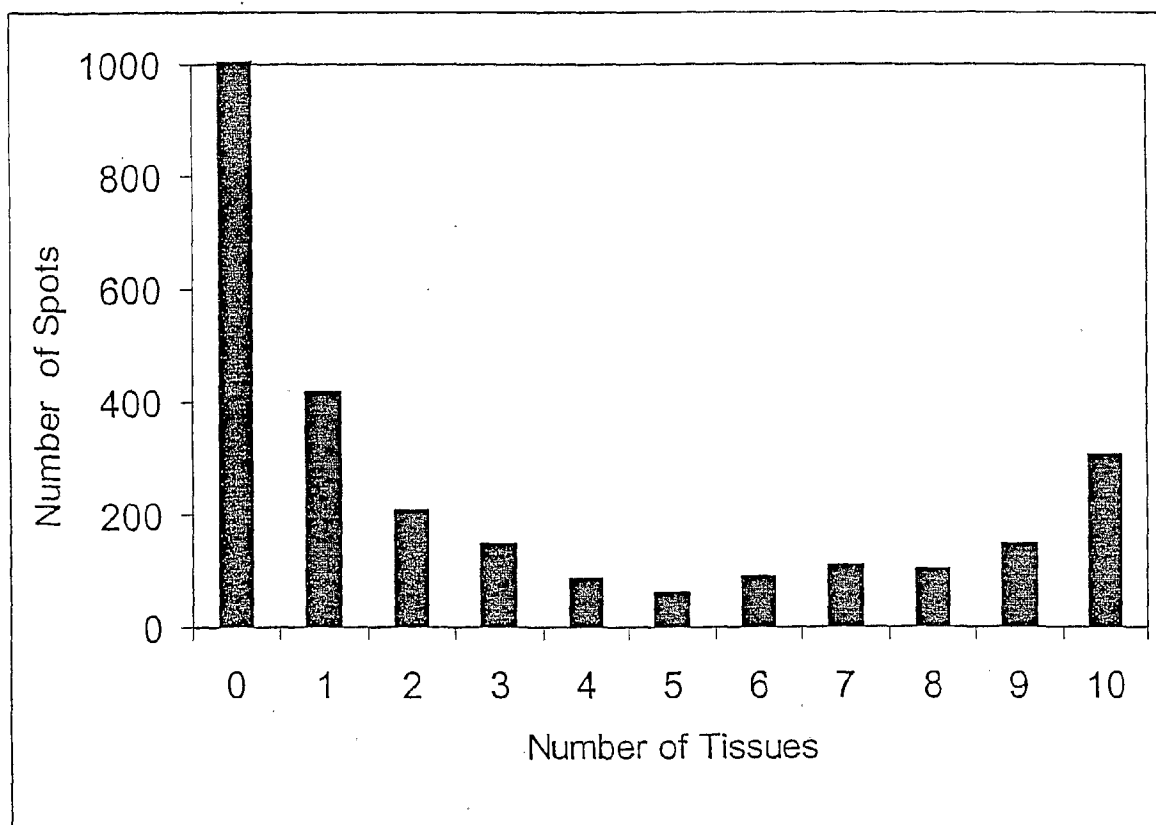


Fig. 6

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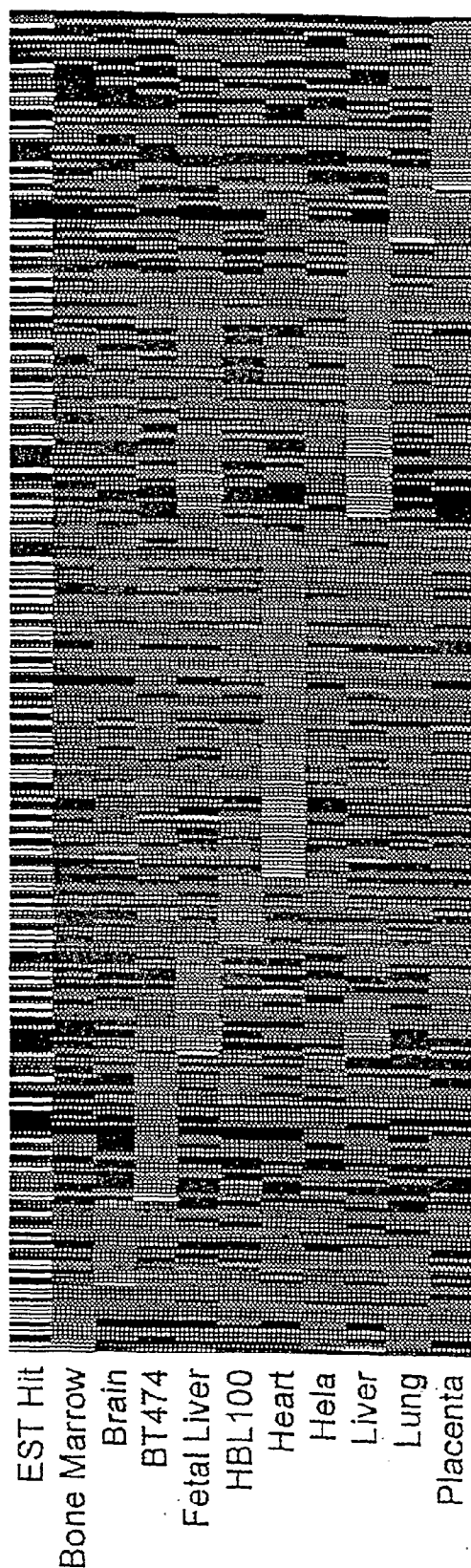


Fig. 7a

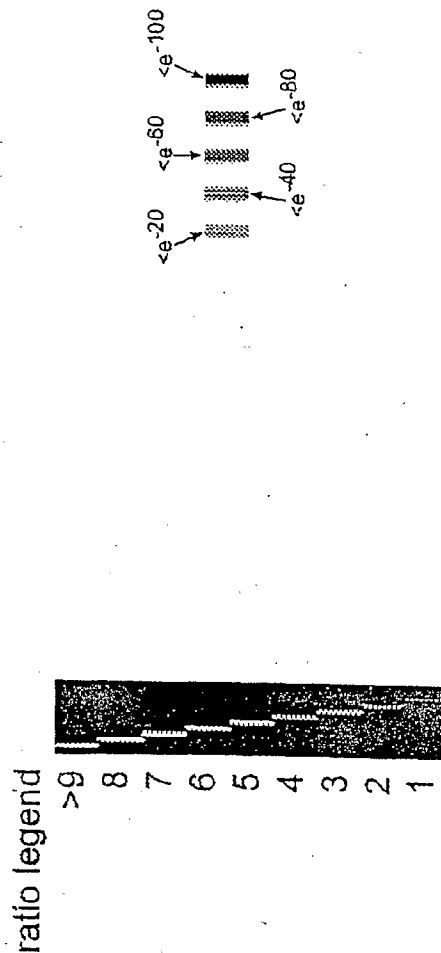


Fig. 7b

Fig. 7c

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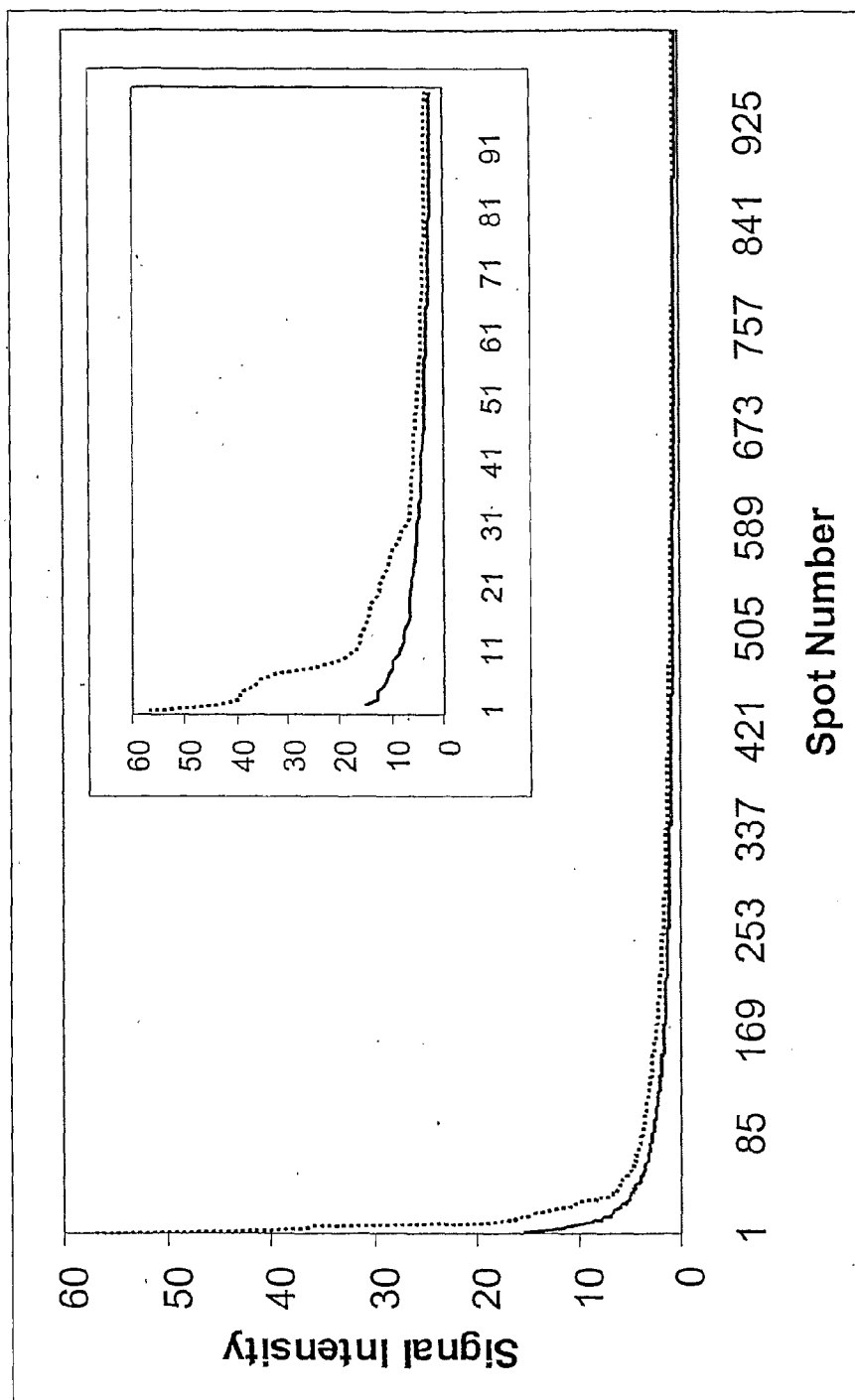


Fig. 8

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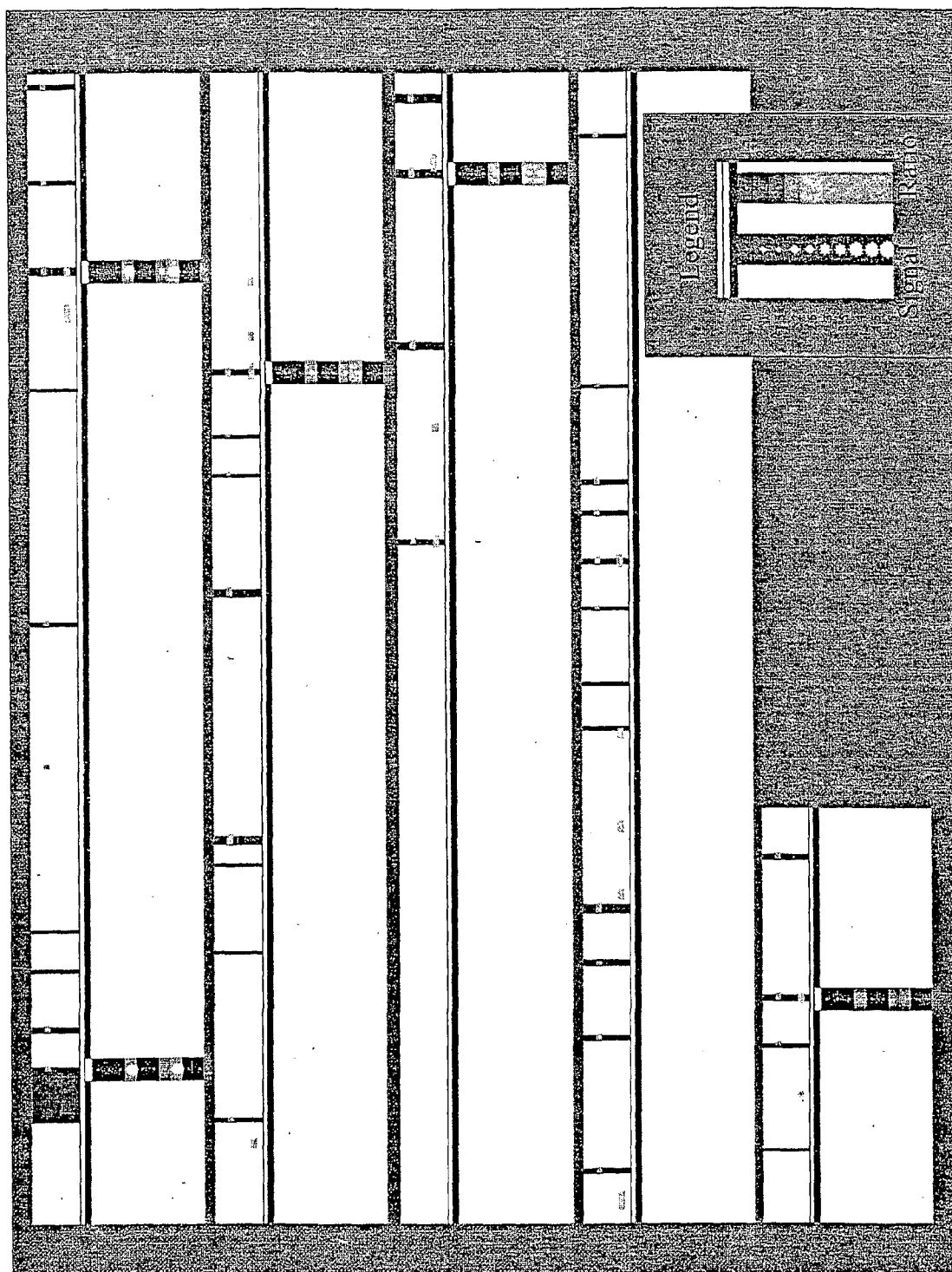


Fig. 9

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Fig. 10

